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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 05:18:47 ; Search time 908.004 Seconds
(without alignments)
17413.610 Million cell updates/sec

Title: US-10-688-676A-1

Perfect score: 2671

Sequence: 1 aagatgggtctctaccgcat.....aaataaaattggcaaaa 2671

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	2671	6	ABK83964 Human CDN
2	2671	100.0	2671	12	Adj74847 Marker ge
3	2671	100.0	2671	12	Adq37893 DNA encod
4	2660	99.6	3103	9	Aad57515 Human enz
5	2644.2	99.0	2844	6	Abi60541 Human lip
6	1306	48.9	2048	10	Abt42155 Toxicity
7	1272	47.6	1992	12	Adj75763 Marker ge
8	1055.6	39.5	2311	13	Ads09997 Human the
9	1030.4	38.6	2302	13	Ads09995 Human the
10	1016.4	38.3	2368	13	Adq39008 Human SNP
11	1016.4	38.1	2867	13	Adq39009 Human SNP
12	1013.6	37.9	2343	13	Aac58018 Arachidon
13	918.6	34.4	2218	13	Ads09996 Human the
14	901.6	33.8	2227	13	Ads11347 Human the
15	901.6	33.8	2227	13	Ads11348 Human the
16	901.6	33.8	2227	13	Adg11349 Human the
17	515.6	19.3	584	12	Adm99845 Human ALO
18	514	19.2	584	12	Adm99844 Human ALO
19	382.6	14.3	2420	3	Aad24665 Human 5-1
20	382.6	14.3	2484	3	Aaa35131 Human ade

21	382.6	14.3	2484	3	AAF21253	Aaf21253 Human low
22	382.6	14.3	2484	10	ADe85077	Adc85077 Farnesyl
23	382.6	14.3	2484	10	ABz96947	Abz96947 Human nuc
24	382.6	14.3	2484	10	ACf63369	Acf63369 Human lip
25	382.6	14.3	2484	11	ABD20796	Abd20796 Human pul
26	382.6	14.3	2497	3	AAA35132	Aaa35132 Human ade
27	382.6	14.3	2497	3	AAF21254	Aaf21254 Human low
28	382.6	14.3	2497	6	ABL65632	Abi65632 Lung canc
29	382.6	14.3	2497	6	ABL67646	Abi67646 Oesophagu
30	382.6	14.3	2497	6	ABL67509	Abi67509 Thyroid c
31	382.6	14.3	2497	6	ABT11115	Abt11115 Human 5-1
32	382.6	14.3	2497	6	ABK83762	Abk83762 Human CDN
33	382.6	14.3	2497	6	AA24664	Aad24664 Human 5-1
34	382.6	14.3	2497	8	ACA89905	Acc89905 Gene diff
35	382.6	14.3	2497	8	ACC57722	Acc57722 Human 5-1
36	382.6	14.3	2497	10	ABZ96948	Abz96948 Human nuc
37	382.6	14.3	2497	11	ADI31829	Adi31829 Human CDN
38	382.6	14.3	2497	11	ABD20797	Abd20797 Human pul
39	382.6	14.3	2497	13	ADP54501	Adp54501 Human PRO
40	382.6	14.3	2500	3	AAA35130	Aaa35130 Human ade
41	382.6	14.3	2500	3	AAF21252	Aaf21252 Human low
42	382.6	14.3	2500	10	ABZ96946	Abz96946 Human nuc
43	382.6	14.3	2500	11	ABD20795	Abd20795 Human pul
44	382.6	14.3	11151	3	AAA35133	Aaa35133 Human ade
45	382.6	14.3	11181	3	AAF21255	Aaf21255 Human low

ALIGNMENTS

RESULT 1

ABK83964

ID ABK83964 standard; cDNA; 2671 BP.

XX AC ABK83964;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #535.

XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX KW viral infection; parasitic infection; protozoal infection;

XX KW fungal infection; sterile inflammatory disease; psoriasis;

XX KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

XX KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

XX KW adult respiratory distress syndrome; inflammatory bowel disease;

XX KW Crohn's disease; ulcerative colitis; periodontal disease;

XX KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX XX (GENE-) GENE LOGIC INC.

XX PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX PI WPI; 2002-435328/46.

XX DR Detecting granulocyte activation by detecting differential expression of

XX PT genes associated with granulocyte activation, which serves as diagnostic

XX PT markers that is useful for monitoring disease states and drug toxicity.

XX PS Claim 1; SEQ ID NO 535; 114pp; English.

XX XX The invention relates to detecting (M1) granulocyte (GC) activation

XX CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

XX CC

DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g., psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2671 BP; 580 A; 743 C; 718 G; 630 T; 0 U; 0 Other;

Query Match 100.0%; Score 2671; DB 6; Length 2671;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAGATGGGTCTTACCGCATCCGGGTGTCCACTGGGGCCCTCGCTCTATGCGGTTCCAAAC	60
Db	1	AAGATGGGTCTTACCGCATCCGGGTGTCCACTGGGGCCCTCGCTCTATGCGGTTCCAAAC	60
Qy	61	AACCAAGTGCAGCTGTGGTGGCCAGCAGCGGGAGCGCGCTCGGGAAGCGACTG	120
Db	61	AACCAAGTGCAGCTGTGGTGGCCAGCAGCGGGAGCGCGCTCGGGAAGCGACTG	120
Qy	121	TGGCCCGCACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCG	180
Db	121	TGGCCCGCACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCG	180
Qy	181	CTGCTGTTTGTGAACCTGCCAAACGCGACCTCTTAAAGACAGCGCTGTGCGAAC	240
Db	181	CTGCTGTTTGTGAACCTGCCAAACGCGACCTCTTAAAGACAGCGCTGTGCGAAC	240
Qy	241	TGGATCTCTGTGACGGCCCGGAGCGGGAGCGAGGTTCAGTTCCCTCTGTTACCGCTGG	300
Db	241	TGGATCTCTGTGACGGCCCGGAGCGGGAGCGAGGTTCAGTTCCCTCTGTTACCGCTGG	300
Qy	301	GTGAGGGCAACGGCGTCTTGAGCTCTGCTGAAAGGACCGGCGCGACTGTGGCGAGGAC	360
Db	301	GTGAGGGCAACGGCGTCTTGAGCTCTGCTGAAAGGACCGGCGCGACTGTGGCGAGGAC	360
Qy	361	CCTCAGGCGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAGAGTTGTATC	420
Db	361	CCTCAGGCGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAGAGTTGTATC	420
Qy	421	CGGTGGGGAACCTGGAAGAGCGGTAAATCTGAATATGCTGGGGCCAAACTATATGAC	480
Db	421	CGGTGGGGAACCTGGAAGAGCGGTAAATCTGAATATGCTGGGGCCAAACTATATGAC	480
Qy	481	CTCCCTGTGGATGAGCGATTTCTGGAAAGACAGAGAGTTGACTTTTGAGGTTTCGCTGGCC	540

Db	481	CTCCCTGTGGATGAGCGATTTCTGGAAAGACAGAGAGTTGACTTTTGAGGTTTCGCTGGCC	540
Qy	541	AAGGGGCTGGCGGCACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGAT	600
Db	541	AAGGGGCTGGCGGCACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGAT	600
Qy	601	CTAGATGACTTCAACCGGATTTTCTGGTGTGTGAGCAAGCTGGCTGAGCGGTGCGG	660
Db	601	CTAGATGACTTCAACCGGATTTTCTGGTGTGTGAGCAAGCTGGCTGAGCGGTGCGG	660
Qy	661	GACTCTGGAAGAGATGCTTATTTGGGTACCAAGTTCTTAAATGGGCGCAACCCCGTG	720
Db	661	GACTCTGGAAGAGATGCTTATTTGGGTACCAAGTTCTTAAATGGGCGCAACCCCGTG	720
Qy	721	GTGCTGAGCGCTGTGCTCACTCTGCTCGCTAGTGTCTCCCTCCAGGCAATGAGGAA	780
Db	721	GTGCTGAGCGCTGTGCTCACTCTGCTCGCTAGTGTCTCCCTCCAGGCAATGAGGAA	780
Qy	781	CTGAGGCGGCACTGGAGAGGAGCTGGAGGAGGACACACTGTTGAAAGCTGACTTCTCC	840
Db	781	CTGAGGCGGCACTGGAGAGGAGCTGGAGGAGGACACACTGTTGAAAGCTGACTTCTCC	840
Qy	841	CTGCTGGATGGATCAAGCCCAACGTCTCTGTAGCCAGCAGCCTGGCTGCCCCCT	900
Db	841	CTGCTGGATGGATCAAGCCCAACGTCTCTGTAGCCAGCAGCCTGGCTGCCCCCT	900
Qy	901	CTAGTCATCTGCTGAAATTTGAGGCTGATGGAACTCTTGGCCCATGTCATCAGCTCCAG	960
Db	901	CTAGTCATCTGCTGAAATTTGAGGCTGATGGAACTCTTGGCCCATGTCATCAGCTCCAG	960
Qy	961	CTGCCCCGACAGGATCCCCACCACTCTCCCTTTTCTGCTACGGATCCCCCAATGGCC	1020
Db	961	CTGCCCCGACAGGATCCCCACCACTCTCCCTTTTCTGCTACGGATCCCCCAATGGCC	1020
Qy	1021	TGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCAGCTCCAGTCCATGAGCTGAGTCT	1080
Db	1021	TGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCAGCTCCAGTCCATGAGCTGAGTCT	1080
Qy	1081	CATCTTCTCAGGGGACACTTGATGGCTGAGGTCAATTTGTGGCCACCACTAGGTCGCTG	1140
Db	1081	CATCTTCTCAGGGGACACTTGATGGCTGAGGTCAATTTGTGGCCACCACTAGGTCGCTG	1140
Qy	1141	CGTGGATACATCTTCAAGCTTAAATTCCTCCCACTCGATACACCTTGGAAT	1200
Db	1141	CGTGGATACATCTTCAAGCTTAAATTCCTCCCACTCGATACACCTTGGAAT	1200
Qy	1201	AAGTCCGGGCGCAGGACTGGGCTGGTCTCTGACATGGGAATTTTCGACAGATAATGAGC	1260
Db	1201	AAGTCCGGGCGCAGGACTGGGCTGGTCTCTGACATGGGAATTTTCGACAGATAATGAGC	1260
Qy	1261	ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCTTCTTAACTACAGC	1320
Db	1261	ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCTTCTTAACTACAGC	1320
Qy	1321	TCTTCTGTCCCCCTGATCACTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCTTTC	1380
Db	1321	TCTTCTGTCCCCCTGATCACTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCTTTC	1380
Qy	1381	TATGCCCAAGATGCGCTGCGGCTCTGGGAATCATCTATCGGTATCTGGAAGGAATCGTG	1440
Db	1381	TATGCCCAAGATGCGCTGCGGCTCTGGGAATCATCTATCGGTATCTGGAAGGAATCGTG	1440
Qy	1441	AGTCTCCACTATAAGACAGACGTGGCTGTGAAGAGAGCCAGAGCTGACAGCTGGTGT	1500
Db	1441	AGTCTCCACTATAAGACAGACGTGGCTGTGAAGAGAGCCAGAGCTGACAGCTGGTGT	1500
Qy	1501	CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTTTTA	1560
Db	1501	CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTTTTA	1560
Qy	1561	CAGGCTCGGACAGGTTTGGCACTTTGTACCATGTGTATCTTACCTGACCGGCCAA	1620
Db	1561	CAGGCTCGGACAGGTTTGGCACTTTGTACCATGTGTATCTTACCTGACCGGCCAA	1620

Db 1561 CAGGCTCGGACCAAGTTGGCCACTTTGTCCACATGTGTATCTTACCTGCGACCGGCCAA 1620
Qy 1621 CACGCTCTGTGCACTCGGCGCAGCTGGTACTCTTGGGTGCTTAATGCAACCCCTGC 1680
Db 1621 CACGCTCTGTGCACTCGGCGCAGCTGGTACTCTTGGGTGCTTAATGCAACCCCTGC 1680
Qy 1681 ACGATGGGCTGGCGCCGCAACCCAGGATGCAAGCTGGAGACAGTGTATGGGACA 1740
Db 1681 ACGATGGGCTGGCGCCGCAACCCAGGATGCAAGCTGGAGACAGTGTATGGGACA 1740
Qy 1741 CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCTGGCAGCTGGGCGAGAGC 1800
Db 1741 CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCTGGCAGCTGGGCGAGAGC 1800
Qy 1801 CAGCCCGTTAAGTGGCTGTGGCCAGCATGAGGAGAGTATTTTTCGGGCGCTCAGGCT 1860
Db 1801 CAGCCCGTTAAGTGGCTGTGGCCAGCATGAGGAGAGTATTTTTCGGGCGCTCAGGCT 1860
Qy 1861 AAGGCTGTGCTGAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAATTCAGATC 1920
Db 1861 AAGGCTGTGCTGAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAATTCAGATC 1920
Qy 1921 CGGAATGCAAGCTCGACATGCCCTACGAGTACTTCCGCGCCAGCGTGTGGAACAAGT 1980
Db 1921 CGGAATGCAAGCTCGACATGCCCTACGAGTACTTCCGCGCCAGCGTGTGGAACAAGT 1980
Qy 1981 GTGGCCATCTAAGCGTGCACCCCTTTTGTATTTTTCAGCCCCCATCACCAAGCCACAAG 2040
Db 1981 GTGGCCATCTAAGCGTGCACCCCTTTTGTATTTTTCAGCCCCCATCACCAAGCCACAAG 2040
Qy 2041 CTGACCCCTTCTGGTTATAGCCCTGCGCTCCCAAGTCCCAAGCTTCCGATGTCCAC 2100
Db 2041 CTGACCCCTTCTGGTTATAGCCCTGCGCTCCCAAGTCCCAAGCTTCCGATGTCCAC 2100
Qy 2101 CTTCCCTAGAGGGGACCTTTTCATGCTCTCGACCCAGTCAACACATTTTACTCTAGA 2160
Db 2101 CTTCCCTAGAGGGGACCTTTTCATGCTCTCGACCCAGTCAACACATTTTACTCTAGA 2160
Qy 2161 GGCATCACCTGGGACCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Db 2161 GGCATCACCTGGGACCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Qy 2221 TCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
Db 2221 TCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
Qy 2281 TTTCAAGACTAGATAGGGGATATAATACATTTACTCCACACCTTTTATGAATCAAT 2340
Db 2281 TTTCAAGACTAGATAGGGGATATAATACATTTACTCCACACCTTTTATGAATCAAT 2340
Qy 2341 ATGATTTTTTTTGTGTTAAGACAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2400
Db 2341 ATGATTTTTTTTGTGTTAAGACAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2400
Qy 2401 GTGCGCATCACCGGCTCAGTGCAGCTTCAAGCTTCTGGGCTCAAAATGATCTCCAC 2460
Db 2401 GTGCGCATCACCGGCTCAGTGCAGCTTCAAGCTTCTGGGCTCAAAATGATCTCCAC 2460
Qy 2461 TCAGCTCTCTGAGTGGGACTACGCTCATGCCATCATGCCATCATGCCATCATGCCATCAT 2520
Db 2461 TCAGCTCTCTGAGTGGGACTACGCTCATGCCATCATGCCATCATGCCATCATGCCATCAT 2520
Qy 2521 TATTTTTCGTTGAGACGGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2580
Db 2521 TATTTTTCGTTGAGACGGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2580
Qy 2581 AAATTGAGTTTAAATAAATAAAGTTGTTTACGCTAAAGATGAAAGAACTAGGAC 2640
Db 2581 AAATTGAGTTTAAATAAATAAAGTTGTTTACGCTAAAGATGAAAGAACTAGGAC 2640
Qy 2641 TGAATCTATTTTAAATAAATAAATATGGCAAG 2671
Db 2641 TGAATCTATTTTAAATAAATAAATATGGCAAG 2671

RESULT 2

ADJ74847

ID ADJ74847 standard; DNA; 2671 BP.

XX ADJ74847;

XX 20-MAY-2004 (first entry)

XX Marker gene SEQ ID NO:99.

XX bronchial asthma; chronic obstructive pulmonary disease;

XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

XX gene therapy; marker gene; gene; ds.

XX Homo sapiens.

XX EP1394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Claim 1; SEQ ID NO 99; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antiseize nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

SQ Sequence 2671 BP; 580 A; 743 C; 718 G; 630 T; 0 U; 0 Other;

Query Match

100.0%; Score 2671; DB 12; Length 2671;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AAGATGGGTCTCTACCGCATCCGGTGTCCACTCGGGGCTCGCTCTATGCGGGTTCCAAC	60
DB	1	AAGATGGGTCTCTACCGCATCCGGTGTCCACTCGGGGCTCGCTCTATGCGGGTTCCAAC	60
QY	61	AACACGGTGACGTGTGGCTGTGCGCCAGCAGCAGGGAGCGGGCTCGGGAAGCGACTG	120
DB	61	AACACGGTGACGTGTGGCTGTGCGCCAGCAGCAGGGAGCGGGGCGCTCGGGAAGCGACTG	120
QY	121	TGSCCGCACGGGGCAAGGACAGNACTCAAGGTGGAGTACCGGAGTATCTGGGGCGG	180
DB	121	TGSCCGCGCACGGGGCAAGGACAGNACTCAAGGTGGAGTACCGGAGTATCTGGGGCGG	180
QY	181	CTGCTGTTTGTGAAACTGGCRAAACGGCACCTCTTAAAGGACGACGCTGGTCTTGCAAC	240
DB	181	CTGCTGTTTGTGAAACTGGCRAAACGGCACCTCTTAAAGGACGACGCTGGTCTTGCAAC	240
QY	241	TGGATCTCTGTGACGGGCCCCGGAGCCGGGACGAGGTCAAGTTCCTTTATACCGTGG	300
DB	241	TGGATCTCTGTGACGGGCCCCGGAGCCGGGACGAGGTCAAGTTCCTTTATACCGTGG	300
QY	301	GTGAGGGCAACCGGCTCTGAGCCTGCTGAAGSCACGGGCCGACGTGTGGGCGAGGAC	360
DB	301	GTGAGGGCAACCGGCTCTGAGCCTGCTGAAGSCACGGGCCGACGTGTGGGCGAGGAC	360
QY	361	CCTCAGGGCTGTTTCAGAAACACCGGGAAGAGAGCTGGAAAGAGAGAAAGTGTATC	420
DB	361	CCTCAGGGCTGTTTCAGAAACACCGGGAAGAGAGCTGGAAAGAGAGAAAGTGTATC	420
QY	421	CGGTGGGGAACTGGAAGGACGGGTTAACTCTGAATATGGCTGGGGCCAAACTATATGAC	480
DB	421	CGGTGGGGAACTGGAAGGACGGGTTAACTCTGAATATGGCTGGGGCCAAACTATATGAC	480
QY	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGTGGCC	540
DB	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGTGGCC	540
QY	541	AAGGGCTGGCCACCTCGCTATCAAGACTCTCTAAATGTTCTGACATTCGTGGAAGAT	600
DB	541	AAGGGCTGGCCACCTCGCTATCAAGACTCTCTAAATGTTCTGACATTCGTGGAAGAT	600
QY	601	CTAGATGACTTCAACCGGATTTTCTGSGTGGTTCAGAGCAAGCTGGCTGAGCGGTGGG	660
DB	601	CTAGATGACTTCAACCGGATTTTCTGSGTGGTTCAGAGCAAGCTGGCTGAGCGGTGGG	660
QY	661	GACTCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGGGCGCAACCCCGTG	720
DB	661	GACTCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGGGCGCAACCCCGTG	720
QY	721	GTGCTGAGGCGCTCTGCTACCTTCCTGCTCGCCTAGTGTTCCTCCAGGCGATGAGGAA	780
DB	721	GTGCTGAGGCGCTCTGCTACCTTCCTGCTCGCCTAGTGTTCCTCCAGGCGATGAGGAA	780
QY	781	CTGACGCCCCAGCTGGAGAGGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTCTCC	840
DB	781	CTGACGCCCCAGCTGGAGAGGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTCTCC	840
QY	841	CTGCTGTGATGGGATCAAGGCCAAGCTCATCTCTGTAGCCAGCAGCACTGTGGCTGCCCT	900
DB	841	CTGCTGTGATGGGATCAAGGCCAAGCTCATCTCTGTAGCCAGCAGCAGCTGTGGCTGCCCT	900
QY	901	CTAGTCATGCTGAAATTTGACGCTGATGGGAACCTCTGCCCATGGTTCATCCAGCTCCAG	960
DB	901	CTAGTCATGCTGAAATTTGACGCTGATGGGAACCTCTTGSCCATGGTTCATCCAGCTCCAG	960
QY	961	CTGCCCCGACAGGATCCCCACACCTCCCTTTCTTGCCCTACGGATCCCCCAATGGCC	1020
DB	961	CTGCCCCGACAGGATCCCCACACCTCCCTTTCTTGCCCTACGGATCCCCCAATGGCC	1020
QY	1021	TGGCTTCTGCGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCATGAGCTGCAGFTCT	1080

Db	732		GTCTGAGGCGTCTGCTCACCTTCTCTGCTCGCCTAGTGTTCCTCCAGGCATGGAGAA	791
Qy	781		CTGCAGGCCACGTGAGAAAGAGCTGGAGGGAGGCACACTGTTCCGAGCTCAGTCTCTCC	840
Db	792		CTGCAGGCCCAGCTGAGAAAGAGCTGGAGGGAGGCACACTGTTCCGAGCTCAGTCTCTCC	851
Qy	841		CTGCTGATGGGATCAAGGCCAACGCTCATTTCTGTAGCCAGCAGCACCTGGCTGCGCCT	900
Db	852		CTGCTGATGGGATCAAGGCCAACGCTCATTTCTGTAGCCAGCAGCACCTGGCTGCGCCT	911
Qy	901		CTAGTCAATGCTGAAATTTGCACGCTGATGGGAAACTCTTGCCCATGCTCATTCAGCTCCAG	960
Db	912		CTAGTCAATGCTGAAATTTGCACGCTGATGGGAAACTCTTGCCCATGCTCATTCAGCTCCAG	971
Qy	961		CTGCCCCGACAGGATCCCAACACCTCCCTTTTCTTGCTACGATCCCCCAATGGCC	1020
Db	972		CTGCCCCGACAGGATCCCAACACCTCCCTTTTCTTGCTACGATCCCCCAATGGCC	1031
Qy	1021		TGGCTTCTGCGAAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCATGAGTGCAGTCT	1080
Db	1032		TGGCTTCTGCGCAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCATGAGTGCAGTCT	1091
Qy	1081		CATCTTCTGAGGGACACTTGTATGGCTGAGGTCAATTTGTTGTGGCCACCATGAGTGCCTG	1140
Db	1092		CATCTTCTGAGGGACACTTGTATGGCTGAGGTCAATTTGTTGTGGCCACCATGAGTGCCTG	1151
Qy	1141		CCGTGCAATACATCTATCTTCAAGCTTATAATTTCCCACTCGGATACACCTTGGAAAT	1200
Db	1152		CCGTGCAATACATCTATCTTCAAGCTTATAATTTCCCACTCGGATACACCTTGGAAAT	1211
Qy	1201		AACGTCCGGGCGAGGACTGGGCTGCTCTGACATGGGAATTTTCGACAGATAATGAGC	1260
Db	1212		AACGTCCGGGCGAGGACTGGGCTGCTCTGACATGGGAATTTTCGACAGATAATGAGC	1271
Qy	1261		ACTGTTGGGGAGGCCAGTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGC	1320
Db	1272		ACTGTTGGGGAGGCCAGTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGC	1331
Qy	1321		TCCCTTCTGTCCTCCCTGATGACTTGGCCGACGGGGGCTCTGGAGTGAGTCTTCTCTTC	1380
Db	1332		TCCCTTCTGTCCTCCCTGATGACTTGGCCGACGGGGGCTCTGGAGTGAGTCTTCTCTTC	1391
Qy	1381		TATGCCAAGATCGCTCGGCTCTGGGAAATCATCTATCGGTATGGGAAGAAATCGTG	1440
Db	1392		TATGCCAAGATCGCTCGGCTCTGGGAAATCATCTATCGGTATGGGAAGAAATCGTG	1451
Qy	1441		AGTCTCCATATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACTGGTGT	1500
Db	1452		AGTCTCCATATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACTGGTGT	1511
Qy	1501		CGAGATCACTGAAATCGGGCTGCAGGGGCCAGGACCGAGGGTTCTGTGCTCTTTA	1560
Db	1512		CGAGATCACTGAAATCGGGCTGCAGGGGCCAGGACCGAGGGTTCTGTGCTCTTTA	1571
Qy	1561		CAGGCTGGGACAGGTTTGCCACTTTGTACCATGTGATCTTCACTGCACGCGCAA	1620
Db	1572		CAGGCTGGGACAGGTTTGCCACTTTGTACCATGTGATCTTCACTGCACGCGCAA	1631
Qy	1621		CACGCTCTGTGCACCTGGGGCAGCTGSACTGGTACTCTTGGGTGCTTAATGCACTCTGC	1680
Db	1632		CACGCTCTGTGCACCTGGGGCAGCTGSACTGGTACTCTTGGGTGCTTAATGCACTCTGC	1691
Qy	1681		ACGATGGGCTGCCCCGCCAACACAGGATGCAACGCTGGAGACAGTGTATGGCGACA	1740
Db	1692		ACGATGGGCTGCCCCGCCAACACAGGATGCAACGCTGGAGACAGTGTATGGCGACA	1751
Qy	1741		CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGACAGCG	1800
Db	1752		CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGACAGCG	1811
Qy	1801		CAGCCCGTTATGGTGGCTGTGGGCGCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCCT	1860

[illegible]

1380 CTATGCCCAAGATGCGCTCGGGCTCTGGGAATCATCTATCGTATGTGGAAGGAATCGT 1439
1812 CTATGCCCAAGATGCGCTCGGGCTCTGGGAATCATCTATCGTATGTGGAAGGAATCGT 1871
1440 GAGTCTCCACTATAAGACAGAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTG 1499
1872 GAGTCTCCACTATAAGACAGAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTG 1931
1500 TCAGAGATCACTGAATCGGGCTGCAAGGGGCCAGAGCCGAGGGTTCCTGTCTCTTT 1559
1932 TCAGAGATCACTGAATCGGGCTGCAAGGGGCCAGAGCCGAGGGTTCCTGTCTCTTT 1991
1560 ACAGGCTCGGGACACGGTTTGCACCTTTGTACCATGTGTATCTTCACTCTGCACCGGCCA 1619
1992 ACAGGCTCGGGACACGGTTTGCACCTTTGTACCATGTGTATCTTCACTCTGCACCGGCCA 2051
1620 ACACGGCTCTGTGCACCTCGGGCAGCTGGACTGGTACTCTTGGTGCCCTAAATGCAACCTTG 1679
2052 ACACGGCTCTGTGCACCTCGGGCAGCTGGACTGGTACTCTTGGTGCCCTAAATGCAACCTTG 2111
1680 CACGATGCGGCTGCCCCCGCCACCAACCAAGGATGCAACGCTGGAGACAGTATGGCGAC 1739
2112 CACGATGCGGCTGCCCCCGCCACCAACCAAGGATGCAACGCTGGAGACAGTATGGCGAC 2171
1740 ACTGCCCAACTCTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAGACG 1799
2172 ACTGCCCAACTCTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAGACG 2231
1800 CCAGCCCGTTATGTTGGCTGTGGCCAGACATGAGGAGGATATTTTCGGGCCCTGAGCC 1859
2232 CCAGCCCGTTATGTTGGCTGTGGCCAGACATGAGGAGGATATTTTCGGGCCCTGAGCC 2291
1860 TAAGGCTGTGCTGAAGAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATTAAGGAATTCAGAT 1919
2292 TAAGGCTGTGCTGAAGAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATTAAGGAATTCAGAT 2351
1920 CCGGAATGCAAAAGCTGCACATGCCCTACGATGACCTGCGGCCAGCGTGTGGAAACAG 1979
2352 CCGGAATGCAAAAGCTGCACATGCCCTACGATGACCTGCGGCCAGCGTGTGGAAACAG 2411
1980 TGTGGCCATCAAGCGTGCACACCTTTTGGTTATTTTCAAGCCCCCATCAACCAAGCCACAA 2039
2412 TGTGGCCATCAAGCGTGCACACCTTTTGGTTATTTTCAAGCCCCCATCAACCAAGCCACAA 2471
2040 GCTGACCCCTTCTGTGTATAGCCCTGCCCTCCCAAGTCCACCCCTTCCCATGTCCCA 2099
2472 GCTGACCCCTTCTGTGTATAGCCCTGCCCTCCCAAGTCCACCCCTTCCCATGTCCCA 2531
2100 CCCTCCCTAGAGGGCACCCTTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAG 2159
2532 CCCTCCCTAGAGGGCACCCTTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAG 2591
2160 AGGCATCACCTGGGACCTTACTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2219
2592 AGGCATCACCTGGGACCTTACTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2651
2220 CTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2279
2652 CTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2711
2280 ATTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAA 2339
2712 ATTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAA 2771
2340 TATGATTTTTTTTGTGTGTTAAGACAGAGTCTCACTTTTGACACCCAGCGCTGGAGTGCAG 2399
2772 TATGATTTTTTTTGTGTGTTAAGACAGAGTCTCACTTTTGACACCCAGCGCTGGAGTGCAG 2831
2400 TGGTGCCATCACACGCTCACTGACGCTCAGGCTCCTGGCTCAATGATCTCTCCAC 2459
2832 TGGTGCCATCACACGCTCACTGACGCTCAGGCTCCTGGCTCAATGATCTCTCCAC 2891

RESULT 5
ABL60541

ID ABL60541 standard; cDNA; 2844 BP.

XX ABL60541;

XX 27-AUG-2002 (first entry)

XX Human lipid metabolism enzyme (LME)-5 cDNA (clone Id: 7484270CB1).

XX Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective; gene;
XX nontropic; cerebrotective; antiparkinsonian; antialzheimer's; vaccine;
XX antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;
XX gene therapy; protein therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 107..2161

XX /tag= a

XX /product= "lipid metabolism enzyme"

XX /note= "LME-5"

XX WO200229036-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031302.

XX 06-OCT-2000; 2000US-0238388P.

XX 13-OCT-2000; 2000US-0240616P.

XX 02-NOV-2000; 2000US-0245719P.

XX 08-NOV-2000; 2000US-0247503P.

XX 17-NOV-2000; 2000US-0249503P.

XX (INCY-) INCYTE GENOMICS INC.

XX PA Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;

XX PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;

XX Lall PG, Tribouley CM;

XX WPI; 2002-315862/35.

XX DR P-PSDB; ABB08005.

XX Lipid Metabolism Enzymes and nucleic acids, useful for preventing,

XX diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-

XX Jakob disease.

XX Claim 5; Page 124-125; 127pp; English.

XX The invention relates to human lipid metabolism enzymes (LMEs) and

XX encoding polynucleotides. The LMEs can be expressed by standard

XX recombinant technology. The LME polypeptides, polynucleotides and

XX modulators may be used in the prevention, diagnosis and treatment of

XX diseases associated with inappropriate LME expression such as cancer

XX (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.

CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome
CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
CC pectoris and mitral valve prolapse). The present sequence represents the
CC human LME-5 encoding cDNA
XX
SQ

Sequence 2844 BP; 620 A; 777 C; 781 G; 666 T; 0 U; 0 Other;

Query Match 99.0%; Score 2644.2; DB 6; Length 2844;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2652; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 AAGATGGGTCTTACCGCATCCGCGTGCACCTGGGGCCCTCGCTCTATCGCGTTCACAC 60
DB 170 AAGATGGGTCTTACCGCATCCGCGTGCACCTGGGGCCCTCGCTCTATCGCGTTCACAC 229
QY 61 AACACAGGTGCAGTGTGGTGTGGCGCAGCAGCGGGAGCGCGCTCCGGGAAGCGACTG 120
DB 230 AACACAGGTGCAGTGTGGTGTGGCGCAGCAGCGGGAGCGCGCTCCGGGAAGCGACTG 289
QY 121 TGGCCCGCAGCGGGCAGGAGACAGAACTCAAGGTGGAAAGTACCGGAGTATCTGGGGCCG 180
DB 290 TGGCCCGCAGCGGGCAGGAGACAGAACTCAAGGTGGAAAGTACCGGAGTATCTGGGGCCG 349
QY 181 CTGCTGTTGTGAACCTGCGCAACCGGCACCTCCTTAAGGACGACGCTGTTCTGCAAC 240
DB 350 CTGCTGTTGTGAACCTGCGCAACCGGCACCTCCTTAAGGACGACGCTGTTCTGCAAC 409
QY 241 TGGATCTCTGTGACGGGCCCCGAGCGCGGGACGAGGTCAAGTTCCTTTGTACCGCTGG 300
DB 410 TGGATCTCTGTGACGGGCCCCGAGCGCGGGACGAGGTCAAGTTCCTTTGTACCGCTGG 469
QY 301 GTGGAGGGCAACGGCGTCTGAGCTCTGCTGAAGCACCAGCGCGCACTGTGGCGAGGAC 360
DB 470 GTGGAGGGCAACGGCGTCTGAGCTCTGCTGAAGCACCAGCGCGCACTGTGGCGAGGAC 529
QY 361 CCTCAGGCGCTCTCCAGAAACACCGGAGAGAGCTGGAAGAGAGAGGAGTGTAC 420
DB 530 CCTCAGGCGCTCTCCAGAAACACCGGAGAGAGCTGGAAGAGAGAGGAGTGTAC 589
QY 421 CCGTGGGGAACCTGGAAGACGGGTAAATCTGAAATATGGCTGGGGCCAAACTATATGAC 480
DB 590 CCGTGGGGAACCTGGAAGACGGGTAAATCTGAAATATGGCTGGGGCCAAACTATATGAC 649
QY 481 CTCCTCTGTGATGAGCGATTTCTGAAGACAAGAGAGTTGACTTTGAGGTTTCGTGGCC 540
DB 650 CTCCTCTGTGATGAGCGATTTCTGAAGACAAGAGAGTTGACTTTGAGGTTTCGTGGCC 709
QY 541 AAGGGGCTGGCGACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTGGAGGAT 600
DB 710 AAGGGGCTGGCGACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTGGAGGAT 769
QY 601 CTAGATGACTTCAACCGGATTTCTGGTGTGTGCTCAGAGCAAGCTGGCTGAGCGCTGGG 660
DB 770 CTAGATGACTTCAACCGGATTTCTGGTGTGTGCTCAGAGCAAGCTGGCTGAGCGCTGGG 829
QY 661 GACTCTCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGGCGCCAAACCCGCTG 720
DB 830 GACTCTCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGGCGCCAAACCCGCTG 889
QY 721 GTGCTGAGCGCTCTGCTCACTTCCTGCTCCCTAGTGTTCCTCCAGGCAATGAGGAA 780
DB 890 GTGCTGAGCGCTCTGCTCACTTCCTGCTCCCTAGTGTTCCTCCAGGCAATGAGGAA 949
QY 781 CTGACGGCCACCTGGAGAAGAGCTGGAGGAGGACACACTGTTGAACTGACTTCTCC 840
DB 950 CTGACGGCCACCTGGAGAAGAGCTGGAGGAGGACACACTGTTGAACTGACTTCTCC 1009
QY 841 CTGCTGGATGGGATCAAGGCCAACGTCATTCTCTGTAGCAGCAGCACCTGGCTGCCCT 900
DB 1010 CTGCTGGATGGGATCAAGGCCAACGTCATTCTCTGTAGCAGCAGCACCTGGCTGCCCT 1069
QY 901 CTAGTCATGCTGAAATTTGACGCTGATGGGAAACTCTTTGCCCATGCTCATCCAGCTCCAG 960

DB 1070 CTAGTCATGCTGAAATTTGACGCTGATGGAAACTCTTGGCCCATGCTCATCCAGCTCCAG 1129
QY 961 CTGCCCCGCACACAGGATCCCCACACCTCCCTCTTTTCTTGGCTTACGAGTCCCCCAATGGCC 1020
DB 1130 CTGCCCCGCACACAGGATCCCCACACCTCCCTCTTTTCTTGGCTTACGAGTCCCCCAATGGCC 1189
QY 1021 TGGCTTCTGGCCAAATGCTGGGTGGGAGCTCTGACTTCCAGCTCATGAGCTGCACTCT 1080
DB 1190 TGGCTTCTGGCCAAATGCTGGGTGGGAGCTCTGACTTCCAGCTCATGAGCTGCACTCT 1249
QY 1081 CATCTTCTGAGGGGACACTTGTATGCTGAGGTCAATTTGTGGCCACCATGAGGTGCTCTG 1140
DB 1250 CATCTTCTGAGGGGACACTTGTATGCTGAGGTCAATTTGTGGCCACCATGAGGTGCTCTG 1309
QY 1141 CCGTCGATACATCTCTTCAAGCTTATAATTTCCCCACCTCGCATACACCTTGGAAATTT 1200
DB 1310 CCGTCGATACATCTCTTCAAGCTTATAATTTCCCCACCTCGCATACACCTTGGAAATTT 1369
QY 1201 AACGTCGGGGCAGAGACTGGGCTGCTCTGATCATGGGNAATTTTCGACAGATAATGAGC 1260
DB 1370 AACGTCGGGGCAGAGACTGGGCTGCTCTGATCATGGGNAATTTTCGACAGATAATGAGC 1429
QY 1261 ACTGTCGGGGGAGGCCACGTCAGCTGCTCAAGCAAGCTTGGAGCTTCTTCAACCTACAGC 1320
DB 1430 ACTGTCGGGGGAGGCCACGTCAGCTGCTCAAGCAAGCTTGGAGCTTCTTCAACCTACAGC 1489
QY 1321 TCCTTCTCTGCCCTTGATGACTTGGCCGACCGGGGGCTCTCGGAGTGAAGTCTTCTCTTC 1380
DB 1490 TCCTTCTCTGCCCTTGATGACTTGGCCGACCGGGGGCTCTCGGAGTGAAGTCTTCTCTTC 1549
QY 1381 TATGCCAAAGATGCGCTCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGAAATCGTG 1440
DB 1550 TATGCCAAAGATGCGCTCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGAAATCGTG 1609
QY 1441 AGTCTCCACTATAAGACAGAGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGT 1500
DB 1610 AGTCTCCACTATAAGACAGAGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGT 1669
QY 1501 CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAGGAGCCGAGGGTTCTCTCTCTTTA 1560
DB 1670 CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAGGAGCCGAGGGTTCTCTCTCTTTA 1729
QY 1561 CAGGCTCGGGACAGGTTTGCACTTTGTGTCACATGTGTATCTTCACTGCAACCGGCCAA 1620
DB 1730 CAGGCTCGGGTCCAGGTTTGCCACTTTGTTCACATGTGTATCTTCACTGCAACCGGCCAA 1789
QY 1621 CAGGCTCTGTGCACTCGGGCCAGCTGGACTGTGTTACTCTTGGGTGCTTAATGCACCTGC 1680
DB 1790 CAGGCTCTGTGCACTCGGGCCAGCTGGACTGTGTTACTCTTGGGTGCTTAATGCACCTGC 1849
QY 1681 ACGATGCGGCTGCCCGCCCAACCAAGGATGCAACGCTGGAGACAGTGTGCGACA 1740
DB 1850 ACGATGCGGCTGCCCGCCCAACCAAGGATGCAACGCTGGAGACAGTGTGCGACA 1909
QY 1741 CTGCCCCAATCTTCCACACAGGCTTCTCTCAGATGTCCATCACTTGGCAGCTGGGCGAGACG 1800
DB 1910 CTGCCCCAATCTTCCACACAGGCTTCTCTCAGATGTCCATCACTTGGCAGCTGGGCGAGACG 1969
QY 1801 CAGCCCGTTATGGTGGCTGTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTCAGCCT 1860
DB 1970 CAGCCCGTTATGGTGGCTGTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTCAGCCT 2029
QY 1861 AAGGCTGTGCTGAAGAAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTTGAGATC 1920
DB 2030 AAGGCTGTGCTGAAGAAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTTGAGATC 2089
QY 1921 CGGAATGCAAGCTGGACATGCCCCCTACAGTACTCTGCGGCCAGCGTGGTGGAAACAGT 1980
DB 2090 CGGAATGCAAGCTGGACATGCCCCCTACAGTACTCTGCGGCCAGCGTGGTGGAAACAGT 2149
QY 1981 GTGGCCATCTAAGCGTCGCGACCTTTGTTATTTTTCAGCCCCCATCCAGAGCCACAG 2040

Db	2150	GTGGCCATCTAAGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCACCAAGCCACAAG 2209	PR	10-JUL-2001; 2001US-0303810P.
Qy	2041	CTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCCAACCCCTTCCCAATGCCAC 2100	PR	28-AUG-2001; 2001US-0315047P.
Db	2210	CTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCCAACCCCTTCCCAATGCCAC 2269	PR	27-SEP-2001; 2001US-0324928P.
Qy	2101	CTCCCTCTAGAGGGGACCTTTTCATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGA 2160	PR	22-OCT-2001; 2001US-0330462P.
Db	2270	CTCCCTCTAGAGGGGACCTTTTCATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGA 2329	PR	01-NOV-2001; 2001US-0330867P.
Qy	2161	GGCATCACCTGGGACCTTACT 2220	PR	21-NOV-2001; 2001US-0331805P.
Db	2330	GGCATCACCTGGGACCTTACT 2389	PR	06-DEC-2001; 2001US-0336144P.
Qy	2221	TCT 2280	PR	19-DEC-2001; 2001US-0340873P.
Db	2390	TCT 2449	PR	21-FEB-2002; 2002US-0357842P.
Qy	2281	TTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAT 2340	PR	21-FEB-2002; 2002US-0357843P.
Db	2450	TTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAT 2509	PR	21-FEB-2002; 2002US-0357844P.
Qy	2341	ATGATTTTTTTTGT 2400	PR	15-MAR-2002; 2002US-0364134P.
Db	2510	ATGATTTTTTTTGT 2569	PR	08-APR-2002; 2002US-0370144P.
Qy	2401	GGTGCATCACACGGCTCACTGCAGCCTCAGCGTCTGGGCTCAATGATCTCCACCC 2460	PR	08-APR-2002; 2002US-0370206P.
Db	2570	GGTGCATCACACGGCTCACTGCAGCCTCAGCGTCTGGGCTCAATGATCTCCACCC 2629	PR	17-APR-2002; 2002US-0372794P.
Qy	2461	TCAGCTCTCTGAGTGTGGGACTAGCAGGCTCATGCGTCTATGCCAGCTCAATATTTTTT 2520	PR	21-APR-2002; 2002US-0371679P.
Db	2630	TCAGCTCTCTGAGTGTGGGACTAGCAGGCTCATGCGTCTATGCCAGCTCAATATTTTTT 2689	XX	(GENE-) GENE LOGIC INC.
Qy	2521	TATTTTCGTGGAGACGGGGCTCACTATGTGTGCTAGGCTGGAAATAGGATTTTGAACCC 2580	PA	Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Blashoff M;
Db	2690	TATTTTCGTGGAGACGGGGCTCACTATGTGTGCTAGGCTGGAAATAGGATTTTGAACCC 2749	PI	WPI; 2003-148464/14.
Qy	2581	AAATTGAGTTTACAAATATAAAAGTTGTTTACGTTAAGATGGAAGAACTAGGAC 2640	DR	Predicting at least one toxic effect of a compound, useful for toxicity
Db	2750	AACTTGAGTTTACAAATATAAAAGTTGTTTACGTTAAGATGGAAGAACTAGGAC 2809	XX	modeling, comprises preparing a gene expression profile of a tissue or
Qy	2641	TGAATCTTTTAAATAAAATATTGG 2665	PT	cell sample exposed to the compound, and comparing the gene expression
Db	2810	TGAGCTATTCTTAATGAAGAGTCG 2834	PT	profile to a database.
DE	RESULT 6		XX	Example 4; Page: 446pp; English.
XX	ABT42155		XX	The invention relates to a novel method of predicting at least one toxic
AC	ABT42155 standard; DNA; 2048 BP.		CC	effect of a compound. The method comprises a gene expression profile of a
XX	ABT42155;		CC	tissue or cell sample exposed to the compound, and comparing the gene
XX	26-JUN-2003 (first entry)		CC	expression profile to a database comprising at least part of the data or
DE	Toxicity modelling related rat gene SEQ ID No 1857.		CC	information given in the specification. The methods are useful for
XX	Toxic effect; gene expression profile; renal toxicity; toxicity marker;		CC	predicting at least one toxic effect of a compound, predicting the renal
KW	database; drug screening; toxicity assay; rat; ds.		CC	progression of a toxic effect of a compound, predicting the renal
XX	Rattus norvegicus.		CC	toxicity of a compound, or identifying toxicity markers in tissues or
XX	W020295000-A2.		CC	cells exposed to known renal toxin. The genes are useful as toxicity
XX	28-NOV-2002.		CC	markers in drug screening and toxicity assays, in monitoring disease or
XX	22-MAY-2002; 2002WO-US016173.		CC	physiological states, or disease progression. This polynucleotide
PR	22-MAY-2001; 2001US-0292335P.		CC	represents a rat DNA sequence relating to the toxic effect database
PR	13-JUN-2001; 2001US-0297523P.		CC	described in the specification. NOTE: The sequence data for this patent
PR	19-JUN-2001; 2001US-0298925P.		CC	did not form part of the printed specification, but was obtained in
PR	10-JUL-2001; 2001US-0303807P.		CC	electronic format directly from the World Intellectual Property
PR	10-JUL-2001; 2001US-0303808P.		CC	Organization

Qy	1	AAGATGGGTCTCTACCGCATCCGCGTGTCCACTCGGGGCGCTCGCTCTATGCGGTTCACAC 60	Query Match	48.9%;	Score 1306;	DB 10;	Length 2048;
Db	17	AGATGGGTGTCTACCGCATCCGCGTGTCCACCGGAGACTCCCAAGTACGGGGCTCCAC 76	Best Local Similarity	78.3%;	Pred. No. 0;		
Qy	61	AACAGGTGCGAGTGTGGTGTGGCGCAGCAGCGGAGCGCGCTCGGGAAGCGACTG 120	Matches 1580;	Conservative	0;	Mismatches 435;	Indels 3; Gaps 1;
Db	77	AACGAGGTCTACCTGTGTGGTTGGACAGCATGGAGAGGCATCTCTCGGGAAGCTGCTA 136					
Qy	121	TGCGCCGCGACGGGCAAGGAGCAGAACTCAAGTGGAAAGTACCGAGTATCTGGGGCCG 180					
Db	137	CGACCCCTGTGGGACTCGGAAGCAGAAATTCAAAGTGAATGTGTCAAGATACCTTGGGCCA 196					
Qy	181	CTGCTGTTTGTGAAGTTCGCGCAACCGCACCTCTTAAAGGACGACGCTGCTTCTGCAAC 240					
Db	197	CTGCTGTTGTAAGAGTGCAGAAATGGCATTTATCTACCGATGACGCGCTGTTCTGCAAC 256					
Qy	241	TGGATCTCTGTGAGGCGGCGCGGAGCC---GGGAGCAGAGTTCAGTTCCTTCTTACCGC 297					
Db	257	TGGATTTCTGTGAAGGGCGCGGAGACCAAGGATCAGATGATGTTTCCCTCTGTACCGA 316					

XX	WPI; 2004-193155/19.
DR	Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX	comparing the expression level of a marker gene in a biological sample
PT	from a subject with the expression level of the gene in a sample from a
PT	healthy subject.
PT	
XX	Claim 14; SEQ ID NO 1015; 241pp; English.
PS	The present invention describes a method of testing for bronchial asthma
XX	or chronic obstructive pulmonary disease. The method comprises
CC	determining the expression level of a marker gene in a biological sample
CC	from a subject, comparing the expression level determined with the
CC	expression level of the marker gene in a biological sample from a healthy
CC	subject, and judging whether the subject has bronchial asthma or chronic
CC	obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC	genes (S1) whose expression levels increase when respiratory epithelial
CC	cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC	whose expression levels decrease when respiratory epithelial cells are
CC	stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC	testing for bronchial asthma or chronic obstructive pulmonary disease;
CC	(2) a kit for screening for a candidate compound for a therapeutic agent
CC	to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC	an animal model for bronchial asthma or chronic obstructive pulmonary
CC	disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC	method for producing an animal model for bronchial asthma or chronic
CC	obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC	asthma or chronic obstructive pulmonary disease, comprising the compound,
CC	a marker gene or an antisense nucleic acid corresponding to a portion of
CC	the marker gene, a ribozyme, a polynucleotide that suppresses the
CC	expression of the gene through an RNAi effect or an antibody recognising
CC	a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC	bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC	probe has been immobilised to assay a marker gene. (1) has respiratory
CC	and antiasthmatic activities, and can be used in gene therapy. The method
CC	is useful for testing for or screening for a therapeutic agent for
CC	bronchial asthma or chronic obstructive pulmonary disease. The present
CC	sequence is used in the exemplification of the present invention.
XX	
SQ	Sequence 1992 BP; 455 A; 537 C; 543 G; 457 T; 0 U; 0 Other;
	Query Match 47.6%; Score 1272; DB 12; Length 1992;
	Best Local Similarity 77.8%; Pred. No. 0;
	Matches 1549; Conservative 0; Mismatches 440; Indels 3; Gaps 1;
Qy	4 ATGGGTCTTACCGGATCCGGTGTCACATGGGGCCTCGCTATTAGCCGGTTCCAACAAC 63
Db	1 ATGGGTGTCTACCGCATCCGGCTCTCCACCGGGACTCCGTGTACCGGGGCTCCAACAAC 60
Qy	64 CAGGTGCAGCTGGCTGGTCGCCAGCACGGGGAGGGCGCTCGGAACGCACTGTGG 123
Db	61 GAGGTCTACTGTGGTTGATTCGACAGCATGGGGAGGATCTCTCGGNACTGTTCGGA 120
Qy	124 CC GGCA CGGGGCAAGGAGACAGAACTCAAGGTGGGAAGTACC GGAGTATCTGGGGCCGCTG 183
Db	121 CCTGTGCGAATCTCGAGGCGAGATTCAGGTGGATGTGTGAGATACCTTTGGGCGCACTG 180
Qy	184 CTGTTTTGAAACTCGCGAAAACGGCACCTCTTAAGGACGACGCTGTTCTGCAACTGG 243
Db	181 CTGTTTTGTAGAGTGCAGAAATGGCATATTCTCAAAGAGGAGCGCTGGTCTCTGCAACTGG 240
Qy	244 ATCTCTGTCAAGGCCCCCGAGCCC--GGGACGAGGTTCAGGTTCCCTTTGATCGGCTGG 300
Db	241 ATTCTGTGAAGGGCCCCCGAGACACAGGATCCGAGTACAGTTCCTCCCTGTTCACGATGG 300
Qy	301 GTGAGGGCAACCGGCGTCTGAGCTTCCTGGAAGGCAACCGGCGGCACTGTGGGGAGGAC 360
Db	301 GTTCAGGCAACCAAGATCTGAACTCCCTGAGGGCACTGGCTGCACCGTGGTGAAGAC 360
Qy	361 CCTCAGGGCTGTTTCAGAAAAACCGGGGAAGAAGAGCTGGAAGAGAGAAAGTTGTAC 420
Db	361 TCTCAAGGCTGTTTCAGGAACACACAGGAGGAGGAACCTGGAAGAAGAGGAGTCTGTAC 420

QY	1501	CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCCCAGGACCGAGGGTTTCCTGTCTCTTTA	1561
Db	1501	CAAGAGATCACTGAGATTGGGTTGCAAGGTGCCAGGACAGAGGCTTCCCCACCTCCCTC	1560
QY	1561	CAGGCTCGGGACAGGTTTGCCACTTTGTGCACCATGTGTATCTTTCACCTGCACCGGCCAA	1620
Db	1561	CAGTCCCGGGCTCAGGCTTGCCACTTCAATCAACCATGTGCATCTTTCATGCACTGCGCAG	1620
QY	1621	CACGCCCTCTGTGCACCTCGGGCCAGCTGGACTGTGGTACTCTTTGGGTGCCTAATGCACCCCTGC	1680
Db	1621	CACCTCTCCATCCATCTTTGGCCAGCTGGATTGGTTCTACTGGGTTCTTAATGCACCCCTGC	1680
QY	1681	ACGATGGGCTGCCCGCCCAACCAACCAAGATGCAACGCTGGAGACAGTGTATGGCGACA	1740
Db	1681	ACCATGGGGCTGCCCAACCACTAAACCAAGGACGCGATGGAGAAAGCTGATGGCCAGC	1740
QY	1741	CTGCCCCAATTCACACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGCGACAGCG	1800
Db	1741	CTGCCCAATCTTAATCAGTCTACTCTCCAGATAAATGTGTTTGGCTCTTGGGCGACAGCG	1800
QY	1801	CAGCCCCGTATGTGGCTGTGGGCCAGCATGAGGAGGATATTTTTCGGGCCCTTGAGCCT	1860
Db	1801	CAGCTGTTATGTGGCTGCCCTGGGCCAGCATTCAGAGGAACTTCCCAACCTTGAGCC	1860
QY	1861	AAGCTGTGCTGAAGAAGTTTCAGAGAGGAGCTGGCTGCTTGGATAAGGAAATTGAGATT	1920
Db	1861	AAAGCTGTGCTGAAGAAGTTTCAGAGAGGAGCTGGCTGCTTGGATAAGGAAATTGAGATT	1920
QY	1921	CGGAATGCAAAGCTGGACATGCCCTACGAGTACCTGCGGCCAGCGTGGTGGAAAACAGT	1980
Db	1921	CGTAAACAAAGCTTGGACATACCTTATAGTACCTTGGCGGCCAGCTGGTGGAAAACAGC	1980
QY	1981	GTGGCCATCTAA	1992
Db	1981	GTGGCCATATGA	1992
RESULT 8			
ADS09997			
ID	ADS09997 standard; DNA; 2311 BP.		
XX	ADS09997;		
XX	16-DEC-2004 (first entry)		
DT	Human therapeutic DNA - SEQ ID 234.		
DE	antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;		
XX	inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;		
KW	aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.		
KW	Homo sapiens.		
OS	WO2004080148-A2.		
XX	23-SEP-2004.		
XX	30-SEP-2003; 2003WO-US030720.		
PF	02-OCT-2002; 2002US-0416186P.		
XX	(NUVE-) NUVELO INC.		
PR	Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;		
XX	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AU, Weng G, Zhou P;		
PA	WPI; 2004-668857/65.		
XX	P-PSDB; ADS10681.		
DR	New polynucleotide, useful in preparing a composition for diagnosing or		
XX	treating inflammatory, neurodegenerative or stem cell disorders, e.g.,		
PT	aplastic anemia or cancer for promoting wound healing.		
XX			

PS	Claim 1; SEQ ID NO 234; 718pp; English.	
XX		
CC	The invention relates to a novel isolated polynucleotide and the encoded	
CC	polypeptide. The molecules of the invention demonstrate antiinflammatory,	
CC	neuroprotective, antianemic, cytostatic and vulnerary activities and may	
CC	be useful in preparing a composition for diagnosing or treating	
CC	inflammatory, haematopoietic, immune, neurodegenerative or stem cell	
CC	disorders, such as aplastic anaemia or cancer, as well as for promoting	
CC	wound healing. The molecules may also be utilised during gene therapy	
CC	procedures. The current sequence is that of a human therapeutic DNA of	
CC	the invention. The current sequence is not shown explicitly within the	
CC	specification but can be accessed from the WIPO web-site.	
XX		
SEQ	Sequence 2311 BP; 541 A; 623 C; 611 G; 536 T; 0 U; 0 Other;	
	Query Match 39.5%; Score 1055.6; DB 13; Length 2311;	
	Best Local Similarity 71.0%; Pred. No. 4.4e-268;	
	Matches 1442; Conservative 0; Mismatches 579; Indels 9; Gaps 3	
QY	4 ATGGGTCTCTACCGCATCCGGTGTCCATCTGGGGCTCGCTCTATGCGGGTTCCACAAC 63	
DB	1 ATGGCAAGTACACGGTCCGGTAGCCACCGGGATTGCTCTCTGCGGGCTCTCCCAAC 60	
QY	64 CAGTGCAGCTGTGGCTGGTCCGCCAGACGCGGGAGGGCGCGCTCGGGAAGCAGCTGTGG 123	
DB	61 CTGTGTCAGCTATGCTGTGGTGGCGAGCAGCGGGAGGCAGACTTAGGGAAGCAGCTGCCA 120	
QY	124 CCCGACGGGGCAAGGACAGAACTCAAGTGGGAAGTACCGGAGTATCTGGGGCCGCTG 183	
DB	121 CCGGTGTGGGGAAGGAGGCAGAGTTTGAGATCGACGTCGCCCCCTGCACCTGGGGCGGCTC 180	
QY	184 CTGTTTGTGAACCTGCGCAACCGCACCTCTCTTAAGGACGACGCTGGTTCTGCAACTGG 243	
DB	181 CTGATGTTGAGCTGGCGAACAACAACGTCGTGTTGAGTCTCGACTGGTTCTGCAAGTGG 240	
QY	244 ATCTCTGTGCAGGGCCCGGAGCGGGGACGAGGTCAGGTTCCCTTGTGTACCGCTGGGTG 303	
DB	241 ATCTCAGTGCAGGGCCCGGGACCCAGCGGAGGCGCTTTTTCCTCTGCTACCGCTGGGTG 300	
QY	304 GAGGGCAACGGCTCTGAGCGCTGCTGAAAGGCACCGCGCGACACTGTGGCGGAGGACCT 363	
DB	301 CAGGGCCACGGAAATATCTGCTGCTGCTGAGGATCTGCGCGGACCGTGAATGACCC 360	
QY	364 CAGGGCTGTTCAGAAACACCGGGAGAAAGAGCTGGAAGAGAGAGGAAG---TTGTAC 420	
DB	361 CAGAACCTGTTTAGAAATATCGGGAACAGGAGCTCGAGGAAGGAAGGCTTCTCTCC 420	
QY	421 CGGTGGGGAACTCGAAGGACGGGTTAATTCGTAATATGGCTGGGGCCAAACTATATGAC 480	
DB	421 AGGTGGGGCTCCTGGAAGATGGGTTAATCTCGCTATAGCAGGGAATAGGCAACCGGAC 480	
QY	481 CTCCTCTGGATGACGATTTCTCGAAGACAGAGAGTGTGACTTTGAGGTTTCGCTGGCC 540	
DB	481 CTTCTTAGGGACAGCGAATTCCTCGAGGATAGGATTTAGACTTTAATGTCTCCCTAGCA 540	
QY	541 AAGGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTGGGAAGGAT 600	
DB	541 AAAGGTTGAAGACTTGGCCATTTAAGGGGACACTGGATTTCTAATAATTGTGTGAAGG 600	
QY	601 CTAGATGACTTCAACCGGATTTCTGGTGTGGTCAGAGCAAGCTGGCTGAGCGCGTGGG 660	
DB	601 CTGGAAGATTTCAAAAAAATTTCCACATGGAAGACTGTCTCGCTGAGCGGGTTTAT 660	
QY	661 GACTCTGGAAGGAAGATGCCCTTATTTGGGTACCAAGTTTCTTAATGGCGCCAAACCCCTG 720	
DB	661 GATTTCTTGGAGAATGATGCCCTTCTTTGGGTACCAAGTTTCTCAATGGTGCAAACCCCATG 720	
QY	721 GTGCTGAGGGCTCTGCTCACTTTCGCTCGCTAGTGTTCCTCCAGGCAATGAGGAA 780	
DB	721 CTCCTGAGGTGTTCTTCAAGGCTCCAGCTGCGCTGGTGTGCTCTCCAGGATGGAAGAC 780	
QY	781 CTGCAGGCCACAGCTGGGAAGGAGCTGGAGGGAGGCACACTGTGTTCCGAAGCTCACTTCTCC 840	

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Db 781 TTGAAGACCCAGCTGGAGAAAGAACTCCAGGCTGGATCTCTGTTTGAAGTGGAATTTCTCC 840
Qy 841 CTGCTGGATGGATCAAGGCAACGTCATTCTCTGTAGCAGCAGCACCTGGCTGCCCT 900
Db 841 TTTCTGGATGGATCAAGGCTAATGTCATCAATTTTAAAGAGCAATGCGTGGAGCCCT 900
Qy 901 CTAGTCATGCTGAAATTTGACGCTGATGGAAATCTCTTGGCCCATGGTCAATCAGCTCCAG 960
Db 901 TTGGTCATGCTGAAGCTTCAGCCTGATGGAGGACTCTTACCCATGTCATCAGCTCCAG 960
Qy 961 CTGCCCCGACAGGATCCCAACACCTCCCTTTCTTGGCTACGATCCCCCAATGGCC 1020
Db 961 CCACCTTGACAGGATGTCCCCACCTCTGCTCTTTCTGCGCTCGCATCCCCCAATGGCC 1020
Qy 1021 TGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCAGCTTCATGAGCTGCACTCT 1080
Db 1021 TGGCTCTGGCCAAAGACTGGGTCCGAGCTCTGATTTTCAAGTTCAGCTGAGCAGTTACAGTCA 1080
Qy 1081 CATCTTCTGAGGGGACACTTTGATGGCTGAGGTCAATTTTGTGGCCACCATGAGGTCCCTG 1140
Db 1081 CATCTCTGAGGGGACACTTTGATGGCTGAGGTCAATTTTGTGGCTCAATGAGAAGCTTG 1140
Qy 1141 CCGTCGATACATCTTATTTCAAGCTTAATTTCCCACTGCGATACACCTGGAATTT 1200
Db 1141 CCTAGCCTCCATCTCTATCAAGCTCTGATCCCCACTTCCGCTACACCATGGCGATC 1200
Qy 1201 AAGCTCGGGCCAGGAGCTGGCTGCTCTGACATGGGAATTTTCACACAGATAATGAGC 1260
Db 1201 AACGCTGGCCAGAGTAGCTTGTCTCGAATGGGGAATTTTGACCTGTGGTGAGC 1260
Qy 1261 ACTGTGGGGGAGGCCACGCTGACGTGCTCAAGCAAGCTGGAGCCTTCCTAACCTACAGC 1320
Db 1261 ACTGTAGTGAAGCCACGCTGGACATTTTCAGAGAGCCATGCTGTTTGACCTATCAT 1320
Qy 1321 TCCTTCTGCTCCCTGATGACTTGGCGACCGGGGCTCTGGGAGTGAAGTTCCTTC 1380
Db 1321 TCCCTCTGCTCTGATGACCTGGCTGACCGGTCTCTGGATGTGAATCTCTCTTT 1380
Qy 1381 TATGCCCAAGATCGCTGGCGCTCTGGAAATCATCTATCGGTATGTGGAAGGAATCGTG 1440
Db 1381 TATGGC---GATGCCATGAGCTGTGGGGAATCATGACCGGTACATGAGGGGATGGTT 1437
Qy 1441 AGTCTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGCTGCAGACCTGGTGT 1500
Db 1438 GGGCTTTTCTACATAGTACCAAGCATGATGAAGATGATAGAGCTGCAGGCTGGTGC 1497
Qy 1501 CGAGAGATCACTGAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTCTGTCTCTTTA 1560
Db 1498 AGAGAGATGACTGAGACTGGACTGCAGAGGGGCCAAGACAGGGGTTCCTCATCTCTTA 1557
Qy 1561 CAGCTCGGACACGAGTTTCCCACTTTGTCCACATGTATCTTCACTGCACCGGCCAA 1620
Db 1558 GAGTCCCGGGCTAGCTCTGCCACTTGTCCACATGTGCACTTTCATGACAGGTGAG 1617
Qy 1621 CAGCCTCTGTGCACTGGGCCAGCTGGACTGTGTTCTTGGGTGCTCAATGACCCCTGC 1680
Db 1618 CATGCTTCAACACCTGGGCCAGCTGACTGTGTTCTCTGGATCCCTAATGCCCCATGC 1677
Qy 1681 ACSATGGGTGCCCCCGCCAAACCAAGATGCAACGCTGGAGACAGTGTATGGGACA 1740
Db 1678 ACCATGCAAGAGCCCCCACCACCTCTCTAAGGATGTGACAGAGAAGGATATAGTGGACTTA 1737
Qy 1741 CTGCCCCAATTTCCACAGGCTTCTCTCCAGATGTCCTACTTGGCAGCTGGCCAGACGC 1800
Db 1738 CTGCCCCAATTTCCACAGGACGATATGCAAAAGACCTTTCACAAAGTTCTTTGGCAGACGC 1797
Qy 1801 CAGCCCTGTATGTGGCTGTGGGCGACATGAGGAGGATATTTTTCGGGCCCTTGAGCCT 1860
Db 1798 CAGCCTCTCATGGTG---AGAGCAACATGAGGAGAAATATTTCTGTGCTCGAGCC 1854
Qy 1861 AAGCTGTGTGAAGAGTTTCAAGGAGAGCTGCTGCTGCTGATTAAGGAAATTTGAGATC 1920
Db 1855 CAAGCTGTGTGAGACAAATTCAGGAGGAACTGGCTTCCATGGACAGGAGATTTGAGGTC 1914
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Qy 1921 CGGAATGCAAAAGCTGGACATGCCCTTACGAGTACCTTGGGCCCCAGCGTGTGGAACAAGT 1980
Db 1915 CGGAATGCAAGTCTCTGGACCTGCTGTGAGTACCTTTGACCCAGCATGTTAGAGAACAGC 1974
Qy 1981 GTGGCCATCTAAGCGTGGCCACCCTTTGGTTATTTTCAGCCCCCATCACCC 2030
Db 1975 GTGACCATCTGAGAGGCTTGGCCCGCTCAGCTCCAAAGCTCCACATCC 2024
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RESULT 9

AD509995
ID ADS09995 standard; DNA; 2302 BP.

XX
AC ADS09995;

DT 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 232.

DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

OS Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI: 2004-668857/65.
DR P-PSDB; ADS10679.

XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

XX Claim 1; SEQ ID NO 232; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX Sequence 2302 BP; 538 A; 623 C; 608 G; 533 T; 0 U; 0 Other;

Query Match 38.6%; Score 1030.4; DB 13; Length 2302;
Best Local Similarity 71.0%; Pred. No. 2e-261;
Matches 1441; Conservative 0; Mismatches 571; Indels 18; Gaps 5;

Qy 4 ATGGGTCTTACCGCATTCGCGTGTCCACTTGGGCCCTCGCTCTATCGCGTTCCACAC 63

Db 1 ATGGGCAAGTACACGCTCCGCGTAGCCACCGGGGATTTCCTCTGGCGGCTCTCCCAAC 60

Qy 64 CAGGTCCAGCTGTGGCTGTTCGCCAGACGCGGAGCGCGCTCGGGAAGCCACTGTGG 123

Db 61 CTGGTCAGCTATGGCTGTGTGGCGGAGCACGGGAGGAGACCTAGGGAAGAGCTGCCA 120

Db 1376 CTCTGTCTCTGACGACCTGGCTGACCGGGGCTGCTGGACTCCAGGTCTCTCTAT 1435
Qy 1384 GCCAAGATGCGCTGGCGCTCTGGGAAATCATCTATCGGTATGTGAAGAAATCGTGA 1443
Db 1436 GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGATCGTCCAC 1495
Qy 1444 CTCACATATAAGACAGACGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGC 1503
Db 1496 CTCCTTACARAGGATGACATAGTAGAGGGGACCTGTGAGCTGAGGCCCTGGTGTGG 1555
Qy 1504 GAGATCACTGAATCGGGCTGCAAGGGGCCCGAGGCTTCTCTCTCTTTACAG 1563
Db 1556 GAGATCAACGAGGTGGGCTGTGCCAGGCCCGAGGCTTCTCTCTCTCTCTCCAG 1615
Qy 1564 GTCGGGACAGGTTTGGCCACTTTGTACCATGTGTATCTTCACTGCAACCGGCCAAGAC 1623
Db 1616 TCCAGAGTCAACTCTGCCATTTCTCTCACCATGTGCTTCCAGCTGCACCTGCCAGCAT 1675
Qy 1624 GCCTCTGTGCACTGGGCCAGCTGGACTGTGTTCTTGGGTGCTTAATGCACCTGCAG 1683
Db 1676 GCGCCATCAACGAGGCCAGCTGGACTGTGTTCTTGGGTGCTTAATGCCTCATGCACA 1735
Qy 1684 ATGCGCTGCCCGCCCAACCAACCAAG---GATGCAACCGCTGGAGACAGTGATGCGACA 1740
Db 1736 ATGCGGATGCCCGCCCAACCAACCAAGGAGATGTGACGATGGCCACAGTGATGGGTCA 1795
Qy 1741 CTGCCCCAATTCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCGAGCGC 1800
Db 1796 CTACCTGATGTCCGGCAGGCTGTCTTCAATGGCCATCTCATGGCATVATGATGCGCGC 1855
Qy 1801 CAGCCCGTTATGGTGGCTGGCCAGCATGAGGAGGATATTTTCGGGCCCTGAGCT 1860
Db 1856 CAGCCAGACATGGTGGCTTGGGCGCACCAAGAAATATTTCTCAGGCCCGCCAGGCC 1915
Qy 1861 AAGGCTGTCTGAAGAAGTTTCAGGAGGAGCTGGCTGCCCTGGATAGGAATTCAGATC 1920
Db 1916 AAGCTGTCTTAACCAATTCGACAGATTTGGAAGCTGAAAGAGATTACAGC 1975
Qy 1921 CGGAATGCAAGCTGGACATGCCCTACGATGATCTTGGGCCCGAGCGTGGTGAAGAAACAGT 1980
Db 1976 CGGAATGAGCAACTTGACTGGCCCTATGAATATCTGAGCCCGAGCTGYATAGAGAACGT 2035
Qy 1981 GTGGCCATCTAGC 1994
Db 2036 GTCACCATCTGAGC 2049

RESULT 11
ADQ39009
ID ADQ39009 standard; DNA; 2867 BP.
XX
AC ADQ39009;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 672.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX

(APPL-) APPLERA CORP.
Cargill M, Devlin J, Iakoubova O;
WPI; 2004-533949/51.
P-PSDB; ADQ39837.
Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
Claim 7; SEQ ID NO 672; 145pp; English.
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
Sequence 2867 BP; 668 A; 826 C; 764 G; 598 T; 0 U; 11 Other;
Query Match 38.1%; Score 1016.4; DB 13; Length 2867;
Best Local Similarity 69.4%; Pred. NO. 1.1e-257;
Matches 1384; Conservative 8; Mismatches 599; Indels 3; Gaps 1;
Qy 4 ATGGGTCTCTACCGCATCCGGCTGTCCACTGGGGCTCGCTCTATGCCGTTCCACAC 63
Db 555 ATGGGCGCTTACCGCATCCGGCTGGCCACCGGGGCTGGCTCTTCTCGGGTCTGTACAC 614
Qy 64 CAGGTGACGTGTGGCTGGCTGGCCAGCACCGGGAGGGGGCTCGGGAAGCACTGTGG 123
Db 615 CGGTGACAGCTTTGGCTGGTGGGACGCGCGGGAGGGGAGCTGAGCTGAGCTGGCG 674
Qy 124 CCGCAGCGGGCAAGAGACAGAACTCAAGTGGAGTACCGGAGTATCTGGGGCGCTG 183
Db 675 CCGCGCGGGCGAGGAGGAGGAGTTTGCATCATGCTTGCAGAGGACTTGGGGCTCTG 734
Qy 184 CTGTTTGTGAACCTGGCAAAAGCGACCTCTTAAGGACGAGCGCTGCTTCTGCACTGG 243
Db 735 CAGTTCGTGAGGCTGCGCAAGCACCACTGGTGTGGACGACGCGTGTCTTGCACCGC 794
Qy 244 ATCTCTGTGACGGGCGCCGAGCGGGGACGAGGTTCCTTGTTCACCGCTGGGTG 303
Db 795 ATCAGGTGACGGGCGCTTGGAGCTGCGCGAGGTGGCTTCCCGTGTACCGCTGGGTG 854
Qy 304 CAGGCAACCGCGCTCTGAGCTTGCCTGAAGCAACCGGCCCGACCTGTGGGCGAGACCT 363
Db 855 CAGGCGAGGACATCTCTGAGCTTGCCTGAGGCGACCGCCCGCTCCAGGAGACAACTGT 914
Qy 364 CAGGCGCTTCTCCAGAAACACCGGGAAGAGAGAGAGAGAGAGAGTGTGTACCGG 423

Db 915 TTGGACATGTTCCAGAAAGCATCGAGAGAGGAACCTGAAAGACAGACAGCAGATCTTACTGC 974
Qy 424 TGGGGAACCTGGGAAGACGGGTTAAATTCGAAATATGGCTGGGGCCAAACTATATGACCTC 483
Db 975 TGGGCCACCTGGGAAGAGGGTTACCCCTGACCATCGCTGCAGACCCTGAAGATGATCTA 1034
Qy 484 CTTGTGGATGAGCGATTTCTGGAAGACAGAGAGTTGACCTTTTGAGGTTTCGCTGGCCAAAG 543
Db 1035 CCTCCAAATATGAGATTCATGAGGAGAGAGGCTGGACCTTTGAAATGGACACTGAAGGCA 1094
Qy 544 GGCTGGCCGACCTCGTATCAAGAAGCTCTCTAAATGTTCTGACCTTGTGGAAGGATCTA 603
Db 1095 GGCGCTCTGGAGATGGCCCTCAAAACRTGTTTACACCCCTCGCTGAGCTCTCTGGAATCCCTTA 1154
Qy 604 GATGACTTTAAACCGGATTTCTCGTGTGGTTCAGAGCAAGCTGGCTGAGCGCTGGCGGAC 663
Db 1155 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCTGGCTGAGAGGTTTCGCCAG 1214
Qy 664 TCCTGGAAGGAAGATGCTTTATTTGGGTACACAGTTTCTTAATGGCCCAACCCCGTGGTG 723
Db 1215 TGCTGGCAGGATGATGAGTTGTTTCAGCTACCACTTCTCAATGGTGCCAAACCCCATGCTG 1274
Qy 724 CTGAGGGCTCTGCTACCTCTCTGCTGCTAGTGTTCCTCCAGGCACTGAGGAAGCTG 783
Db 1275 TTGAGAGCTCGACCTCTCTGCCCTCCAGGCTAGTGTGCTGCCCTCRGGGATGGAAGAGCTT 1334
Qy 784 CAGGCCAGCTGGGAAGGAGCTGGAGGAGGACACTGTTGAAAGCTGACTTCTCCCTG 843
Db 1335 CRGGCTCACTGGAGAAGAACTTCAGATGGTTCCTGTTTGAAGCTGACTTCATCCTT 1394
Qy 844 CTGGATGGATCAAGGCCAACGTCATTCTCTGTAGCCAGCAGACCTGGCTGCCCTCTTA 903
Db 1395 CTGGATGGAATTCAGCCCAAGTGATCCGAGGAGAGAACTACCTGGCTGCCCCCTC 1454
Qy 904 GTATGCTGAAATGTGAGCCTGATGGGAACCTCTTGCCCATGTCTATCCAGCTCAGCTG 963
Db 1455 GTTATGCTGAAGATGGAGGCCAATGGGAAGCTCAGGCCCATGTGTCTATCCAGATTCAGCCT 1514
Qy 964 CCCGACAGAGATCCCCACACCTCCCTTTTCTGCTACGATCCCCCAATGGCTGG 1023
Db 1515 CCARCCAGCTCTCCAAACCCCAACACTGTTCTGCTCCTCAGACCCCACTTGCTGG 1574
Qy 1024 CTTCTGSCCAAAATGCTGGTGCAGCTCTGACTTCCAGCTCCATGAGCTGCATGCTCAT 1083
Db 1575 CTCTGSCAAAGTCTGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC 1634
Qy 1084 CTTCTGAGGGGACACTGTGAGCTGAGTCAATTTGTTGGCCACCATGAGTGCCTGCCG 1143
Db 1635 TTGCTGAACACKACACCTGGTGGCTGAGTCACTGCTGTGCCCACTGCGGTGCTCCCA 1694
Qy 1144 TCGATACATCTTCTCAAGCTTATATTTCCACCTGGATACACCTCGGAAATTAAC 1203
Db 1695 GGACTGACCCCATCTTCAAGTCTCTGATCCCCCATATCCGCTACACCATGGAANTCAAC 1754
Qy 1204 GTCCGGSCCAGGATGGGCTGTCTGACATGGGAATTTTCGACCAGATAATGAGCACT 1263
Db 1755 ACCGGSCCCGGACCAACTCATCTCAGATGGAGGAATTTTGTAAAGGCAGTGAGCACA 1814
Qy 1264 GGTGGGGGAGCCACGTGAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGTCC 1323
Db 1815 GGTGGAGGGGGCCATGTACAGTTGCTCCGTGGGGGCGCAGCTCAGCTGACCTACTGCTCC 1874
Qy 1324 TTCTGTCCCTCATGACTTTGGCCACCGGGGCTCCTGGAGTGAAGTCTTCTCTCTAT 1383
Db 1875 CTCTGTCTCTGACGACCTTGGCTGACCGGGGCTGCTGGGACTCCAGGTGCTCTCTAT 1934
Qy 1384 GCCCAAGATCGCTGCGCTCTGGGAATCATCTATCGGTATGTGGAAGGAATCGTGAGT 1443
Db 1935 GCCCATGATGTTTACGGCTCTGGAGATCATTTGCCAGGTATGTGGAGGGGATCGTCCAC 1994
Qy 1444 CTCACATATAAGACAGCTGGCTGTGGAAGACGACCCAGAGCTGACAGCTGGTGTGGA 1503
Db 1995 CTCTTTTACCARAGGGATGACATAGTGAAGGGGACCTCTGAGCTGCAGGCTGGTGTGCGG 2054

Qy 1504 GAGATCACTGAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTCTCTCTTTACAG 1563
Db 2055 GAGATCAGGAGGTGGGGCTGTGCCAGGCCAGGACCGAGGTTTCCCTGCTCTCTCCAG 2114
Qy 1564 GTCGGGACAGGTTTGGCACCCTTTGTCCACATGTGTATCTTCACTGACACGGCCACAC 1623
Db 2115 TCCAGAGTCAACTCTGCCATTTCTCCACCATGTGCGTCTTCACGTGCACTGCCAGCAT 2174
Qy 1624 GCCTGTGTGCACCTGGGCCAGCTGGACTGTGTACTCTTGGGTGCTTAATCACCCTGCACG 1683
Db 2175 GCGGCATCAACAGGGCCAGCTGGACTGGTATGTCTGGGTCCCTAATGCTCCATGCACA 2234
Qy 1684 ATGCGCTGCCCCGCCCAACCAAG---GATGCAACGCTGGAGACAGTGTATGGCGACA 1740
Db 2235 ATGCGGATGCCCCGCCCAACCAAGGAAGATGTGACGATGGCCACAGTATGGGTCA 2294
Qy 1741 CTGCCCACCTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGCAGACGC 1800
Db 2295 CTACCTGATGTCCGGCAGGCTGTCTTCAATGGCCATCTCATGGCATTTGATGCGCCG 2354
Qy 1801 CAGCCGTTATGTGCTGTGGCCAGCATGAGGAGGAGTATTTTCGGGGCCTTGAGCCT 1860
Db 2355 CAGCCAGACATGTGCTCTGGGGCCACCAAGAAATATTTCTCAGGCCCAAGGCC 2414
Qy 1861 AAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTGGCTGCCCTCGATAAGAAATTTGAGATC 1920
Db 2415 AAGCTGTGCTAAACCAATTTCCGAAACAGATTTGGAAGAGCTGAAAAGGAGATTACAGCC 2474
Qy 1921 CGAATGCAAGCTGGACATGCCCTACGAGTACCTGCGGCCAGCGTGGTGGAAACAGT 1980
Db 2475 CGGAATGAGCAACTTGACTGGCCCTATGAATATCTGAAGCCAGCTGTATAGAGAACGT 2534
Qy 1981 GTGGCCATCTAAGC 1994
Db 2535 GTACCATCTGAGC 2548

RESULT 12
AAC58018

ID AAC58018 standard; DNA; 2343 BP.

XX AAC58018;

AC AC
XX XX
DT 25-JAN-2001 (first entry)

XX Arachidonic acid metabolism related genomic biallelic marker #652.

XX Human; biallelic marker; arachidonic acid metabolism; genotyping;
detection; hybridisation; phenotype; SNP; polymorphic base;
single nucleotide polymorphism; hybridisation assay; sequencing assay;
specific amplification assay; identification; ERBM; 12-LO-RBM;
eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.

XX Homo sapiens.

OS OS
XX XX
PN WO20004771-A2.

XX 17-AUG-2000.

PD 11-FEB-2000; 2000WO-IB000184.

PF 12-FEB-1999; 99US-0119917P.

PR 23-MAR-1999; 99US-00275267.

PR 07-MAY-1999; 99US-0133200P.

XX (GEST) GENSET.

PA Blumenfeld M, Bougueleret L, Chumakov I;

XX WPI; 2000-571881/53.
DR P-PSDB; AAB24019.

XX XX

PT Novel biallelic markers useful for detecting conditions and genotypes
PT associated with arachidonic acid metabolism.

PS Claim 70; Page 797-799; 802pp; English.

XX The present invention describes polynucleotides including biallelic
CC markers derived from genes involved in arachidonic acid metabolism and
CC from genomic regions flanking those genes. Methods from the present
CC invention may be used to select individuals for clinical trials and
CC predict responses to treatment with drugs. The polynucleotides may be
CC used in hybridisation assays, sequencing assays and specific
CC amplification assays for identifying an eicosanoid-related biallelic
CC marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
CC segment of nucleotides containing an ERBM. The polynucleotides are useful
CC in diagnostic kits. The markers may be used to detect conditions and
CC genotypes associated with arachidonic acid metabolism. AAC57367 to
CC AAC58018 and AAB24019 and AAB24020 represent sequences used in the
CC exemplification of the present invention. N.B. Polymorphic bases (single
CC nucleotide polymorphisms also known as SNPs) in the polynucleotide
CC sequences from the present invention have been given as their
CC corresponding degenerate bases e.g. a polymorphic base of C or T has been
CC given as Y

XX Sequence 2343 BP; 511 A; 688 C; 636 G; 495 T; 0 U; 13 Other;

Query Match 37.9%; Score 1013.6; DB 3; Length 2343;
Best Local Similarity 69.2%; Pred. No. 5.7e-257;
Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGGTCTCTACGCATCCGGTGTCCACTGGGGCTCGCTCTATGCCGGTTCACACAC 63

DB 40 ATGGGCGGTACCGCATCCGCGTGGCCACCGGGGCTGGCTCTTCCTCCGGGTCGTACAC 99

QY 64 CAGGTGCAGCTGTGGTGTGGCCAGCAGCGGAGCGCGCTCGGGAAGCAGCTGTGG 123

DB 100 CGGTGCAGCTTTGGTGTGGGACCGCGGGAGCGGAGCTGGAGCTGAGCTGTGG 159

QY 124 CCGCAGCGGGGCAAGGAGACAGAACTCAAGTGGAGTGCAGAGTATCTGGGGCGGTG 183

DB 160 CCGGCGGGGCGAGGAGGAGGTTGATCATGACGTTGCAGAGACTTGGGGCTCCTG 219

QY 184 CTGTTTGTGAACCTGGCGAAACCGGACCTCTTAAGGACGAGCCTGTCTTGCACCTGG 243

DB 220 CAGTTCTGAGGCTGGCGAAGCACCCTTGGCTGGTGGAGCAGCGGTCTTGCACCGC 279

QY 244 ATCTCTGTCAGGGCCCGGAGCGGGGACGAGTCAAGTTCCTTTTACCGCTGGGTG 303

DB 280 ATCAGGTCAGGGCCCTGGAGCTTCGGGAGGTGGCCCTTCCGCTGCTACCGCTGGGTG 339

QY 304 GAGGGCAACGGGGTCTCTGAGCCTGCTGAAGGCACCGGCGCACCTGTGGCGGAGGACCT 363

DB 340 CAGGGCGAGGACATCTGAGCCTGCCCCGAGGGCACCGCCCGCTGCCAGGACAACTGCT 399

QY 364 CAGGGCTTTTCCAGAAACACCGGGAAGAGAGCTGGGAAGAGAGAGAGTGTACCGG 423

DB 400 TTGGACATTTCCAGAAGCATCGAGAGAAGAACTGAAAGACAGACAGCAGATCTACTG 459

QY 424 TGGGGAACCTGGAAGCAGGGTTAATCTGAATATGCTGGGGGCCAACTATATGACCTC 483

DB 460 TGGGCCACTTGGAGGAGAGGGTTACCCCTGACCATCGCTGCGACCCGTAAGGATGATCTA 519

QY 484 CCTGTGGATGAGCGATTTCTGGAAGCAAGAGAGTTGACTTTTGGGTTTCGCTGGGCCAAG 543

DB 520 CCTCCAAATATGAGATTCCATGAGGAGAGAGGCTGAGCTTTGTAATGGACACTGAAGGCA 579

QY 544 GGGCTGGCGGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTGTCTGGGAAGATCTA 603

DB 580 GGGGCTCTGGAGATGGCCCTCAACRTGTTTACACCCCTCTGAGCTCTCTGGAATGCTCTA 639

QY 604 GATGACTTCAACCGGATTTCTGGTGTGTCTGAGCAAGCTGGCTGAGCGCTGGCGGAC 663

DB 640 GAAGACTTTGATCAGATCTTCTGGGGCCAGGAAGAGTGGCCCTGGCTGGAAGGTTGGCCAG 699

QY 664 TCCTGGAAGGAAGATGCTCTTATTTGGGTACAGTTTCTTAATGGCGCCACCCCGTGGTG 723

DB 700 TGCTGGCAGGATSATAGTTGTTTACAGTACCAGTTCTCAATGGTGCCCAACCCCATGCTG 759

QY 724 CTGAGCGCTCTGCTCACCTTCCTGCTAGTGTTCCTCCAGGATCGAGGAAGTG 783

DB 760 TTGAGYCTCGACCTCTGCTCCCTCAGGCTAGTGTGCTCCCTCRGGATGGAAGCTT 819

QY 784 CAGGCCCTAGCTGGAGAAGGAGCTGGAGGGAGGACACATGTTTGGAAAGCTGACTTCTCCCTG 843

DB 820 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGTTTCCCTGTTTGAAGCTGACTTCTCCTT 879

QY 844 CTGGATGGATCAAGGCCCAACGTCATCTCTGTAGCAGCAGCACCTGGCTGCCCTCTA 903

DB 880 CTGGATGGAATTTCCAGCCCAACGTCATCCGAGGAGAGAAGCAATACCTGGCTGCCCTCTC 939

QY 904 GTCATGCTGAAATTCAGCCCTGATGGGAAACTCTTTGGCCCATGTCATCCAGCTCCAGCTG 963

DB 940 GTTATGCTGAAGATGGAGCCCAATGGGAAGCTGAGAGCCCATGGTTCATCCAGATTCAGCCT 999

QY 964 CCGCGCACAGGATCCCAACCACTCCCTTTTCTTGGCTTACGGATCCCCCAATGGCCTGG 1023

DB 1000 CCAACRCCCGAGCTCTCCAAACCCCAACACTGTTCTCTGCTCAGACCCCGCACTTGGCTGG 1059

QY 1024 CTTCTGGCCAAATGCTGGGTGGGAGCTCTGATCTCCAGCTCCATGAGCTGAGTCTCAT 1083

DB 1060 CTCCTGGCAAGTCTCTGGGTCCGAAATTTTCAGATTTCCAACTGCACGAGATCCAGTATCAC 1119

QY 1084 CTTCTGAGGGGACACTTCATGCTGAGTCAATGTTGTGGCCACCATGAGTGCCTGCCG 1143

DB 1120 TTGCTGAAACACACCTCTGGTGGCTGAGTCACTGCTGCGCCACCATGCGGTGCCCTCCA 1179

QY 1144 TCGATACATCTTCTCAAGCTTATAATTCGCCACCTGCCGATACACCTCGTGAATTAAC 1203

DB 1180 GGACTGCAACCCATCTTCAAGTCTCTGATCCCCCATATCCGCTACACCATGGAATCAAC 1239

QY 1204 GTTCGGGCGAGACTGGGCTGTCTGACATGGGAATTTTCGACAGANAATAGCACT 1263

DB 1240 ACCCGGGCCGAGACCAACTCATCTCAGATGAGGAAATTTTGTGAAGCAGTGAAGACA 1299

QY 1264 GGTGGGGAGGCCACGTGCTCAAGACGCTGGAGCCTTCTTAACCTACAGCTCC 1323

DB 1300 GGTGAGGGGGCCATGTACAGTTGCTCCGTGGGCGGAGCTCAGTGAACCTACTGCTCC 1359

QY 1324 TTCTGTCCCTCTGATGACTTGGCCGACCGGGGGCTCTCTGGGAGTGAAGTCTTCTTCTAT 1383

DB 1360 CTCTGTCTCTCTGAGCACTTGGCTGACCGGGGGCTGCTGGGACTCCAGGTGCTCTCTAT 1419

QY 1384 GCGCAAGATGCGCTGCGGCTCTGGGAATCATCTATCCGTTATGTGGAAAGAAATCGTGAGT 1443

DB 1420 GCGCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGATCGTCCAC 1479

QY 1444 CTCACATATAGACAGAGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGTGCA 1503

DB 1480 CTCCTTCTACAPAGGAGATGACATAGTGAAGGGGGACCCCTGAGCTGACGCTGGTGTGCG 1539

QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTACAG 1563

DB 1540 GAGATCAGGAGGTGGGCTGTGCCAGGCCAGGACCGAGGTTCCTGTCTCTTCCAG 1599

QY 1564 GCTCGGGAACAGGTTTGCACCTTGTCAACATGTGTATCTTCACTGACCGGGCCAAACAC 1623

DB 1600 TCCAGAGTCAACTCTGCCATTTCTCACCATTGTGCGTCTTCACGTCACTGCCAGCAT 1659

QY 1624 GCCTGTGTGCACTGGGCGAGCTGAGCTGTACTCTTGGGTGCCCTTAATGCACTCCGACG 1683

DB 1660 GCGGCATCAACCAAGGGCCAGCTGGACTGGTATGCTGGGTCCCTTAATGCTCCATGCACA 1719

QY 1684 ATGCGGCTGCCCGGCCCAACCAACG--GATGCAACGCTGGAGACAGTGTATGCGGACA 1740

DB 1720 ATGCGGATGCCCGGCCCAACCAACG--GATGCAACGCTGGAGACAGTGTATGCGGACA 1779

QY 1741 CTGCCCAACTTCCACCAAGGCTTCTCTCCAGATGTCCATCATCTTGGCAGCTGGGCGACG 1800

Db 1780 CTACCTGATGTCGGCAGGCGCTGCTCTCAATGGCCATCTCATGGCATCTGAGTCGCCGC 1839
QY 1801 CAGCCGTTATGCTGCTGCGCCAGCATGAGGAGGATATTTTCGGGCGCTGAGCCT 1860
Db 1840 CAGCCAGACATGCTGCTCTCGGGCCACCAAGAAAAATATTTCTCAGGCCCCAAGCCC 1899
QY 1861 AAGGCTGTGCTGAAGAAGTTTCAGGAGGAGCTGGCTGCCCTGGATTAAGAAATTTGAGATC 1920
Db 1900 AAGCTGTGCTAAACCAATTCGAAACAGATTTGAAAAAGCTGAAAAAGAGATTACAGCC 1959
QY 1921 CGAATGCAAAAGCTGACATGCCCTACGAGTACCTCGGCCCCAGCGTGGTGGAAAAACAGT 1980
Db 1960 CGGAATGAGCAACTGACTGGCCCTATGAATATCTGAAGCCACGCTGCATAGAGAACAGT 2019
QY 1981 GTGGCCATCTAAGC 1994
Db 2020 GTCACCATCTGAGC 2033

RESULT 13

ADS09996
ID ADS09996 standard; DNA; 2218 BP.

XX AC

ADS09996;

XX 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 233.

XX anti-inflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

PI Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
DR P-PSDB; ADS10680.

XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anaemia or cancer for promoting wound healing.

XX Claim 1; SEQ ID NO 233; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate anti-inflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX Sequence 2218 BP; 511 A; 600 C; 585 G; 522 T; 0 U; 0 Other;

Query Match 34.4%; Score 918.6; DB 13; Length 2218;

Best Local Similarity 68.0%; Pred. No. 7.3e-232;

Matches 1379; Conservative 0; Mismatches 549; Indels 101; Gaps 3;
QY 4 ATGGGCTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGCGGGTCCCAACAC 63
Db 1 ATGGGCAAGTACACGGTCCGCTAGCCACCGGGGATTTGCTCCTGGCGGGCTCTCCCAAC 60
QY 64 CAGGTGCAGCTGTGGCTGGTCCGCCAGCACCGGGGAGGCGCGCTCCGGGAAGCAGCTGTGG 123
Db 61 CTGGTGCAGCTATGCTGGTGGCGAGCACCGGGAGGAGACCTAGGGAAGCAGCTGCCA 120
QY 124 CCGCACCGGGGAGAGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCGGCTG 183
Db 121 CCGGTGTGGGAAAGAGAGCGAGATTGAGATCGACGCTCCCTCGCACCTGGGGCGCCTC 180
QY 184 CTGTTTGTGAACCTCGCAAAACGGCACCTCTCTTAAGGACGAGCGCTGGTCTGCAACTGG 243
Db 181 CTGATGGTGAAGCTGCGCAAAACAAACGCTGCTGTGTGAGTCTCGACTGGTCTTGCAGTGG 240
QY 244 ATCTCTGTGCAGGCGCCCGGAGCCCGGGGACGAGGTCAAGTTCCTTTGTTTACCGCTGGGTG 303
Db 241 ATCTCAGTGCAGGCGCCCGGGGACCCAAAGCGAGGCGCTTTTCCCTCGCTACCGCTGGGTG 300
QY 304 GAGGCAACGCGCTCCTGAGCCTGCTGAAGCACCGGCCCGCACCTGTGGGCGAGGACCT 363
Db 301 CAGGGCCACGGAATTTATCTGCTGCTGTAGGGTA----- 334
QY 364 CAGGGCTGTTTCCAGAAACACCGGGGAGAGAGCTGGAAGAGAGAAAGTTGTACCGG 423
Db 335 -----GG 336
QY 424 TGGGGAACCTGGAAGACGGGTAAATTCGAAATATGGTGGGGCCAAACTATATGACCTC 483
Db 337 TGGGCTCTCGAAAGATGGGTAAATCTGCTATAGCAGGGAATAGGCAACCGGACCTT 396
QY 484 CTTGTGATGACCGATTTCTGGAAGACAAGAGATTGACTTTGAGGTTTCGCTGGCCAG 543
Db 397 CCTAGGACGAGCGATTTCTCGAGGATAAGGATTTAGACTTTTAATGTCTCCCTAGCAAA 456
QY 544 GGGCTGGCGGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTGGAAGGATCTA 603
Db 457 GGGTTGAAGGACTTGGCCCAATTAAGGGACACTGGATTTCTATAAATTTGTGAAAGGCTG 516
QY 604 GATGACTTCAACCGGATTTTCTGGTGTGAGAGAGCTGGCTGAGCGCTGCGGGAC 663
Db 517 GAAGATTTCAAAAAAATATTTCCACATGSAAGACTGTCTCGCTGGCTGAGCGGTATGAT 576
QY 664 TCCTGGAAGGAAGATGCTTATTTGGGTACAGTTTCTTAATGGCGCCCAACCCCGTGGTG 723
Db 577 TCTTGAAGAATGATGCTCTTTTGGGTACCAAGTTTCTCAATGGTGCAAAACCCCATGCTC 636
QY 724 CTGAGCGCTGCTCACCTTCTGCTGCTAGTGTTCCTCCAGGCATGGAGAACTG 783
Db 637 CTGAGGTGTTTCTCAAGGCTCCAGCGCTGCTGGTGTGCTCCAGGGATGGAAGACTTG 696
QY 784 CAGGCCACAGCTGGGAAGGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTCTCCCTG 843
Db 697 AAGACCCAGCTGGAGAAGAACTCCAGGCTGATCTCTGTTTGAAGTGAATTTCTCCTTG 756
QY 844 CTGGATGGGATCAAGGCCAAACCTCATTTCTGTAGCAGCAGCACCTGCTGCCCTCTA 903
Db 757 CTGGATGGAGTCAAGCCTAAATGTCTCATTTTTTAAGCAGCAATGCGTGGCAGCCCCCTTG 816
QY 904 GTCATGCTGAATTCAGCGCTCATGGAACTCTTGGCCATGTCATCCAGCTCCAGCTC 963
Db 817 GTCATGCTGAAGCTTCAGCCTGATGAGGACTCTTACCCTGATGTCATCCAGCTCCAGCCA 876
QY 964 CCGCGCACAGGATCCCCACCACTCCCTTTTCTTGGCTACGGATCCCCCAATGGCCTCG 1023
Db 877 CTTGACACGAGTGTCCCCCACCTCTGCTCTTTTGTGCCCTCGCATCCCCCATGGCCTGG 936
QY 1024 CTTCTGGCCAAATGTGGGTGGCGAGCTCTGACTTCCAGCTCCAGCTCCAGCTGACTGCTCAT 1083
Db 937 CTCCTGGCCAAAGACCTGGGTCCGGAGCTCTGATTTTCCAGCTCCAGCAGTTTACAGTCACAT 996

Db	1896	-----	Db	869	GGTTGGGCTTTTCTAATAAGTGTGACCAAGCCATGAAGATGATCTAGAGCTGAGGCCTTG	810
Qy	424	TGGGGAACCTGGAAGACGGTTAATCTCAATATGCTGGGCCAAACTATATGACCTC	Qy	1497	GTGTCAGAGATCACTGAAATCGGCTGCAAGGGGCCAGGACCGAGGCTTTCTGTCTC	1556
Db	1889	TGGGGCTCTCGAAGATGGTGGTTAAATCCCTCTATAGCAGGAATAGGCAACCGGACCTT	Db	809	GTGTCAGAGATGATGAGACTGGACTGAGAGGGGCCCAAGACCAGGGGTTCTCATCTC	750
Qy	484	CTGTGGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGTGGCCAAAG	Qy	1557	TTTACAGGCTCGGACCAAGGTTTGCACTTTGTCCACCATGTGTATCTTCACTGTGACCCGG	1616
Db	1829	CCTAGGACGAGCGATTCCTCGAGGATAGGATTTAGACTTTAATGTCTCCCTAGCAAA	Db	749	CTTAGAGTCCCGGCTCAGCTCTGCCACTTTGTCCACCATGTGCATCTTCAATGCACAG	690
Qy	544	GGCTGGCCGACCTCGCTATCAAAAGACTCTTAAATGTTCTGACTTGTGGAAAGATCTA	Qy	1617	CCAAACAGCGCTGTGACCTGGCCAGCTGAGCTGCTACTCTTGGTGCCCTAATGCACC	1676
Db	1769	GGTTGAAGGACTTGGCCATTAAAGGGACACTGGAATTCATAAATTTGTGAAAAGGCTG	Db	689	TCAGCATGCTTCAACCACTGGCCAGCTGACTGGTACTCTCTGGATCCCTAATGGCCC	630
Qy	604	GATGACTTCNAACGGATTTTCTGGTGTGTGTCAGAGCAAGCTGGCTGAGCGCTGGGGAC	Qy	1677	CTGCACGATGCGGCTGCCCCGCCCAACCAAGGATGCAACGCTGGAGACAGTGTATGTC	1736
Db	1709	GAAGATTTCAAAAATAATTTCCCAATGGAAGACTGTCTGGCTGAGCGGGTTATGAT	Db	629	ATGCAACATGCAAGAACCCGCCCATCTCTAAGATGTGACAGAGAGGATATAGTGA	570
Qy	664	TCCTGAAAGGAAGATGCTTTATTTGGGTACCACTTTCTTAATGGCGCCAAACCCCGTGGT	Qy	1737	GACATGCGCCAACTTCCACAGGCTTCTTCAGATGTCCATCATCTTGGCAGCTGGGCG	1796
Db	1649	TCTTGGAGAAATGATGCTTCTTTGGGTACCACTTTCTCAATGGTGCAAAACCCCATGCTC	Db	569	CTTACTTGCCCAATCTCCACCAAGCATGATGCAAAAGACCTTCAAAAAGTTCTCTGGCAG	510
Qy	724	CTGAGGCTCTGCTCACCCTTCTGCTGTGCTAGTGTTCCTCCAGGCAATGGAAGAACTG	Qy	1797	AGCCAGCCGCTTATGTTGGCTGTGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGA	1856
Db	1589	CTGAGGTGTTCTCAAGGCTCCAGGCTGCTGCTGCTCCAGGGATGGAAGACTTG	Db	509	ACGCCAGCGCTGTCAT-----GATGAGGAGAAATATTTCTCTGGTCTCTGA	465
Qy	784	CAGGCCAGCTGGAAGAGCTGGAGGGAGGCACACTGTTTGAAGCTGACTTCTCCCTG	Qy	1857	GCCTAAGGCTGTGCTGAAGAAGTTCCAGGAGGAGCTGGCTGCCCTGGATAAGAAATTGA	1916
Db	1529	AAGACCCAGCTGGAAGAAAGACTCCAGGCTGGATCTCTGTGTAAGTGAATTTCTCCTTG	Db	464	GCCCAAGCTGTGTGAGACAAATTCAGGAGGAACTGGCTTCCATGGACAGGAGATTGA	405
Qy	844	CTGGATGGGATCAAGGCCAACGTCAATTTCTGTAGCCAGCAGCACCTGGCTGCCCTCTA	Qy	1917	GATCCGGAATCAAAAGCTGGACATGCCCTPACAGTACCTGCGGCCAGCGTGTGGA-AA	1975
Db	1469	CTGGATGGAGTCAAGCTTAATGTCTCATCTTTTAAGCAGCAATGCGTGGCAGCCCTTG	Db	404	GGTCCGGAATCAGTCTCGAACCTGCGTGTGAGTACCTTTGACCCAGCATGCTAGAGAA	345
Qy	904	GTATGCTGAAATTTGAGGCTGATGGGAAACTCTTGCCCATGTATCCAGCTTCCAGCTG	Qy	1976	ACAGTGTGCCATCTAAG	1993
Db	1409	GTGCTGTGAAGCTTCAGCCTGATGAGGACTCTTACCCATGCTCATCCAGCTCCAGCCA	Db	344	ACAGCTGACCATCTGAG	327
Qy	964	CCCCGACAGGATCCCCACACCTCCCTTTCTTGCCTACGATCCCCCATGGCCTGG	RESULT 15			
Db	1349	CCTTGACACGAGTGTCCCCACCTCTGCTCTTTCTGCCCCGATCCCCCATGGCCTGG	ADSL1348/c			
Qy	1024	CTTCTGCCAAAATGCTGGGTGCCAGCTCTGACTTCCAGCTCCATCAGCTGCAGTCTCAT	ID	ADSL1348	standard; DNA; 2227 BP.	
Db	1289	CTCCTGGCCAGACCTGGGTCCGGAGCTCTGATTTCCAGCTGCAGAGTTACAGTCACT	XX	AC	ADSL1348;	
Qy	1084	CTTCTGAGGGGACACTTGTATGGCTGAGGTCATTTGTGTGGCCACCATGAGGTGCTGCCG	XX	XX	16-DEC-2004 (first entry)	
Db	1229	CTGCTGAGGGGACACTTGATTTGCTGAGGTTATTGCTGTGGCTACAATGAGAAGCTTGCCT	DE	Human therapeutic contig DNA - SEQ ID 1585.		
Qy	1144	TCGATACATCTATCTTCAAGCTTATAATTCGCCACCTCGGATACACCCCTGGAAATAAC	XX	antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;		
Db	1169	AGCCTCCATCTATACAAAGCTCCTGATCCCCCACTTCGCTACACCATGGCGATCAAC	KW	inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;		
Qy	1204	GTCCGGGCCAGGACTGGGCTGCTCTGACATGGGAATTTTCACACAGATAATGAGCACT	KW	aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.		
Db	1109	ACGCTGGCCAGAGTAGTCTTGCTCCGAATGGGAAATTTTGACCTGGTGTGAGCACT	XX	Homo sapiens.		
Qy	1264	GGTGGGGAGGCCAGCTGACGTGCTCAAGCAAGCTGGAGCCTTCCTAACCTACAGCTCC	XX	WO2004080148-A2.		
Db	1049	GGTAGTGAAGCCACGCTGGACATCTTTCAGAGAGCCATGCTTGTGTGACCTATCATTC	PD	23-SEP-2004.		
Qy	1324	TTCTGTCCCCCTATGACTTGGCCGACCGGGGCTCTGGAGTGAAGTCTTCTCTAT	XX	30-SEP-2003; 2003WO-US030720.		
Db	989	CTCTGTCTCTGATGACCTGGCTGACCGGCTGCTGGATGGAATCTCTCTTTAT	PR	02-OCT-2002; 2002US-0416186P.		
Qy	1384	GCCCAAGATCGCTGCGGCTCTGGGAAATCATC-----TATCGGTATGTGGAAGGAAT	XX	(NUVE-) NUVELO INC.		
Db	929	GGCTAAGATGCCATCAGGCTGTGGGNAATCATCAGCCGGGAATAGGTACGTGAGGGGAT	XX	Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;		
Qy	1437	CGTAGTCTCCATATAAGACACAGCTGGTGTGTAAGACGACCCAGAGCTGACAGCTTG	PI	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;		
			XX	WPI; 2004-668857/65.		
			DR	P-PSDB; ADS11946.		
			XX	New polynucleotide, useful in preparing a composition for diagnosing or		
			PT	treating inflammatory, neurodegenerative or stem cell disorders, e.g.,		

PT aplastic anemia or cancer for promoting wound healing.
XX Example 2; SEQ ID NO 1585; 718bp; English.
PS
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC DNA of the invention. The current sequence is not shown explicitly within
CC the specification but can be accessed from the WIPO web-site.
XX Sequence 2227 BP; 527 A; 589 C; 600 G; 511 T; 0 U; 0 Other;
SQ
Query Match 33.8%; Score 901.6; DB 13; Length 2227;
Best Local Similarity 68.3%; Pred. No. 2.3e-227;
Matches 1364; Conservative 0; Mismatches 529; Indels 105; Gaps 4;
QY 4 ATGGGTCTCTACCGCATCCGCGTGTCCACTGGGGCTCGCTCTATGCCGGTTCACAAAC 63
DB 2227 ATGGGCAAGTACACGCTCCGCGTAGCCACCGGGGATTTGCTCTGGCGGCTCTCCCAAC 2168
QY 64 CAGGTGAGCTGTGGCTGTGCGCCAGCACGGGAGCGCGCTCGGGAAGCAGCTGTGG 123
DB 2167 CTGGTGCAGCTATGGCTGTGGTGGCGAGCACGGGAGGCGAGCTAGGGAAGCAGCTGCCA 2108
QY 124 CCGCACGGGCAAGGAGACAGAACTCAAGTGGAAAGTACCGGAGTATCTGGGGCGCGTG 183
DB 2107 CCGGTGTGGGAAGAGGAGCAGAGTTGAGATCGACGTCCCCCTGCACCTGGGGCGCCCTC 2048
QY 184 CTGTTTGTGAAACTGCGCAAAACGGCACCTCTTTAAGGACGACGCCCTGGTTCTGCAACTGG 243
DB 2047 CTGATGTTGAAGCTGCGCAAAACACAACGCTGCTTTCAGTCTCGACTGGTTCTGCAAGTGG 1988
QY 244 ATCTCTGTGAGGGCCCGGAGCGGGGAGGAGTCAAGTTCCTTGTTCACGCTGGGTG 303
DB 1987 ATCTCAGTGCAGGGCCCGGAGCCCAAGGGCGGCGCTTTTTCCTCCCTGCTACCGCTGGGTG 1928
QY 304 GAGGGCAACGGCTCTGAGCCCTGCTGAAGGCACCGCGCGACCTGTGGGCGAGGACCTT 363
DB 1927 CAGGGCCACGAAATATCTGCTTGCCTGAGG----- 1897
QY 364 CAGGGCTGTGTCAGAAACACACGGGAAGAGAGCTGGAAAGAGAGAAAGTTGTACCGG 423
DB 1896 -----GTACTGG 1890
QY 424 TGGGAAACTGGAAGACGGGTTAAATCTGAATATGCTGGGCGCCAAACTATATGACCTC 483
DB 1889 TGGGGCTCTGGAAGATGGGTTAAATCTGCTTATAGAGGAATAGGCAACCGGACCTT 1830
QY 484 CTTGTGGATGAGGATTTCTGGAAGACAGAGATTTGACTTTGAGCTTTGCTGGCGCAAG 543
DB 1829 CCTAGGGAAGAGGATTTCTCGAGGATAAGGATTTAGACTTTAATGTCTCCCTAGCAAAA 1770
QY 544 GGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTTGCTGGGAAGATCTA 603
DB 1769 GGGTTGAAGGACTTGGCCATTAAAGGGGACACTGGATTTCTAATAATTTGTGAAAGGCTG 1710
QY 604 GATGACTTCAACCGGATTTTCTGGTGTGTGTGTCAGAGCAAGCTGGCTGAGCGCGTGGGGAC 663
DB 1709 GAAGATTTCAAAAAAATAATCCACATGGAAGACTGTCTGGCTGAGCGGGTTTATGAT 1650
QY 664 TCTTGAAGAGAGATGCTTATTTGGTACCAAGTTTCTTAATGGCGCAACCCCGTGGT 723
DB 1649 TCTTGAAGAGATGATGCTTCTTTGGGTACCAAGTTTCTCAATGGTGCAAAACCCCATGCTC 1590
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Job time : 922.004 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 11:52:27 ; Search time 5546.35 Seconds
(without alignments)
18330.926 Million cell updates/sec

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Perfect score: 2671
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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	986.2	36.9	1809	9 AY415838	AY415838 Mus muscu
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4	943.4	35.3	2410	3 AK036898	AK036898 Mus muscu
5	943.4	35.3	2993	3 AK087724	AK087724 Mus muscu
6	919.4	34.4	2301	3 AK036960	AK036960 Mus muscu
7	867.8	32.5	898	5 BQ957032	BQ957032 AGENCOURT
8	815.8	30.5	997	5 BQ276406	BQ276406 AGENCOURT
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10	728.4	27.3	781	5 BM976589	BM976589 UI-CF-EN1
11	690.4	25.8	727	6 CB305836	CB305836 UI-CF-EN1
12	632.4	23.7	682	7 CR767490	CR767490 DKF2p468J
13	619	23.2	620	5 BX644955	BX644955 DKF2p781M
14	609	22.8	622	5 BM975468	BM975468 UI-CF-EN1
15	572	21.4	701	5 BM981991	BM981991 UI-CF-EN1
16	549.6	20.6	921	2 BE538114	BE538114 601062748
17	547	20.5	2216	3 AK079232	AK079232 Mus muscu
18	526	19.7	537	5 BX282722	BX282722 BX282722
19	498.8	18.7	758	7 CO575440	CO575440 AGENCOURT
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ALIGNMENTS

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DEFINITION Homo sapiens ALOX15 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY415836 genomic survey sequence.
ACCESSION AY415836
VERSION AY415836.1 GI:39771796
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1809)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1809)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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AY415838
ACCESSION
VERSION AY415838.1 GI:39771798
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1809)
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PubMed 14671302
REFERENCE 2 (bases 1 to 1809)
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Carilli, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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Matches 1180; Conservative 0; Mismatches 629; Indels 0; Gaps 0;

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LOCUS      2964 bp      mRNA      linear      HTC 13-JAN-2003
DEFINITION Homo sapiens, Similar to arachidonate lipxygenase, epidermal,
clone IMAGE:5270337, mRNA.
ACCESSION BC041851
VERSION   BC041851.1 GI:27693128
KEYWORDS  HTC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 2964)
            Direct Submission
            Submitted (23-DEC-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Niklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www.shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 74 Row: k Column: 5
This clone has the following problem: frame shifted.

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ORIGIN
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Best Local Similarity 70.3%; Pred. No. 2.3e-187;
Matches 1337; Conservative 0; Mismatches 530; Indels 34; Gaps 3;

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QY 197 TGGGAAACGGACCTCTTAGGACGACGCTGTTCTGCACTGGATCTCTGTGCGAGG 256
DB 857 TGGCGAAACACAAACGCTGCTTGTGAGTCTCGACTGGTTCTGCAAGTGGATCTCAGTGCAGG 916
QY 257 GCCCGGAGCGGGGACGAGGTTCAGGTTCCTTGTTCACCGCTGGGTGGAGGGCAACGGCG 316
DB 917 GCCCGGGACCCNAGCGGGCGCTTTTCCCTGTCTACCGCTGGGTGGAGGGCCACGGNA 976
QY 317 TCTGAGCTGCTGTAAGGACCGGCGCACTGTGGCGAGGACCTCTAGGCGCTGTTCC 376
DB 977 TTATCTGCTGCTGAGGGTACTGCGCGGACCGCTGAGTGTATACCCCGCAAGAACCTGTTTA 1036
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1145 GATTCTCGAGGATAAGGATTTAGACTTTTAAATGCTCCTCTAGCAAAAGGGTTGAAGGACT 1204
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1865 GTAGCTTTGTCTCCGAATGGGGAATTTTGGACCTGGTGGTGGAGCACTGGTAGTGAAGCC 1924
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DEFINITION
Mus musculus adult female vagina cDNA, RIKEN full-length enriched
library, clone:930022G08 product:arachidonate 12-lipoxygenase,
full insert sequence.
ACCESSION
AK036898
VERSION
AK036898.1 GI:26331797
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2 10349636
PUBMED
11042159
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
99279253
MEDLINE
PUBMED
10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2 20499374
PUBMED
11042159
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitesuna, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Tanaka, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (KISA) system--384-format

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JOURNAL
MEDLINE
PUBMED
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JOURNAL
MEDLINE
PUBMED
AUTHORS
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JOURNAL
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FEATURES
source
CDS

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sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2410)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Chemical Research, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
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2410

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QY	1981	GTGGCCATCTAAG	1993

Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillarary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2301)
Adachi, J., Aizawa, K., Akimura, T., Atakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submision

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

source

1. 2301

/organism="Mus musculus"

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12. 2017

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putative"

ORIGIN

Query Match

Best Local Similarity

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34.4%; Score 919.4; DB 3; Length 2301;

67.0%; Pred No. 5.6e-180;

Conservative 0; Mismatches 646; Indels 17; Gaps 2;

2;

2;

2;

2;

2;

2;

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Db 12 ATGGGCGCTTATCCGCGTCCGGTGTGTGTCTCTGGGCGCTGGCTCTTCTTCCGGATCCCTCAAC 71
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QY 350 TGGGCGAGGACCTCAGGGCCTGTTCCAGAAACACCGGAAAGAGAGCTGGAAGAGAGAA 409
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QY 410 GGAAGTTGTACCGTGGGGAACTGGAAGAGCGGGTTAAATCTGAATATGGCTGGGGCA 469
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Qy 1430 AAGGAATCGTAGTCTCCATATAAGACAGAGCTGGCTGTGAAGACGACCCAGAGCTGC 1489
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Db 1872 CAGACCCAGGACCAAGCTGTGCTCAGGCAATTTCAAGCAGATTTGGACAATTTGGAGA 1931
Qy 1907 AGGAATTCAGATCCGGAATGCAAGCTGGAATGCAATGCTTACAGTACCTCAAGCCAGCC 1966
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Qy 1967 TGGTGAATAACAGTGTGGCCATCTAAG 1993
Db 1992 GCATAGAGAACAGTATCACCATCTGAG 2018
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RESULT 7

BQ957032

LOCUS

DEFINITION BQ957032 8794383 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6370474

5', mRNA sequence.

ACCESSION BQ957032

VERSION BQ957032.1

KEYWORDS GI:22372510

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (Bases 1 to 898)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/BTP/Gazdar

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2543 row: b column: 11

High quality sequence stop: 642.

FEATURES

source

1..898

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/tissue_type="large cell carcinoma"

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/clone_lib="NIH_MGC_18"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match 32.5%; Score 867.8; DB 5; Length 898;
Best Local Similarity 98.5%; Pred. No. 2.9e-169;
Matches 875; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 301 GTGGAGGGCAACCGCGTCTCTGAGCTGTGCTGAAGCAACCGCGGCACTGTGGGCGAGGAC 360
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Qy 361 CCTCAGGGCTGTTCCAGAAACACCGGAGAGAGCTGGAGAGAGAGAGAGTTGTAC 420
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RESULT 8
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LOCUS
DEFINITION BQ276406 997 bp mRNA linear EST 07-MAY-2002
5', mRNA sequence.
ACCESSION BQ276406
VERSION BQ276406.1 GI:20486614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 997)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCW2114 row: j column: 12
High quality sequence stop: 715.
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Site_2: XhoI; CDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN
Query Match 30.5%; Score 815.8; DB 5; Length 997;
Best Local Similarity 99.3%; Pred. No. 1.8e-158;
Matches 839; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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QY 1886 AGGAGCTGGCTGCCCTGGATTAAGGAAATTTAGATCCGGAATGCAAGCTGGACATGCCCT 1945
Db 301 AGGAGCTGGCTGCCCTGGATTAAGGAAATTTAGATCCGGAATGCAAGCTGGACATGCCCT 360
QY 1946 ACAGTACCTGGCGCCAGCGTGTGGAACAGTGTGGCCATCTTAAGCGTGGCACCT 2005
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Db 841 CAGCC 845
RESULT 9
CA311119/c
LOCUS
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CA311119
ACCESSION UI-CF-FNO-afc-b-13-0-UI 3', mRNA sequence.
769 bp mRNA linear EST 04-NOV-2002

VERSION	CA311119.1	GI:24529217	
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ORGANISM	Homo sapiens		
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AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBLISHED	8889548		
COMMENT	Contact: McCray, PB McCray Lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.regen.com) or from Open Biosystems (www.openbiosystems.com). The following repetitive elements were found in this cDNA sequence: 1-39, >AT rich#low complexity (matched compliment) 123-332, >ALU 442-503, >(GGAA)n#Simple_repeat Seq primer: M13 FORWARD POLYA=Yes.		
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DB	769	GAGATCCGGAATGCAAAAGCTGGACATGCCCTACGAGTACCTCGCGCCCGCAGCGTGGTGGAA	710
QY	1975	ACAGTGTGGGCATCTAGAGCTGCGCACCCCTTTGGTTATTTTCAGCGCCCATCCCAAGC	2034
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QY	2035	CACAGCTGACCCCTCGTGGTTATAGCCCTCGCCCTCCCAAGTCCCAAGCTCTTCCCATG	2094
DB	650	CACAGCTGACCCCTCGTGGTTATAGCCCTCGCCCTCCCAAGTCCCAAGCTCTTCCCATG	591
QY	2095	TCCACCCCTCCCTAGAGGGGACACCTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTAC	2154

sequence: 1-39, >AT_rich#Low complexity (matched compliment)
123-332, >ALU 442-503, >(GGAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
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/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not.I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS shr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 27.3%; Score 728.4; DB 5; Length 781;
Best Local Similarity 98.6%; Pred. No. 2.4e-140;
Matches 754; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 1906 AAGGAAATGAGATCGGAATCGGAATCGACATGCGCTACGAGTACCTGGGCCCCAGC 1965
DB 777 AGGGAATGAGATCGGAATCGGAATCGGACATGCGCTACGAGTACCTGGGCCCCAGC 718
QY 1966 GTGGTGGAAAACAGTGTGGCCATCTAAGCGTCGCCACCCCTTTGTTTATTTAGCCCCCAT 2025
DB 717 GTGGT-GAAAACAGTGTGCATCTNAAGCGTCGCCACCCCTNT-GTTATTTAGCCCCCAT 660
QY 2026 CACCCCAAGCCAAAGCTGACCCCTTCGTGTTATAGCCCTGCCCCCAAGTCCACCCCT 2085
DB 659 CACCCCAAGCCAAAGCTGACCCCTTCGTGTTATAGCCCTGCCCCCAAGTCCACCCCT 600
QY 2086 CTTCCCATGTCCACCCCTCCCTAGAGGGGCACCTTTTCATGTCTCTGCACCAGTGAAC 2145
DB 599 CTTCCCATGTCCACCCCTCCCTAGAGGGGCACCTTTTCATGTCTCTGCACCAGTGAAC 540
QY 2146 ACATTTTACTCTAGAGGCATCACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTTC 2205
DB 539 ACATTTTACTCTAGAGGCATCACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTTC 480
QY 2206 CTATCTTCTTC 2265
DB 479 CTATCTTCTTC 420
QY 2266 CAATTATATAATCATTTCAAGACTAGAATAGGGGGATATATACATATTACTCCACACC 2325
DB 419 CAATTATATAATCATTTCAAGACTAGAATAGGGGGATATATACATATTACTCCACACC 360
QY 2326 TTTTATGAATCAATATGATTTTTTTTGTGTTTGAAGACAGAGTCTCACTTTGACACCC 2385
DB 359 TTTTATGAATCAATATGATTTTTTTTGTGTTTGAAGACAGAGTCTCACTTTGACACCC 300
QY 2386 AGGCTGGAGTCAGTGGTGCCTACACAGGCTCACTGACGCTCAGGCTCAGGCTCTGGGCTCA 2445

Db 299 AGGCTGGAGTCAGTGGTGGCCATCACACGGCTCACTGCAGCCTCAGCGTCTCGGCTCA 240
QY 2446 AATGATCTCTCCAGCTCAGCCTCCTGAGTAGCTGGAGTACAGGCTATGCCATCATGCC 2505
Db 239 AATGATCTCTCCAGCTCAGCCTCCTGAGTAGCTGGAGTACAGGCTATGCCATCATGCC 180
QY 2506 CAGCTAATATTTTTTTTATTTTCGTGGAGACGGGCGCTCACATATGTTGCTAGGCTGGA 2565
Db 179 CAGCTAATATTTTTTTTATTTTCGTGGAGACGGGCGCTCACATATGTTGCTAGGCTGGA 120
QY 2566 TAGGATTTTGAACCCAAATTCAGTGTAAACAATAATAAAAGTGTGTTTACGCTAAAGATG 2625
Db 119 TAGGATTTTGAACCCAAATTCAGTGTAAACAATAATAAAAGTGTGTTTACGCTAAAGATG 60
QY 2626 GAAAGAACTAGGACTGAACTATTTTAAATAATAATATTTGGCAAA 2670
Db 59 GAAAGAACTAGGACTGAACTATTTTAAATAATAATATTTGGCAAA 15

RESULT 11
CB305636/c
LOCUS
DEFINITION
UI-CF-EN1-aed-p-02-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
CB305636
ACCESSION
CB305636.1 GI:28846147
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 727)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 123-332, >ALU 442-503, >(GGAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1. .727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-aed-p-02-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h TAG LIB=UI-CF-EN1 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match		25.8%;	Score 690.4;	DB 6;	Length 727;
Best Local Similarity		99.6%;	Pred. No. 1.8e-132;		
Matches 713;		Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2;
QY	1956	GCGGCCAGCGTGGTGGAAACAGTGTGGCCATCTTAAGCGTGCACACCTTTGGTTATTT	2015		
Db	727	GCGGCCAGCGTGGT-GAAAAACAGTGTGGCCATCTAAGCGTGCACACCTTTGG-TATTT	670		
QY	2016	CAGCCCCATCACCCAGGCACAGCTGACCCCTCGTGGTTATAGCCCTGCCCTCCCAA	2075		
Db	669	CAGCCCCATCACCCAGGCACAGCTTACCCCTCGTGGTTATAGCCCTGCCCTCCCAA	610		
QY	2076	GTCCCAACCTCTTCCCATGTCCCAACCTCCCTAGAGGGCACCTTTTCATGTCTCTGCA	2135		
Db	609	GTCCCAACCTCTTCCCATGTCCCAACCTCCCTAGAGGGCACCTTTTCATGTCTCTGCA	550		
QY	2136	CCAGTGAACACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTTCCTTCT	2195		
Db	549	CCAGTGAACACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTTCCTTCT	490		
QY	2196	TCCCTCTTTCCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2255		
Db	489	TCCCTCTTTCCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	430		
QY	2256	CAATAGCCACAAATTATATAATCAATTTCAAGACTAGATAGGGGATATAATACATTT	2315		
Db	429	CAATAGCCACAAATTATATAATCAATTTCAAGACTAGATAGGGGATATAATACATTT	370		
QY	2316	ACTCCACACCTTTTATGAATCAAAATAGATTTTTTTTGGTTTGAAGACAGAGTCTAC	2375		
Db	369	ACTCCACACCTTTTATGAATCAAAATAGATTTTTTTTGGTTTGAAGACAGAGTCTAC	310		
QY	2376	TTTGACACCCAGCTGGAGTGCAGTGGTGCATACACGGCTCACTGCAGCTCAGCT	2435		
Db	309	TTTGACACCCAGCTGGAGTGCAGTGGTGCATACACGGCTCACTGCAGCTCAGCT	250		
QY	2436	CCTGGGCTCAATATGATCTCCCACTCAGCTCCTCAGTAGCTGGGACTACAGGCTCATG	2495		
Db	249	CCTGGGCTCAATATGATCTCCCACTCAGCTCCTCAGTAGCTGGGACTACAGGCTCATG	190		
QY	2496	CAATATGCCAGCTAATATTTTTTTTATTTTGTGGAGACGGGGCTCACTATGTGCT	2555		
Db	189	CAATATGCCAGCTAATATTTTTTTTATTTTGTGGAGACGGGGCTCACTATGTGCT	130		
QY	2556	AGCTGGAATAGGATTTTGAACCCAAATAGTTTAAACAATAAATAAGTTGTTTAC	2615		
Db	129	AGCTGGAATAGGATTTTGAACCCAAATAGTTTAAACAATAAATAAGTTGTTTAC	70		
QY	2616	GCTAAAGATGGAAGAACTAGGACTGAACCTATTTTAAATAAAATTTGGCAAAAG	2671		
Db	69	GCTAAAGATGGAAGAACTAGGACTGAACCTATTTTAAATAAATAATTTGGCAAAAG	14		

RESULT 12

CR767490
LOCUS
DEFINITION
DKFZp468J1413_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DKFZp468J1413 5', mRNA sequence.
ACCESSION
CR767490

VERSION

CR767490.1 GI:52609682

KEYWORDS

Pongo pygmaeus (orangutan)

SOURCE

Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 682)

REFERENCE

1 (bases 1 to 682)
Ottewaelder,B., Obermaier,B., Deutschenbaur,S., Schaiipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

AUTHORS

Ottewaelder,B., Obermaier,B., Deutschenbaur,S., Schaiipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

TITLE

Pongo pygmaeus mRNA (Ottewaelder,B., Obermaier,B.,
Deutschenbaur,S., et al.)

JOURNAL

Unpublished (2004)

COMMENT

Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp468J1413) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp468J1413
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..682
Location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp468J1413"
/tissue type="heart"
/dev stage="adult"
/lab_host="pH10B"
/clone_lib="468 (synonym: phrt1)"
/note="Vector: pSpart1_Sfi; Site_1: SfiI; Site_2: SfiIB"

ORIGIN

Query Match 23.7%; Score 632.4; DB 7; Length 682;
Best Local Similarity 97.6%; Pred. No. 1.9e-120;
Matches 642; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY	1	AAGATGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGCCGGTTCCAAAC	60		
Db	25	AAGATGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGCCGGTTCCAAAC	84		
QY	61	AACAGGTGACAGTGTGGTGGCCAGCACCGGGAGGGCGGCTCGGGAGGCACTG	120		
Db	85	AACAGGTGACAGTGTGGTGGCCAGCACCGGGAGGGCGGCTCGGGAGGCACTG	144		
QY	121	TGGCCCGCACGGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCG	180		
Db	145	TGGCCCGCACGGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCG	204		
QY	181	CTGCTGTTTGTGAACACTCGCAACCGCACCTCTCTTAAGGACGACGCTGTTCTGCAAC	240		
Db	205	CTGCTGTTTGTGAACACTCGCAACCGCACCTCTCTTAAGGACGACGCTGTTCTGCAAC	264		
QY	241	TGGATCTCTGTGACGGGCCCGAGCCGGGACGAGGTCCAGTTCCTTGTACCGCTGG	300		
Db	265	TGGATCTCTGTGACGGGCCCGAGCCGGGACGAGGTCCAGTTCCTTGTACCGCTGG	324		
QY	301	GTGGAGGCAACCGCGTCTCGAGCCTGCTCAAGGCACCGCGCAGCTGTGGCGGAGAC	360		
Db	325	GTGGAGGCAACCGCGTCTCGAGCCTGCTCAAGGCACCGCGCAGCTGTGGCGGAGAC	384		
QY	361	CCTCAGGGCCTGTTCCAGAAACACCGGGAAGAGAGCTGGAGAGAGGAAGTTGTAC	420		
Db	385	CCTCAGGGCCTGTTCCAGAAACACCGGGAAGAGAGCTGGAGAGAGGAAGTTGTAC	444		
QY	421	CGTGGGGAACCTGGAAGGACGGGTTAATTTCTGAATATGGCTGGGGCCAAATATATGAC	480		

Db 445 CGTGGGGAACACTGGAAGATGGGTAAATCTGAATGTGGCTGGGCGCAAACTATGTGAC 504
 Qy 481 CTCCTGTGGATGACGAGTCTTCTGGAACAAGAGATGTGACTTTGAGGTTTCGCTGCC 540
 Db 505 CTCCTGTGGATGACGAGTCTTCTGGAACAAGAGATGTGACTTTGAGGTTTCGCTGCC 564
 Qy 541 AAGGGCTGGCGGCTCGCTATCAAGACACTCTCTAAATGTTCTGACTTGTCTGGAGGAT 600
 Db 565 AAGGGCTGGCGGCTCGCTATCAAGACACTCTTAAATGTTCTGACTTGTCTGGAGGAT 624
 Qy 601 CTAGATGACTTCAACCGGATTTCTGGTGTGTCTGAGACAGCTGGCTGAGCGCTGC 658
 Db 625 CTAGATGACTTCAACCGGATTTCTGGTGTGTCTGAGACAGCTGGCTGAGCGTGC 682

RESULT 13

BX644955 620 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFZp781M0636_r1.781 (synonym: h1ccc4) Homo sapiens cDNA clone
 DEFINITION DKFZp781M0636_5', mRNA sequence.

ACCESSION BX644955
 VERSION BX644955.1 GI:34479288

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,

Fobo, G., Han, M. and Wiemann, S.

TITLE EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp781M0636) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1. .620

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="caxon:9606"

/clone="DKFZp781M0636"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="781 (synonym: h1ccc4)"

/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;

cDNA-collection"

ORIGIN

Query Match

Best Local Similarity 23.2%; Score 619; DB 5; Length 620;

Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 GCTCTATCCGGTTCCAAACACAGGTGACGTGTGGTTCGGCCACGACGGGAGGC 101

Db 2 GCTCTATCCGGTTCCAAACACAGGTGACGTGTGGTTCGGCCACGACGGGAGGC 61

Qy 102 GCGCTCGGGAAGCAGTGTGGCCGACGGGCGAGGACAGACTCAAGGTGGAAGT 161

Db 62 GCGCTCGGGAAGCAGTGTGGCCGACGGGCGAGGACAGACTCAAGGTGGAAGT 121

Qy 162 ACCGAGTATCTGGGGCGCTGCTTTGTGAACCTGCGCAACGGCACCTCTCTTAAGGA 221

Db 122 ACCGAGTATCTGGGGCGCTGCTTTGTGAACCTGCGCAACGGCACCTCTCTTAAGGA 181

Qy 222 CGACGCTGGTTCTGCAACTGGATCTCTGTGACGGGCCCCCGGACCGAGGTGAC 281
 Db 182 CGACGCTGGTTCTGCAACTGGATCTCTGTGACGGGCCCCCGGACCGAGGTGAC 241
 Qy 282 GTTCCCTTGTACCGCTGGGTGGAGGGCAACGGCGTCTCTGAGCCTGCTGAAAGCACCGG 341
 Db 242 GTTCCCTTGTACCGCTGGGTGGAGGGCAACGGCGTCTCTGAGCCTGCTGAAAGCACCGG 301
 Qy 342 CCGCACTGTGGGCGGAGACCTCTCAGGCGCTGTTCCAGAAACACCGGGAAGAGAGCTGGA 401
 Db 302 CCGCACTGTGGGCGGAGACCTCTCAGGCGCTGTTCCAGAAACACCGGGAAGAGAGCTGGA 361
 Qy 402 AGAGAGAGGAGTGTACCGGTGGGGAACCTGGAAGGACGGGTAAATCTCTGAATATGSC 461
 Db 362 AGAGAGAGGAGTGTACCGGTGGGGAACCTGGAAGGACGGGTAAATCTCTGAATATGSC 421
 Qy 462 TGGGGCCAAACTATATGACCTCCCTGTGGATGAGCGATTTCTGGAAGACAAGAGAGTTGA 521
 Db 422 TGGGGCCAAACTATATGACCTCCCTGTGGATGAGCGATTTCTGGAAGACAAGAGAGTTGA 481
 Qy 522 CTTTGAGGTTTCGCTGGCCAAAGGGCTGGCGGACCTCGCTATCAAAAGACTCTCTTAAATGT 581
 Db 482 CTTTGAGGTTTCGCTGGCCAAAGGGCTGGCGGACCTCGCTATCAAAAGACTCTCTTAAATGT 541
 Qy 582 TCTCACTTGTCTGGAAGGATCTAGATGACTTCAACCGGATTTCTGCTGTGTGTCAGAGCAA 641
 Db 542 TCTCACTTGTCTGGAAGGATCTAGATGACTTCAACCGGATTTCTGCTGTGTGTCAGAGCAA 601
 Qy 642 GCTGGCTGAGCGCTGCGG 660
 Db 602 GCTGGCTGAGCGCTGCGG 620

RESULT 14

BM975468/c

LOCUS BM975468

DEFINITION UI-CF-EN1-acv-i-02-0-UI.81 UI-CF-EN1 Homo sapiens cDNA clone

UI-CF-EN1-acv-i-02-0-UI 3', mRNA sequence.

ACCESSION BM975468

VERSION BM975468.1 GI:19593059

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Bonaldo, M.F., Lennon, G. and Soares, M.B.

1 (bases 1 to 622)

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

sequence: 123-332, >ALU 442-503, >(GGAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1. .622

/organism="Homo sapiens"

FEATURES

source


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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acv.i-02-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UI-CF-EN1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polyn linker; Site 1: Ecor I; Site 2: Not I ;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s) : Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldio, Lemon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CAGCCACAGG.
TAG TATSSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGCT"

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ORIGIN

[illegible]

Best Local Similarity 99.1%; Pred. No. 6.4e-108;		Matches 575; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	1814	TGGCTGTGGCCAGCATGAGGAGAGTATTTTTCGGGCCCTGAGCCTAAGGCTGTGCTCA	1873
Db	701	TGGCTGTGGCCAGCATGAGGAGAGTATTTTTCGGGCCCTGAGCCTAAGGCTGTGCTGA	642
QY	1874	AGAACTTCAGGAGAGAGCTGGCTGCGTGGATAAGGAAATTGAGATCCGGAATGCAAAAGC	1933
Db	641	AGAACTTCAGGAGAGAGCTGGCTGCGTGGATAAGGAAATTGAGATCCGGAATGCAAAAGC	582
QY	1934	TGGACATGCCCTACGAGTACCTGGCGCCAGCGTGTGGAACACAGTGTGGCCATCTAAG	1993
Db	581	TGGACATGCCCTACGAGTACCTGGCGCCAGCGTGTGGAACACAGTGTGGCCATCTAAG	522
QY	1994	CCTCGCCACCCCTTTGGTTATTTTCAGCCGCCCATCACCCCAAGCCACAAAGCTGACCCCTTCGT	2053
Db	521	CCTCGCCACCCCTTTGGTTATTTTCAGCCGCCCATCACCCCAAGCCACAAAGCTGACCCCTTCGT	462
QY	2054	GTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCAATGTCACCCCTCCCTAGAGGG	2113
Db	461	GTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCAATGTCACCCCTCCCTAGAGGG	402
QY	2114	GCACCTTTTCATGTCTCTGACCCAGTGACACATTTTACTCTAGAGGCATCACCTGGG	2173
Db	401	GCACCTTTTCATGTCTCTGACCCAGTGACACATTTTACTCTAGAGGCATCACCTGGG	342
QY	2174	ACCTTACTCCTCTTTCCCTTCTCTTCTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCT	2233
Db	341	ACCTTACTCCTCTTTCCCTTCTCTTCTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCT	282
QY	2234	TTCCTCATTCAGATCTATATGGCAAAATAGCCCAATATATAAATCAATTCAAAGACTAGA	2293
Db	281	TTCCTCATTCAGATCTATATGGCAAAATAGCCCAATATATAAATCAATTCAAAGACTAGA	222
QY	2294	ATAGGGGATATATACATATTTACTCCACACCTTTTATGAATCAATATGATTTTTTTGT	2353
Db	221	ATAGGGGATATATACATATTTACTCCACACCTTTTATGAATCAATATGATTTTTTTGT	162
QY	2354	TGTTGTTAAGACAGAGTCTCCTTTTGACACCCAGGCTGA	2393
Db	161	TGTTGTTAAGACAGAGTCTCCTATGTTGCCCTAGGCTGA	122

Search completed: July 19, 2005, 21:20:53
Job time : 5557.35 secs

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result	No.	Score	Query Match	Length	DB	ID	Description
	1	2671	100.0	2671	6	CQ776413	Sec0776413
	2	2671	100.0	2671	9	HUMLOX15A	M23892 Humara
	3	2671	100.0	2671	11	G28561	G28561 SHGO
	4	2669.4	99.9	2707	9	BC029032	HonBC029032
	5	2644.2	99.0	2844	6	AX535974	SecAX535974
	6	1640.4	61.4	2881	4	FIGLOX12A	FIGLOX12A
	7	1583.6	59.3	2884	4	BOV1ZLLIP	M81320 Bos t
	8	1583.6	59.3	2884	4	BOV1ZLLPOX	M62516 Bovini
	9	1511.6	56.6	2897	4	S96247	S96247 12-1
	10	1480.6	55.4	2777	4	OC121IIP	Z977654 Oryct
	11	1465.8	54.9	3614	4	RABCS15L	M27214 Oryct
	12	1316.6	49.3	2216	10	S69383	S69383 12-1
	13	1306	48.9	2048	10	RATLIPPOX	LO6040 Rati
	14	1299.8	48.7	2482	10	BC081546	BC081546 M
	15	1299.8	48.7	2485	10	EC056625	EC056625 M
	16	1275.2	47.7	2413	10	MUS1ZLLIPOX	L34570 Mus
	17	1272	47.6	1992	6	CQ777329	SecCQ777329
	18	1272	47.6	1992	10	MMU04331	MusU04331
	19	1058.2	39.6	2237	10	MMU39200	MusU39200

Db	181	CTGCTGTTTGTGAAACTGCGCCAAACCGGCACCTCTCTTAAGGACGACGCGCTGGTTCTTGCAC	240
Qy	241	TGATCTCTCTGACGGGCCCCGAGCGGGGACGAGGTCAAGTTTCCCTTGTATACCGCTCG	300
Db	241	TGATCTCTCTGACGGGCCCCGAGCGGGGACGAGGTCAAGTTTCCCTTGTATACCGCTCG	300
Qy	301	GTGAGGGCAACCGCGTCTTGAGCGCTCTGAAAGGCAACCGGCCGCACTGTGGGCGAGGAC	360
Db	301	GTGAGGGCAACCGCGTCTTGAGCGCTCTGAAAGGCAACCGGCCGCACTGTGGGCGAGGAC	360
Qy	361	CCTCAGGGCTGTTCCAGAAACACCGGGAAGAGCTGGAGAGAGAGGATGTTAT	420
Db	361	CCTCAGGGCTGTTCCAGAAACACCGGGAAGAGCTGGAGAGAGAGGATGTTAT	420
Qy	421	CGTGGGAACTGGAAGGACGGTTAATCTCGAATATGCTGGGCGCAACTATATGAC	480
Db	421	CGTGGGAACTGGAAGGACGGTTAATCTCGAATATGCTGGGCGCAACTATATGAC	480
Qy	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGATTGACTTTGAGGTTTCGTGGCC	540
Db	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGATTGACTTTGAGGTTTCGTGGCC	540
Qy	541	AAGGGCTGCGGACCTCGCTATCAAAAGACTCTCTAAATGTTCTGACTTCTCTGGAAGGAT	600
Db	541	AAGGGCTGCGGACCTCGCTATCAAAAGACTCTCTAAATGTTCTGACTTCTCTGGAAGGAT	600
Qy	601	CTAGTACATTTCAACCGGATTTTCTGCTGTGGTCAGAGCAAGCTGCTGAGCGCTGCCG	660
Db	601	CTAGTACATTTCAACCGGATTTTCTGCTGTGGTCAGAGCAAGCTGCTGAGCGCTGCCG	660
Qy	661	GACTCTCTGGAAGGAATGCTTATTTGGGTACAGGTTTCTTAATGGCGCAACCCCGTG	720
Db	661	GACTCTCTGGAAGGAATGCTTATTTGGGTACAGGTTTCTTAATGGCGCAACCCCGTG	720
Qy	721	GTGCTGAGCGCTCTGCTCACTTCTGCTCGCTAGTGTTTCCCTCCAGGCATGGAAGAA	780
Db	721	GTGCTGAGCGCTCTGCTCACTTCTGCTCGCTAGTGTTTCCCTCCAGGCATGGAAGAA	780
Qy	781	CTGAGCGCCAGCTGGAGAGGAGCTGGAGGAGGCACACTGTTCCGAAGCTGACTTCTCC	840
Db	781	CTGAGCGCCAGCTGGAGAGGAGCTGGAGGAGGCACACTGTTCCGAAGCTGACTTCTCC	840
Qy	841	CTGCTGATGGGATCAAGGCGCAACGTCATTTCTGTAGCCAGCAGCACCTGGCTGCCCT	900
Db	841	CTGCTGATGGGATCAAGGCGCAACGTCATTTCTGTAGCCAGCAGCACCTGGCTGCCCT	900
Qy	901	CTAGTCATGTGAAATTCGACGCTGATGGGAAACTCTTTGCCCATGTCATCAGCTCCAG	960
Db	901	CTAGTCATGTGAAATTCGACGCTGATGGGAAACTCTTTGCCCATGTCATCAGCTCCAG	960
Qy	961	CTGCCCCGACAGGATCCCCACCTCTTCTGCTCAGGATCCCCCAATGGCC	1020
Db	961	CTGCCCCGACAGGATCCCCACCTCTTCTGCTCAGGATCCCCCAATGGCC	1020
Qy	1021	TGGCTTCTGCGAAATCTGGGTGCGCAGCTCTGACTTCCAGTCCATGAGCTGCAGTCT	1080
Db	1021	TGGCTTCTGCGCAATCTGGGTGCGCAGCTCTGACTTCCAGTCCATGAGCTGCAGTCT	1080
Qy	1081	CATCTTCTGAGGGACACTTGATGGCTGAGGTCATTTGTCGCCACCATGAGGTGCTG	1140
Db	1081	CATCTTCTGAGGGACACTTGATGGCTGAGGTCATTTGTCGCCACCATGAGGTGCTG	1140
Qy	1141	CCGTGCGATACATCTCTATCTTCAAGCTTTAATTTCCCACTTGGGATACCCCTGGAAATT	1200
Db	1141	CCGTGCGATACATCTCTATCTTCAAGCTTTAATTTCCCACTTGGGATACCCCTGGAAATT	1200
Qy	1201	AACGTTCGGGCGAGCTGGGCTGCTCTGACATGGGAATTTTCGACCAGATAATGAGC	1260
Db	1201	AACGTTCGGGCGAGCTGGGCTGCTCTGACATGGGAATTTTCGACCAGATAATGAGC	1260
Qy	1261	ACTGGTGGGGAGCCACGTGCAGCTCTCAAGCAAGCTGGAGCTTCTTAACTCAGC	1320
Db	1261	ACTGGTGGGGAGCCACGTGCAGCTCTCAAGCAAGCTGGAGCTTCTTAACTCAGC	1320

Qy	1321	TCCTTCTGTCCTCCCTGATGACTTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCCCTTC	1380
Db	1321	TCCTTCTGTCCTCCCTGATGACTTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCCCTTC	1380
Qy	1381	TATGCCCAAGATCGCTCGGGCTCTCGGAAATCATCTATCGTATGTCGGAAGAAATCGTG	1440
Db	1381	TATGCCCAAGATCGCTCGGGCTCTCGGAAATCATCTATCGGTAATGTGGAGAAATCGTG	1440
Qy	1441	AGTCTCCACTATAAGACAGACGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGT	1500
Db	1441	AGTCTCCACTATAAGACAGAGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGT	1500
Qy	1501	CGAGAGATCACTGAATTCGGGCTGCAAGGGGCCACGAGCGAGGGTTTCTGTCTCTTTA	1560
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Qy	1561	CAGGCTCGGACACAGGTTTGCCACTTTGTCAACCATGTGTATCTTCACTGCACCGGCCAA	1620
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Qy	1621	CAGCCTCTGTGCACTCTGGGCGAGCTGGAATGTGTACTCTTGGGTGCTTAATGCACCTGTC	1680
Db	1621	CAGCCTCTGTGCACTCTGGGCGAGCTGGAATGTGTACTCTTGGGTGCTTAATGCACCTGTC	1680
Qy	1681	ACGATCGGCTGCCCGGCCAACCCACCAAGGATGCAACGCTGAGACAGTGTATGGCGGACA	1740
Db	1681	ACGATCGGCTGCCCGGCCAACCCACCAAGGATGCAACGCTGAGACAGTGTATGGCGGACA	1740
Qy	1741	CTGCCCAAATTCCACACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAGACGC	1800
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Qy	1801	CAGCCCGTTATGTTGCTGTGGGCGAGCATGAGGAGGATATTTTTCGGGCCCTGAGCCT	1860
Db	1801	CAGCCCGTTATGTTGCTGTGGGCGAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCCT	1860
Qy	1861	AAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTGGCTGCCCTGGATAAGGAAATTGAGATC	1920
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Qy	1921	CGAAATGCAAACTGAGCATGCCCCTACGAGTACTCTGGGCCCGCAGGTGTGTGGAAAAACAGT	1980
Db	1921	CGAAATGCAAACTGAGCATGCCCCTACGAGTACTCTGGGCCCGCAGGTGTGTGGAAAAACAGT	1980
Qy	1981	GTGCGCATCTAAGCTCGCCACCTTTTGGTTATTTTCAGGCCCCCATCACCCAGGCCACAAG	2040
Db	1981	GTGCGCATCTAAGCGTGCACCCCTTTTGGTTATTTTCAGCCCCCATCACCCAGGCCACAAG	2040
Qy	2041	CTGACCCCTTCGTGGTTATAGCCCTCCCAAGTCCCAAGTCCCAAGTCCCAAGTGTGCCAC	2100
Db	2041	CTGACCCCTTCGTGGTTATAGCCCTCCCAAGTCCCAAGTCCCAAGTGTGCCAC	2100
Qy	2101	CCTCCCTAGAGGGGCACTTTTCATGGTCTCTGCAACCGAGTGAACATTTTACTCTAGA	2160
Db	2101	CCTCCCTAGAGGGGCACTTTTCATGGTCTCTGCAACCGAGTGAACATTTTACTCTAGA	2160
Qy	2161	GGCATCACCTGGGACCTTACTCTCTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220
Db	2161	GGCATCACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220
Qy	2221	TCCT	2280
Db	2221	TCT	2280
Qy	2281	TTTTCAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAT	2340
Db	2281	TTTTCAGACTAGAAATAGGGGGATATAATACTATTACTCCACACCTTTTATGAATCAAT	2340
Qy	2341	ATGATTTTTTTTGTGTTTGAAGACAGAGTCTCACTTTTGACCCAGGCTGGAGTGCAGT	2400
Db	2341	ATGATTTTTTTTGTGTTTGAAGACAGAGTCTCACTTTTGACCCAGGCTGGAGTGCAGT	2400

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Db 2401 GGTGCAATCACACGGCTCACTGAGCCTCAGCGCTCGGGCTCAAAATGATCCTCCAC 2460
QY 2461 TCAGCCTCCTGAGTAGTGGGACTACAGGCTCATGCCATCATGCCAGCTAATATTTTT 2520
Db 2461 TCAGCCTCCTGAGTAGTGGGACTACAGGCTCATGCCATCATGCCAGCTAATATTTTT 2520
QY 2521 TATTTTCGTGGAGAGCGGGCCTCATTATGTTGCCCTAGGCTGGAATAGATTTGAACC 2580
Db 2521 TATTTTCGTGGAGAGCGGGCCTCATTATGTTGCCCTAGGCTGGAATAGATTTGAACC 2580
QY 2581 AAATTTGAGTTTAACTAATAAAGTTGTTTACCTTAAAGATGGAAGAACTAGGAC 2640
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Db 2641 TGAATCTATTTTAAATAATATTGCAAAAG 2671

RESULT 2
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LOCUS Human 15-lipoxygenase mRNA, complete cds.
DEFINITION M23892
ACCESSION M23892.1 GI:187190
VERSION 15-lipoxygenase.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2671)
Signal.E., Craik.C.S., Highland.E., Grunberger.D., Costello.L.L.,
Dixon.R.A. and Nadel.J.A.
Molecular cloning and primary structure of human 15-lipoxygenase
Biochem. Biophys. Res. Commun. 157 (2), 457-464 (1988)
89076270
MEDLINE 3202857
PUBMED
COMMENT Original source text: Human reticulocyte, cDNA to mRNA, clone
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Query Match 100.0%; Score 2671; DB 9; Length 2671;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 AACACAGTGTGAGCTGTGGCTGGCCAGCACGCGGAGGCGCGCTCGGGAAGCAGCTG 120
121 TGGCCCGCACGGGCGAGGACACAGAACTCAAGGTGGAAGTACCGAGTATCTGGGGCG 180
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301 GTGAGGGCAACGGGCTCTGAGCCTGCTCAAGGACCGGCGGCACTGTGGGCGAGGAC 360
301 GTGAGGGCAACGGGCTCTGAGCCTGCTCAAGGACCGGCGGCACTGTGGGCGAGGAC 360
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QY	1201	AAGCTCCGGCCAGGACTGGCTGGTCTCTGACATGGGAATTTTCACAGATATATGAGC	1260
Db	1201	AAGCTCCGGCCAGGACTGGCTGGTCTCTGACATGGGAATTTTCACAGATATATGAGC	1260
QY	1261	ACTGGTGGGGAGGCCACAGCTGACGTGCTCAAGCAAGCTGGAGCTTCCTAACCTACAGC	1320
Db	1261	ACTGGTGGGGAGGCCACAGCTGACGTGCTCAAGCAAGCTGGAGCTTCCTAACCTACAGC	1320
QY	1321	TCCTTCTGTCCTCCCTGATGACTTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCCTTC	1380
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QY	1381	TATGCCAAGATCGCTGGGCTCTGGGAAATCATCTATCGGTATGTGGAGGATCGTG	1440
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QY	1681	ACGATGGGCTGCCCGCCCAACCAAGGATGCAACGCTGGAGACAGTGTATGGGACA	1740
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QY	1801	CAGCCCTTATGTGGCTGTGGCCAGCATGAGGAGTATTTTCGGGCCCTGAGCCT	1860
Db	1801	CAGCCCTTATGTGGCTGTGGCCAGCATGAGGAGTATTTTCGGGCCCTGAGCCT	1860
QY	1861	AAGGCTGTGTAAGAAAGTTTCAGGAGGAGCTGGCTGCCCTGGATAGGAAATTTGAGATC	1920
Db	1861	AAGGCTGTGTAAGAAAGTTTCAGGAGGAGCTGGCTGCCCTGGATAGGAAATTTGAGATC	1920
QY	1921	CGAATGCAAGCTGAGCATGCCCTACAGTACTCTGGGCCACAGCTGGTGGAAACAGT	1980
Db	1921	CGAATGCAAGCTGAGCATGCCCTACAGTACTCTGGGCCACAGCTGGTGGAAACAGT	1980
QY	1981	GTGGCCATCTAAGCGTCGACACCTTTGGTTATTTTACGCCCCCATCACCCCAAGCAAG	2040
Db	1981	GTGGCCATCTAAGCGTCGACACCTTTGGTTATTTTACGCCCCCATCACCCCAAGCAAG	2040
QY	2041	CTGACCCCTTCTGGTGTATAGCCCTTCCCAAGTCCCAACCTCTTCCCATGTGCCAC	2100
Db	2041	CTGACCCCTTCTGGTGTATAGCCCTTCCCAAGTCCCAACCTCTTCCCATGTGCCAC	2100
QY	2101	CCTCCCTAGAGGGCACCTTTTATGTCTCTGACCCAGTGAACATTTTACTCTAGA	2160
Db	2101	CCTCCCTAGAGGGCACCTTTTATGTCTCTGACCCAGTGAACATTTTACTCTAGA	2160
QY	2161	GGCATCACCTGGGACCTTACTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220
Db	2161	GGCATCACCTGGGACCTTACTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220

QY	2221	TCT	2280
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QY	2281	TTTCAAGACTAGAAATAGGGGATATAAATACATATTTACTCCACACCTTTTATGAATCAAAAT	2340
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RESULT 3

G28561
LOCUS SHGC-35280 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G28561
ACCESSION G28561.1 GI:1408376
VERSION
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2671)
AUTHORS Olivier, M. and Cox, D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TGGTATAGCCCTGCCCTC
Primer B: GTGGCTATTTGCCATATAGATCTG
STS size: 214
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:									
MgCl2:		2.5 mM							
KCl:		50 mM							
Tris-HCl:		20 mM							
pH:		8.3							
Prepared with primer pairs provided by Sandoz, derived from M23892									
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Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	AACCAAGTGCACCTGTGGCTGGTGGCCAGCACCGGGAGGCGGCGCTCGGGAAGCAGCTG	120						
Db	61	AACCAAGTGCACCTGTGGCTGGTGGCCAGCACCGGGAGGCGGCGCTCGGGAAGCAGCTG	120						
QY	121	TGGCCCGCACGGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTTGGGGCCG	180						
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QY	181	CTGCTGTTTGTGAACCTCGCAACCGGCACCTCTTAAAGGACGACGCTGTGTTCTGCAAC	240						
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QY	241	TGGATCTCTGTGACGGGCGCGGAGCCGGGACAGAGTCAGGTTCCCTTGTATACCGCTGG	300						
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QY	301	GTGGAGGGCAACGGGTCTGAGCTGCTCAAGGCAACCGGCGCATGTGGGCGGAGGAC	360						
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QY	361	CTCAGGGCGCTTCCAGAAACACCGGGAAGAGAGCTGGAAAGAGAGAGAAAGTTGTAC	420						
Db	361	CTCAGGGCGCTTCCAGAAACACCGGGAAGAGAGCTGGAAAGAGAGAGAAAGTTGTAC	420						
QY	421	CGGTGGGAAACTGGAAGGACGGGTAAATCTGAATATGGCTGGGGCAAACCTATATGAC	480						
Db	421	CGGTGGGAAACTGGAAGGACGGGTAAATCTGAATATGGCTGGGGCAAACCTATATGAC	480						
QY	481	CTCCCTGTGGATGACGGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC	540						
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QY	541	AAGGGCTGGCGGACCTCGCTATCAAGACTCTCTAAATGTTCTTGACTCTGCGAAGGAT	600						
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QY	601	CTAGATGACTTCAACCGGATTTCTGGTGTGGTCAAGCAAGCTGGCTGAGCGCGTCGG	660						
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RESULT 4
LOCUS   BC029032
DEFINITION Homo sapiens arachidonate 15-lipoxygenase, mRNA (cDNA clone
ACCSSION BC029032
VERSION   BC029032.1 GI:20809660
KEYWORDS MGC.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2707)
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AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerf, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2707)

Strausberg, R.

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulesed, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 50 Row: a Column: 3

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502054.

FEATURES

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gene

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2670; Conservative 0; Mismatches 1; Indels 0;

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RESULT 6

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LOCUS Pig arachidonate 12-lipoxygenase mRNA, complete cds.

DEFINITION M31417 GI:164536
arachidonate 12-lipoxygenase; lipoxygenase.
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (Bases 1 to 2881)
Yoshimoto, T., Suzuki, H., Yamamoto, S., Takai, T., Yokoyama, C. and
Tanabe, T.

TITLE Cloning and sequence analysis of the cDNA for arachidonate
12-lipoxygenase of porcine leukocytes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (6), 2142-2146 (1990)
MEDLINE 90192763
PUBMED 2315307

COMMENT Original source text: Porcine leukocyte, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by S.Yamamoto, 17-JAN-1990.

FEATURES

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14. .2005

mRNA

CDS

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ORIGIN

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Query Match      61.4%; Score 1640.4; DB 4; Length 2881;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1861; Conservative 0; Mismatches 346; Indels 3; Gaps 1;
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DEFINITION M81320 M61716
ACCESSION M81320.1 GI:162587
VERSION lipoxigenase.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 2884)
AUTHORS De Marzo, N., Sloan, D.L., Dicharry, S., Highland, E. and Sigal, E.
TITLE Cloning and expression of a new isoform of 12-lipoxygenase:
Evidence that the enzyme from bovine tracheal epithelium is the
homologue of the human 15-lipoxygenase
JOURNAL Unpublished (1991)
COMMENT Original source text: Bos taurus trachea cDNA to mRNA.
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ACCESSION S96247
VERSION S96247.1 GI:246172
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Bovinae; Bos
1 (bases 1 to 2897)
De Marzo,N., Sloane,D.L., Dicharry,S., Highland,E. and Sigal,E.
Cloning and expression of an airway epithelial 12-lipoxigenase
Am. J. Physiol. 262 (2 Pt 1), L198-L207 (1992)
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		Db	1563 CTACAGTCAAGGACCGAGCTTTGCCACTTTGTGACCATGTATCTTACCTGACCTGGT	1622
		Qy	1618 CAACAGCTCTGTGCACTGCGGCGAGCTGAGTGTACTCTTGGGTGCTTAATGACCC	1677
		Db	1623 CAGACTCTCTCACTCACTGCGGCGAGCTGAGTGTACTCTTGGGTGCTTAATGACCC	1682
		Qy	1678 TGCAGATCGGCTGCCCGCCCAACCAAGGATGCAACGCTGAGACAGTGTGGCG	1737
		Db	1683 TGCAATCGGCTGCCCGCCCAACCGACCAAGGATGTGACACTGGAGAAAGTGTGGCA	1742
		Qy	1738 ACCTGCCCAACTTCCACAGGCTTCTTCCAGATGTCCATCTTGGCAGCTGGGCGA	1797
		Db	1743 ACCTGCCCAACTTCCATCAGGCTTCTTCCAGATGTCCATCTTGGCAGCTGGGCGA	1802
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Query Match	56.6%; Score 1511.6; DB 4; Length 2897;			
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Matches 1716; Conservative	0; Mismatches 319; Indels 3; Gaps 1;			
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Qy	181 CTGCTGTTTGTGAACTGCGCAACCGGCACCTCTTAAAGACACGCGCTGTTCTGCAAC	240		
Db	183 CTGCTGTTGTTGAAATTCGCAACCGGCACCTCTCTCGGATGATGCTGTGTTCTGCAAC	242		
Qy	241 TGGATCTGTGACGGGCGCGGAGCC --- GGGGACGAGTCAAGTTCCTTGTTCACGC	297		
Db	243 TGGATCTCCGTGCGAGGCGCGCGGCGCAGTGGGAAACAGTTCAGGTTCCGCTGCTATCGC	302		
Qy	298 TGGGTGAGGCGACGCGCTCTGAGCTGCTGAGGCGACCGCGCAGCTGTGGGCGAG	357		
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Qy	478 GACCTCCTGTGATGAGCGATTTCTGGAAGACAGAGAGTTCAGCTTGAAGTTTCGCTG	537		
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Db	543 ACCAAGGGGTGGCGCACCTAGCCATCAAAAGACTCTTTAAACATTTCTGACTTCTGGA	602		
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Db 1863 CCCAAGGCTGTGCTAAAGAAGTTTACGGAGGAGCTGGCTCCCTTGGAAAAGACATAGAG 1922
Qy 1918 ATCCGAATGCAAAAGCTGACATGCTTACGAGTACCTCGGGCCGACGCTGGTGGAAAC 1977
Db 1923 ATCCGGAATGCCAGCTGAGCTGGCTACGAAATACCTCGGCCCGACGCTGGTGGAAAC 1982
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RESULT 10
OC12LIP 2777 bp mRNA linear MAM 11-JUN-1998
LOCUS Oryctolagus cuniculus mRNA for 12-lipoxygenase.
DEFINITION 297654
ACCESSION 297654
VERSION 1
KEYWORDS 12-lipoxygenase.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1
AUTHORS Berger M., Schwarz K., Thiele H., Reimann I., Huth A.,
Borgraber S., Kuhn H. and Thiele B.J.
TITLE Simultaneous expression of leukocyte-type 12-lipoxygenase and
reticulocyte-type 15-lipoxygenase in rabbits
J. Mol. Biol. 278 (5), 935-948 (1998)
MEDLINE 98263260
PUBMED 9600854
REFERENCE 2 (bases 1 to 2777)
AUTHORS Thiele B.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1997) Institute of Biochemistry, University
of Clinics Charite, Humboldt-University, Hessische Str 3-4, Berlin
D-10115, Germany
COMMENT Related sequence: Cell 89:597-606 (1997).
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/cell_type="monocytes"
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15..2006
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polya_signal
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ORIGIN

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Query Match 55.4%; Score 1480.6; DB 4; Length 2777;
Best Local Similarity 80.5%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 424; Indels 9; Gaps 4;

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Db 12 AAGATGGGTGTCTATCGCGCTCTGCGGTGTCCACCGGGGCTCGATCTAGCGGGCTCCAAA 71
Qy 61 AACCAAGGTGACGCTGTGGCTGGTCCGCCAGACCGGGAGGGCGCGCTCGGGAAGGACATG 120
Db 72 AACAAAGTGGAGCTGTGGCTGGTGGCCAGCAGCGAGAGGTGGAGCTCGGTCGTCCTG 131
Qy 121 TGGCCCGCACCGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCGG 180
Db 132 CGGCCCTCACGMAACAAGGAGGAGGAATCAAGGTGAACGTTTCCAAAGTACCTGGGATCG 191
Qy 191 CTGCTGTTTGTGAACCTGGGCAACCGGCACCTCTTAAAGGACGACGCTGGTTCGCAAC 240
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Qy 241 TGGATCTCTGTGACGGGCCCGGAGCC--GGGGACGAGGTCAAGTTCCTTGTGTACCGC 297
Db 252 TGGATCTCTGTGACGGGCCCTCGGGCCGCTGAGGACAAGTACTGTTCCCGTGTACCGC 311
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Db 792 GAGCTGAGGCGGCTGGAGAGGAGCTCAAGGAGGAGCAGCTGTTTGAAGGCGGCTTC 851
Qy 838 TCCCTGTGATGAGATCAAGGCGCAACCTCAATCTCTGTAGCAGCAGCAGCAGCTGCTGCC 897
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Db 85 AACAAAGTGGAGCTGTGGCTGTTGGCCAGCAGCGAGAGGTGGAGCTCGGGTCGTGCGCTG 144
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Qy 1918 ATCCGGAATGAAAGCTGGACATGCCCTTACGAGTACTTGGGCCCGAGGCTGGTGGAAAC 1977
Db 1945 GTCCGGAATGAAAGCTGGACATACCTTATGAGTACTTGGGCCCGAGCTTGTGGAGAAC 2004
Qy 1978 AGTGTGCCATCTAAGC 1994
Db 2005 AGTGTGCCATTTGAGC 2021

RESULT 12

S69383
LOCUS S69383 2216 bp mRNA linear ROD 23-SEP-1994
DEFINITION 12-lipoxygenase [rats, pineal glands, mRNA, 2216 nt].
ACCESSION S69383
VERSION S69383.1 GI:545793
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2216)
Hada, T., Hagiya, H., Suzuki, H., Arakawa, T., Nakamura, M., Matsumoto, S.,
Yoshimoto, T., Yamamoto, S., Azekawa, T., Morita, Y. et al.


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QY 1618 CAACAGCCTCTGTGACCTGGCCAGCTGGACTGGTACTCTTGGTGCTTAATGACCC 1677
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RESULT 13
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LOCUS Ratius norvegicus 12-lipoxygenase mRNA, complete cds.
DEFINITION
ACCESSION L06040
VERSION L06040.1 GI:205212
KEYWORDS lipoxygenase.
SOURCE Ratius norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2048)
AUTHORS Watanabe,T., Medina,J.F., Haeggstrom,J.Z., Radmark,O. and Samuelsson,B.
TITLE Molecular cloning of a 12-lipoxygenase cDNA from rat brain
JOURNAL Eur. J. Biochem. 212 (2), 605-612 (1993)
MEDLINE 93185682
PUBMED 844196
COMMENT Original source text: Rattus norvegicus (strain Sprague-Dawley) brain mRNA.
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Matches 1580; Conservative 0; Mismatches 435; Indels 3; Gaps 1;
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QY 61 AACAGGTGACGTGTGTGCTCGGCAGCACCGGGAGCGGCTCGGGAGCGACTG 120
Db 77 AACGAGGTCTACCTGTGTGGTTGGACAGCATGGAGAGGCATCTCTCGGGAAGCTGCTA 136
QY 121 TGGCCCGCACCGGCAAGGACAGAACTCAAGTGGAGTACCGGAGTATCTGGGGCG 180
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QY 181 CTGCTGTTTGTGAACCTGCGCAACCGGCACCTCTCTTAAGGACGACGCTGGTTCGCAAC 240
Db 197 CTGCTGTTCTAAGATGCGAATAATGGCATTTATCTACGGATGACGCTGGTTCGCAAC 256
QY 241 TGGATCTCTGTGAGGGCCCGGAGCC- - -GGGACGAGGTGAGGTTCCTTGTTCACGC 297
Db 257 TGGATTTCTGTAAGGGCCCGGAGACCAAGGATCAGAGTACATGTTCCCTCTGTTCACGA 316
QY 298 TGGGTGAGGGCAACGGGTCTCTGAGCTGCTGAAGSCACCGCGCAGTGTGGGCGAG 357
Db 317 TGGGTTCAGGGCAGAAAGCATCTGAGCCTCTCGAGGCACTGGCTGACCGCTGTGAA 376
QY 358 GACCTCAGGGCCTGTTCCAGAAACACCGGAAGAGAGCTGGGAAGAGAGAGAGTGTG 417
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Db	977	GAATGCCCCAAACTGGTCTACTCCACACCTATTTTACGCGCTCGATCCCCCAATG	Mus musculus arachidonate 15-lipoxygenase, mRNA (cdna clone		
Qy	1018	GCTGTGCTTGTGCCCCAAATGCTGGTGGCAGCTCTGACTTCAGTTCATGATGCTGCAAG	MGC:78162 IMAGE:3671948), complete cds.		
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Db	1097	GCTCATCTTGTGAGGGGACATTTGATGGCTGAGTCTTTGCTGTGGCCACCATGAGGTGC	Mus musculus (house mouse)		
Qy	1138	CTGCGCTGATATACCTCTTCAAGCTTATAATCCCACTCGGATACACCTGGAA	Mus musculus		
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Qy	1198	ATTAACTCCGGCCAGGACTGGCTGCTCTGACATGGGAATTTTCGACCAATGATG	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
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Qy	1258	AGCACTGGTGGGGAGCCAGCTGCAGCTCTCAAGCAAGCTGGAGCTTCTTAACCTAC	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,		
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			Direct Submission		
			Submitted (01-SEP-2004) National Institutes of Health, Mammalian		
			Gene Collection (MGC), Cancer Genomics Office, National Cancer		
			Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
			USA		
			NIH-MGC Project URL: http://mgc.nci.nih.gov		
			Contact: MGC help desk		
			Email: cgabbs@mail.nih.gov		
			Tissue Procurement: Jeffrey Green M.D.		
			cdna Library Preparation: Life Technologies, Inc.		
			cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
			DNA Sequencing by: Sequencing Group at the Stanford Human Genome		
			Center, Stanford University School of Medicine, Stanford, CA 94305		
			Web site: http://www-shgc.stanford.edu		
			Contact: (Dickson, Mark) mcd@paxil.stanford.edu		
			Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,		
			R. M.		
			Clone distribution: MGC clone distribution information can be found		
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Query Match      48.7%; Score 1299.8; DB 10; Length 2482;
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Title: US-10-688-676A-1

Perfect score: 2671

Sequence: 1 aagatgggtctctaccgcat.....aaataaaatttgcaaaag 2671

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1013.6	37.9	2343	3	US-09-641-638-652
2	1013.6	37.9	2343	4	US-10-170-097-423
3	382.6	14.3	2496	4	US-09-949-016-5821
4	382.6	14.3	2497	4	US-09-023-655-1155
5	382.6	14.3	2497	4	US-10-071-411A-3
6	382.6	14.3	2497	4	US-09-949-016-109
7	342.8	12.8	2685	3	US-09-061-768A-1
8	342.8	12.8	2685	4	US-09-764-246-1
9	342.8	12.8	2685	4	US-09-949-016-156
10	341.2	12.8	2674	4	US-09-949-016-3041
11	332	12.4	3384	4	US-09-547-435-29
12	330.4	12.4	2316	4	US-09-547-435-5
13	330.4	12.4	2701	4	US-09-547-435-1
14	327.8	12.3	2307	4	US-09-799-451-803
15	327.8	12.3	2604	4	US-09-547-435-23
16	318.6	11.9	432	3	US-09-641-638-435
17	318.6	11.9	432	4	US-10-170-097-435
18	303	11.3	3205	3	US-09-061-768A-3
19	303	11.3	3205	4	US-09-764-246-3
20	276	10.3	1383	4	US-09-547-435-11
21	276	10.3	1848	4	US-09-547-435-9
22	276	10.3	2316	4	US-09-547-435-27
23	274.2	10.3	2469	3	US-09-087-727-1
24	274.2	10.3	2469	4	US-09-853-053-1
25	274.2	10.3	2469	4	US-09-949-016-155
26	200.6	7.5	391	3	US-09-641-638-423
27	200.6	7.5	391	3	US-09-641-638-424

28	200.6	7.5	391	4	US-10-170-097-423	Sequence 423, App
29	200.6	7.5	391	4	US-10-170-097-424	Sequence 424, App
30	199.4	7.5	391	3	US-09-641-638-420	Sequence 420, App
31	199.4	7.5	391	3	US-09-641-638-421	Sequence 421, App
32	199.4	7.5	391	4	US-10-170-097-420	Sequence 420, App
33	199.4	7.5	391	4	US-10-170-097-421	Sequence 421, App
34	199	7.5	391	3	US-09-641-638-419	Sequence 419, App
35	199	7.5	391	3	US-09-641-638-422	Sequence 422, App
36	199	7.5	391	4	US-10-170-097-419	Sequence 419, App
37	199	7.5	391	4	US-10-170-097-422	Sequence 422, App
38	192.8	7.2	1441	4	US-09-547-435-13	Sequence 13, Appl
39	188.8	7.1	1005	4	US-09-547-435-7	Sequence 7, Appl
40	188.8	7.1	1470	4	US-09-547-435-3	Sequence 3, Appl
41	188.8	7.1	1938	4	US-09-547-435-25	Sequence 25, Appl
42	176.6	6.6	239	5	PCT-US93-08106-7	Sequence 7, Appl
43	176.6	6.6	239	5	PCT-US93-08106-8	Sequence 8, Appl
44	176.6	6.6	239	5	PCT-US94-00089-15	Sequence 15, Appl
45	176.6	6.6	239	5	PCT-US94-00089-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-641-638-652
; Sequence 652, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSSET 051Cp1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 652
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..39
; NAME/KEY: CDS
; LOCATION: 40..2031
; NAME/KEY: 3'UTR
; LOCATION: 2032..2343
; NAME/KEY: allele
; LOCATION: 366
; OTHER INFORMATION: 10-343-231 : deletion of C
; NAME/KEY: allele
; LOCATION: 605
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 712
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 766
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 804
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G

[illegible]

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Db 1660 GCGCCATCAACAGGSCCAGCTGGTATGTCCTGGTCCCTAATGCTCCATGCACA 1719
QY 1684 ATGGGGTGGCCCGCCCAACACCAAG---GATGCAAGCTGGAGACAGTATGGCGACA 1740
Db 1720 ATGGGATGGCCCGCCCAACCAAGCAAGAAAGATGTGACGAGGCCACAGTATGGGGTCA 1779
QY 1741 CTGCCCCAATTCACACAGGCTTCTCCACAGATGCCATCACTGGCAGCTGGCGACAGCC 1800
Db 1780 CTACCTGATGTCGGCAGGCTGTCTTCAATGGCCATCTCATGGCATCTGAGTCGCCGC 1839
QY 1801 CAGCCCGTTATGTTGGCTGTGGCCAGCATGAGGAGGATATTTTCGGGCCCTGAGCCT 1860
Db 1840 CAGCCAGACATGTGCTCTGGGGCCACCAAGAAATATTTCTCAGGCCCAAGCCC 1899
QY 1861 AAGCTGTGCTGAAGAAGTTCCAGGAGGAGCTGGCTGCCCTGATAGAAATTTGATC 1920
Db 1900 AAGCTGTGCTAAACCAATTTCCAGACAGATTTGGAAGAGCTGGAAGGAGATTACAGCC 1959
QY 1921 CGGAATGCAAGCTGGACATGCTCAGAGTACCTCGGCCAGCGTGGTGGAAACAGT 1980
Db 1960 CGGAATGAGCACTTGACTGGCCCTATGAATATCTGAAGCCAGCTGCATAGAGAACAGT 2019
QY 1981 GTGCCCATCTAAGC 1994
Db 2020 GTCAACCATCTGAGC 2033

RESULT 2
US-10-170-097-652
; Sequence 652, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T14XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 652
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..39
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..2031
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 2032..2343
; FEATURE:
; NAME/KEY: allele
; LOCATION: 366
; OTHER INFORMATION: 10-343-231 : deletion of C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 605
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; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 712
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 766
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 804
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 821
; OTHER INFORMATION: 10-347-220 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1004
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1049
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1123
; OTHER INFORMATION: 10-349-216 : deletion of CTG
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1131
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1491
; OTHER INFORMATION: 10-507-170 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1742
; OTHER INFORMATION: 10-340-112 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1760
; OTHER INFORMATION: 10-340-130 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1941
; OTHER INFORMATION: 10-341-116 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 2144
; OTHER INFORMATION: 10-341-319 : polymorphic base C or T
; US-10-170-097-652

Query Match 37.9%; Score 1013.6; DB 4; Length 2343;
Best Local Similarity 69.2%; Pred. No. 2.9e-261;
Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGGTCTTACCGCATCCGGGTGTCACCTGGGGCTCGCTCTATGCCGGTTCCCAACAC 63
Db 40 ATGGGCCGCTACCGCATCCGGTGGCCACCGGGGCTGGCTCTTCTCCGGGTCGTACAC 99
QY 64 CAGGTGCAGCTGTGGCTGGTCCGCCAGCACCGGGAGGCGCGCTCGGGAAGGACTGTGG 123
Db 100 CGCTGCAGCTTTGGCTGGTGGGACGCGCGGGAGGCGGAGCTGCAGCTGCGG 159
QY 124 CCGCACCGGGCAAGGAGACAGAACTCAAGTGGGAAGTACCGGAGTATCTGGGGCGCTG 183
Db 160 CCGGGCGGGCGAGGAGGAGGTTTGTATCATGACGTTGCAGAGGACTTGGGGCTCCTG 219
QY 184 CTGTTTGTGAACCTGCGCAACGGCAGCTCTCTAAGGACGAGCGCTGTCTGCAACTGG 243
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Db 220 CAGTTCTGTGAGGCTGCGCAAGACCACTGGCTGGTGGACGACGCTGGTGTCTGCGACCGC 279
QY 244 ATCTCTGTGAGGCGCCCGGAGCGGGACAGGTCAGGTTCCCTTGTGTACCGCTGGGTG 303
Db 280 ATACCGTGCAGGGCCCTGGAGCCTGCGGAGGTGGCCCTCCCGTGTCTACCGCTGGGTG 339
QY 304 GAGGGCAACCGCTCTCTGAGCTGCTGAGCTGCTGAGGCAACCGCGCGCACTGTGGCGAGGACCCCT 363
Db 340 CAGGGCGAGGACATCTCTGAGCCTGCCGAGGGCACCGCGCGCTGCCAGGAGACAATGCT 399
QY 364 CAGGGCCTGTTCAGAAACACCGGGAAGAAGCTGGAGAGAGAGAGAGTTGTATCCGG 423
Db 400 TTGGACATGTTCCAGAGCATCAGAGAGAGAACTGAAAGACAGACAGCAGATCTACTGC 459
QY 424 TGGGGAACCTGGAAGGACGGTTTAAATCTCAATATGCTGGGGCCCAAACTATATGACCTC 483
Db 460 TGGGCCACCTTGGAGAGAGAGGTTTACCCCTGACCATCGCTGCACACCGTAAGAGATGATCTA 519
QY 484 CTTGTGGATGAGCGATTCTTGAAGACAAGAGAGTTGACTTTTGAGGTTTGGCTGGCCAAAG 543
Db 520 CCTCCAAATATGAGATTCCATGAGGAGAGAGGCTGGACTTTTGAATGGACACTGAAGGCA 579
QY 544 GGGCTGGCCGACCTGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAGGATCTA 603
Db 580 GGGGCTCTGGAGATGGCCCTCAACRTGTTTTACACCTCTGAGCTCTCTGGAACTGCCTA 639
QY 604 GATGACTTCAACCGGATTTTCTGTGTGGTCAGAGCAAGCTGCTGAGCGCTGCGGGAC 663
Db 640 GAAGACTTTGATCAGATCTTCTGGGCCAGAGAGTGCCCTGGCTGAGAGGTTTCCGCAG 699
QY 664 TCCTGGAAGGAAGATGCTTTATTTGGGTACAGTTTCTTAATGGCGCCCAACCCCGTGGTG 723
Db 700 TGTGGCAGGATGATGAGTTGTTTCACTACAGTTCTCTCAATGGTGCCAAACCCCATGCTG 759
QY 724 CTGAGGGCTCTGCTACCTTCTGCTGCTAGTGTTCCTCCAGGATGGAGGACTG 783
Db 760 TTGAGATGCTCGACTCTCTGCGCTCCAGGCTAGTGTGCTCCCTCGGGATGGAAGAGCTT 819
QY 784 CAGGCCAGCTGGAGAGGAGCTGGAGGGAGGACACTGTTTCAAGCTGACTTCTCCCTG 843
Db 820 CRGCTCACTGGAGAAAGAACTTCAGATGGTTTCCCTGTTGAGCTGACTTTCATCCTT 879
QY 844 CTGATGGATCAAGGCCAACGTCATTCTCTGTAGCAGCAGACCTGGCTGCCCTCTA 903
Db 880 CTGATGGAATTCAGGCCAACGTCATCCGAGGAGAGAACATACCTGGCTGCGCCCTC 939
QY 904 GTATGCTGAAATGACGCTGATGGGAACTCTTGCCCATGTCTCATCCAGCTCCAGCTG 963
Db 940 GTTATGCTGAAGATGGAGGCCCAATGGGAAGCTGCAGCCCATGTCTCATCCAGATTCAGCCT 999
QY 964 CCCGACAGGATCCCCACACCTCCCTTTTCTTGCTACGATCCCCCAATGGGCTGG 1023
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QY 1024 CTTCTGGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCATGAGCTGCACTCTCAT 1083
Db 1060 CTCTGGCAAGTCTGGTCCGAAATTCAGATTTCCACTGACGAGATCCAGTATCAC 1119
QY 1084 CTTCTGAGGGGACACTTGTATGCTGAGGTCAATGTTGTGGCCACCATGAGTGGCTGGCG 1143
Db 1120 TTGTGAAACACKACACTGGTGGTGGTTCATGCTGTGCGCCACCATGGGTGGCTCCCA 1179
QY 1144 TCGATACATCTTCTCAAGCTTATAATTTCCACCTGGGATACACCTCGGAAATTAAC 1203
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QY 1204 GTCCGGCCAGGACTGGGCTGGTCTGTGACATGGGAAATTTTTCGACCAAGATAATGAGCACT 1263
Db 1240 ACCGGGCCCGGACCCCAACTCATCTCAGATGGAGGAATTTTGTAAAGGCACTGAGCACA 1299
QY 1264 GGTGGGGGAGCCACGCTGAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGCTCC 1323
Db 1300 GGTGGAGGGGCCATGTACAGTTGCTCCGTGGGCGCAGCTCAGCTGACCTACTGCTCC 1359

QY 1324 TTCTGTCCCCTGATGACTTGGCCGACCGGGGGCTCTCTGGAGTGAAGTCTTCTTCTAT 1383
Db 1360 CTCTGTCTCTCTGACGACCTGGCTGACCGGGGCTCTCTGGAGTCCAGGCTGCTCTCTAT 1419
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QY 1444 CTCACATTAACAGACAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTCTCGA 1503
Db 1480 CTCCTTACCARAAGGATGACATAGTAGAGGGGACCTCTGAGCTGACGCTGGTCTCGG 1539
QY 1504 GAGATCACTGAAATCGGCTGCAAGGCCCGCAGGACCGAGGGTTTCTCTCTTTACAG 1563
Db 1540 GAGATCAGGAGTGGGCTGTGCCAGGCCAGGACCGAGGTTTCTCTCTCTCTCCAG 1599
QY 1564 GCTCGGGACAGGTTTGGCACCTTTGTCAACATGTGTATCTTCACTGCAACCGGCCAACAC 1623
Db 1600 TCCAGAGTCAACTCTGCCATTTCTCTCAACATGTGTCTTCACTGCACTGCCAGCAT 1659
QY 1624 GCTCTGTGCACCTGGGCCAGCTGGACTGGTACTCTTGGGTGCTTAATGCACCTCTGCACG 1683
Db 1660 GCGCANTCAACAGGCGCAGCTGACTGTGTATGCTGTGGTCCCTTAATGCTCCATGCACA 1719
QY 1684 ATGCGGCTGCCCGCCCAACCCCAAG---GATGCAACGCTGGAGACAGTGTGGCGACA 1740
Db 1720 ATGGGATGCCCGCCACCCACCAACCAAGGAAGATGTGACGAWGGCCACAGTGTGGGTCA 1779
QY 1741 CTGCCCACTTCCACAGGCTTCTCTCAGATGTCCATCACTTGGCAGCTGGCAGACGC 1800
Db 1780 CTACCTGATGTCCGCGAGGCTGTCTTCAATGGCCATCTCATGGCATCTGATGCTGCCGC 1839
QY 1801 CAGCCGTTATGTGCTGTGGCCAGCATGAGGAGGATTTTTCGGGCGCTGAGCCT 1860
Db 1840 CAGCCAGCATGTGCTCTGGGACCAACAAGAAATATTTCTCAGGCCCCAAGCCC 1899
QY 1861 AAGGCTGTCTGAAAGAAAGTTTCAGGGAGGAGCTGGCTGCCCTGGATGAAGAAATTTGAGATC 1920
Db 1900 AAAGCTGTCTAAACCAATTCGAAACAGATTTGGAAAGCTTGAAAGAGAGATTACAGCC 1959
QY 1921 CGAATGCAAGCTGGACATGCCCTACGAGTACTCTGGGCCAGCGCTGGTGGAAACAGT 1980
Db 1960 CGGAATGAGCAACTTGAATGAGTGGCTTATGAATATCTGAAGCCAGCTGCATAGAGAAAGT 2019
QY 1981 GTGGCCATCTAAGC 1994
Db 2020 GTCACCATCTGAGC 2033

RESULT 3

US-09-949-016-5821
; Sequence 5821, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5821
; LENGTH: 2496
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-5821

Query Match 14.3%; Score 382.6; DB 4; Length 2496;
Best Local Similarity 52.5%; Pred. No. 4.1e-92;
Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

QY	126	CGCAGGGGCAAGGACAGACAGAACTCAAGTGGGAGTACCGGAGTATCTGGGSCCGTGT	185
DB	183	CGAGCGTGGCGGTGGATTTACACGCTGACTGTGGACGAGGAACTGGGCGAGATCCA	242
QY	186	GTTTGTGAATTCGCAAAACGGCACCTCTTAAGGACGACGCTGTCTGCAACTGGAT	245
DB	243	GCTGTTCAGATTCGAGAGGCAAGTACTTGGCTGAATGACGACTGTACTGAGTACAT	302
QY	246	CTCTGTGCAAGGCCCCGAGACCGGGAACGAGTCAAGTTCCCTTTGATACCGTGGGTGA	305
DB	303	CACGCTGAAGACGCCC---CAGGGGACTACATCGAGTTCCCTGCTACCGCTGGATCAC	359
QY	306	GGCAACGGGCTCTGAGCTGCTGAAGGACCGGCGGACCTGTGGGCGAGGACCTCA	365
DB	360	CGCGGATGTCGAGGTTGTCTTGAAGGATGACGCGCAAAAGTTGGCCCGAGATGACCAAT	419
QY	366	GGGCTGTTTCCAGAAACACCGGAGAGAGCTGGAAGAGAGAAAGTTGTACCGGTG	425
DB	420	TCACATTTCAAGCAACACCGAGCTTAAGAACTGGAAACCGGCAAAACAATATGATG	479
QY	426	GGGAACTGGAAGGACGGGTTAATCTGAATATGGCTGGGGCCAACTATATGACCTCC	485
DB	480	GATGGAGTGGAAACCTCGGCTTCCCTTGAAGCATCGATGCAAAATGCCACAAGGATTTACC	539
QY	486	TGTGATGAGCATTTCTGGAGACAGAGATGATTTGAGGTTTCCTGGCCCAAGG	545
DB	540	CGTGAATATCCAGTTTGTAGTGAAGAAAGAGTGGACTTTGTCTGAATTTACTCCAAAGC	599
QY	546	GCTGGCCGACCTCGCTATCAAGACT---CTTAATATGTTCTGACTTGTGGAAGATCT	602
DB	600	GATGGAAACCTGTTTCAACCGCTTCAACGCTTCAATGACATGTTCCAGTCTTTTGAATGACTT	659
QY	603	AGATGACTTCAACCGGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	662
DB	660	CGCCGACTTGTGAATACTTTGTCAAGATCAGCAACACTATTTCTGAGCGGTGATGAA	719
QY	663	CTCTGGGAAGGATGCTTATTTGGGTACAGATTTCTTAATGGCGGCAACCCCGTGTG	722
DB	720	TCACTGGCAGGAAGACCTGATGTTTGGCTTACAGTTCTCTGAATGGGTGCAACCTGTGT	779
QY	723	GCTGAGGCGCTGTGCTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	776
DB	780	GATCCGGCGCTGCACAGAGCTGCCGAGAGCTTCCGCTGACCAAGGATGTTAGAGTG	839
QY	777	-----GGAACTGCAGGCCAGCTGGAGAGGAGCTGGAGGGAGGACACTGTTCGAAGC	830
DB	840	CAGCCTGGAGCGGAGCTCAGCTTGGAGCAGAGGTTCCAGCAAGGGAACATTTTCATCGT	899
QY	831	TGACTTCTCTGCTGGATGGAATCAAGGCAAGCTGCA---TTCCTGTAGCCAGCAGCA	887
DB	900	GGACTTTGAGCTGCTGGATGGATCGATGCCAACAACAGACCCCTGCACTCCAGTT	959
QY	888	CTTGGCTGCCCTCTAGTCACTGCAATTTGAGCTGATGGGAACTCTTCCCATGTT	947
DB	960	CTTGGCGCTCCCATCTGCTTGTATGAAGAACTTGGCCCAACAGATTTTCCCATTCG	1019
QY	948	CATCAGCTCCAGCTGCCCGCACAGGATCCCAACCACTCCCTTTTCTTGGCTTACGGA	1007
DB	1020	CATCCAGCTCAACCAATCCCGGAG-----ATGAGAACCTTATTTCTCCCTTCGA	1073
QY	1008	TCCCCCAATGGCTGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCCAGTCCA	1067
DB	1074	TGCAAAATACGACTGCTTTTGGCCAAATCTGGGTGCGCTTCCAGTGAATTCACGTTCA	1133
QY	1068	TGAGTGTGAGTCTCATCTTCTGAGGGGACACTTGTATGGCTGAGGTCATTTGTGGCCAC	1127
DB	1134	CCAGACCATCACCCACCTTCTGCAACACATCTGGTGTCTGAGGTTTTTGGCAATGCAAT	1193

RESULT 4

US-09-023-655-1155
; Sequence 1155, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart

QY	1128	CATGAGGTGCGTGGCTCGATACATCTTCAAGCTTATAATTCGCCACCTCGGATA	1187
DB	1194	GTACCGCCAGCTGCTGTGTGACCCCATTTTCAAGCTGTGTGGCACAGTGAGATT	1253
QY	1188	CACCTCTGGAATTAACGTCGCGGCCAGGACTGGGTGCTCTGTGACATGGGAATTTTGA	1247
DB	1254	CACCATTCGATCAACACCAAGGCCCTGTGAGCAGCTCATCTCGAGTGTGGCTCTTTGA	1313
QY	1248	CCAGATAATGACACTGTGTGGGGAGGCGACGTCGAGCTGTCTCAAGCAAGCTTGGAGCTTT	1307
DB	1314	CAAGGCCAACCCACAGGGGCGGTGGGACGTCGAGATGGTCAGAGGCCCATGAAGA	1373
QY	1308	CTTAACCTTACAGCTCTTCTGTCTTGTCCCTGTGATGACTTGGCGGACCGGGGCTCCTG	1362
DB	1374	CTGACCTATGCTCTCTCTGTCTTCCGAGGCCATCAAGGCCCGGGGCTATGGAGACAA	1433
QY	1363	---GGAGTGAAGTCTTCTTCTATGCCCAAGATCGCTCGGCTCTGGGAAATCATCTA	1418
DB	1434	AGAAGACATCCCTACTACTTCTACCGGAGACGCGGCTCTTGGTGTGGAAAGCATCAG	1493
QY	1419	TCGCTATGTGAAGGAATCGTGAGTCTCCACTATTAAGACAGACGCTGGCTGTGAAGACGA	1478
DB	1494	GACGTTACGCGCGAGGTGTGACATCTACTACGAGGCGGACGAGTGTGTGAGGAGA	1553
QY	1479	CCAGAGCTGACAGCCTGGTGTGAGAGATCACTGAATCGGCTGTGAAGGGGCCAGGA	1538
DB	1554	CCCGAGCTGACGAGACTTCGTGAACGATGTCTACGTGTACGCGATGCGGGGCGCAAGTC	1613
QY	1539	CCGAGGTTTCTGTCTTCTTACAGGCTCGGAGCAGGTTTGCACCTTGTTCACCATGTG	1598
DB	1614	CTCAGGCTTCCCAAGTCGGTCAAGGCGGAGCAGCTGTGCGAGTACCTGACCGTGTG	1673
QY	1599	TATCTTACCTGCACCGGCGCAACAGCCTCTGTGTGACCTGGGCGAGCTGGTGTGCTC	1658
DB	1674	GATCTTACCGCTTCCGCGCAGCAGCGCGGTCACTTTCGCGCAGTACGACTGTGCTC	1733
QY	1659	TGGGTGCTTAATGACCTTGCACGAGTGGGTGCGGCTGCGGCGGCGCAACCAAG---GATGC	1715
DB	1734	CTGGATCCCAATGCGGCCCAACCATCGAGCGCGCGCACCGACTGCGCAAGGGGTGCT	1793
QY	1716	AACGCTGAGACAGATGAGCGGACACTGCCCACTTCCACAGGCTTCTCTCCAGATGTC	1775
DB	1794	GACCATGAGCAGATCGTGGACAGCTGCGGCGGCGCGGCTCTCTGCGCATCTGGG	1853
QY	1776	CATCACTTGGCAGCTGGGCGAGACGCGCGCTTATGTGTGGTGTGGGCGAGCATGAGA	1835
DB	1854	TGCAGTGTGGGCTGTAGCAGTTCAGGAAACGAGCTGTCTTGGGATGTACCCAGA	1913
QY	1836	GGAGTATTTTGGGCGCTGTAGCCTTGAAGCTGTGCTGAAGAAAGTTTCAGGGAGGCTGGC	1895
DB	1914	AGAGCATTTTATCGAAGAGCTGTGAAGGAAGCCATGCGCGATTCGCAAGAACTCGA	1973
QY	1896	TGCCCTGATAAGGAAATGAGATCCGGAATGCAAGCTGACATGCCCTACGAGTACT	1955
DB	1974	GGCCATGTGACGCTGATTTGTGAGCGCAACAGAAAGAGCAGCTGCCATATTTACTACT	2033
QY	1956	GCGGCCAGCTGTGGGAAAACAGTGTGGCATCTAAGCGCTGCGCCACCTTTGGTTATTT	2015
DB	2034	GTCCCAAGACCGGATTCGAAACAGTGTGGCCATCTGAGCACAATGCGCAGTCTCACTGTGG	2093
QY	2016	CAGCCCCCATCACCACGACCAAG	2040
DB	2094	GAAGCCAGCTGCCCGACCCAGATG	2118

QY 1599 TATCTTCACTGACCGGCAACACGCTCTGTGTGACCTTGGGCGAGCTGGAGTGTACTC 1658
Db 1673 GATCTTCACTGCTCGCGCGAGCAGCGCGGTCAACTTTCGGCCAGTACGACTGGTGTCTC 1732
QY 1659 TTGGGTGCTTAATGACACCTGACGATGGGTGCTGCGCCCGCCCAACCAACG--GATGC 1715
Db 1733 CTGGATCCCAATGGCCCGCCCAACCAATGGAGCCCGCCACCGACTGCGCAAGGGGTGGT 1792
QY 1716 AACGCTGGAGACAGTGTATGGGACACTGCCCAACTTCCACAGGCTTCTCTCCAGATGTC 1775
Db 1793 GACCAATTGACGATGCTGTGACACGCTGCGCCGACCGCGCGCTCTCTGTGCTGATCTGGG 1852
QY 1776 CATCACTTGGAGCTGGGAGAGCGGAGCGCCGCTTATGTGGTGTGGGCGCCAGCATGAGGA 1835
Db 1853 TCGAGTGTGGGCGCTGAGCGAGTTCCAGGAAACAGAGCTGTTCCTGGGCAATGATCCCA 1912
QY 1836 GGAGTATTTTTCGGGCGCTGAGCCTAAGGCTGTGCTGAAGAGTTTCAGGAGGAGCTGCG 1895
Db 1913 AGAGCAATTTATCGAGAGCCTGTGAAGAGCCATGGCCGATTCGGCAAGAACTCGA 1972
QY 1896 TCCCTCGGATAAGGAATTTAGATCCGGAATGCAAGCTTGGACATGCCCTACGAGTACTC 1955
Db 1973 GGCCATTTGTACGCTGATTTGCTGAGCGCAACAAAGAGAGCAGCTGCCATATTAATCTACTT 2032
QY 1956 GCGGCCAGCGTGTGGGAAACAGTGTGGCCATCTAAGGTCGCCACCCCTTTGGTTATTT 2015
Db 2033 GTCCCGAGACCGGATTCGGAACAGTGTGGCCATCTGAGCACATCGCCAGTCTCACTGTGG 2092
QY 2016 CAGCCCCCATCAACCAAGCCACAAG 2040
Db 2093 GAAGCCAGCTGCCCGAGCCAGATG 2117

RESULT 5

US-10-071-411A-3

; Sequence 3, Application US/10071411A

; Patent No. 6797475

; GENERAL INFORMATION:

; APPLICANT: Glenn Barnes

; APPLICANT: Joanne Meyer

; TITLE OF INVENTION: Detection of Polymorphisms in the Human

; FILE OF INVENTION: 5-Lipoxygenase Gene

; FILE REFERENCE: MRI-021

; CURRENT APPLICATION NUMBER: US/10/071,411A

; CURRENT FILING DATE: 2002-02-07

; PRIOR APPLICATION NUMBER: 60/267,515

; PRIOR FILING DATE: 2001-02-08

; PRIOR APPLICATION NUMBER: 60/314,248

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2497

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-071-411A-3

Query Match

Best Local Similarity 52.5%; Score 382.6; DB 4; Length 2497;

Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

QY 126 CGCAGCGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGCGCGCTGCT 185
Db 182 CGAGCGTGGCGGTGGATTTCATACGATGCTGTGACGAGGAACCTGGGCGAGATCCA 241
QY 186 GTTGTGAACTGCGCAACCGCACCTCTTAAGACAGCGCTGTGCTGCACTGGAT 245
Db 242 GCTGTGCAATTCGAAAGCGCAAGTACTGGCTGAATGACGACTGGTACCTGGAATACAT 301
QY 246 CTCGTGACGGCCCGGAGCGGGAGCAGGTCAAGTTCCCTGTGTACCGCTGGGTGGA 305
Db 302 CACGCTGAAGACGCCCC--CACGGGACATACATCGAGTTCCCTGCTACCGCTGATCAC 358

QY 306 GGGCAACGCGCTCTGAGCCTGCTGAAAGGCACCGCGCGCACTGTGGGCGAGGACCTCTCA 365
Db 359 CGCGATCTCGAGGTGTCTCTGAGGGATGAGCGGCAAAAGTTGGCCGAGATGACCAAA 418
QY 366 GGGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAAAGATTCTACCGGTG 425
Db 419 TCACATCTCAAGCAACACCGACGTAAGAACTGGAACAACGCGCAAAACAATATCGATG 478
QY 426 GGGAACTTGAAGGACGGGTTAATTTCTGAATATGCTGGGCGCAAACTATATGACCTCCC 485
Db 479 GATGAGTGGAAACCTGCTGCTTCCCTTGAGCATCGATGCCAAAATGCCACAAGATTTACC 538
QY 486 TGTGATGAGGATTTCTGGAAGACAGAGAGTGTGACTTTGAGGTTTCGCTGGCCAAAGG 545
Db 539 CCGTATATCCAGTTTGTAGTGAAGAAAGGAGTGGACTTTGTTCTGAATATTAATCCAAAGC 598
QY 546 GCTGCCGACCTCGCTATCAAGACT---CTCTAAATGCTCTGACTTGTCTGGAAGATCT 602
Db 599 GATGAGAACTGTTTCACTCAACCGTTTCATGCAATGTCACATGTTCCAGTCTTCTTGAATGACTT 658
QY 603 AGATGACTTCAACCGGATTTTCTGCTGTGGTTCAGAGCAAGCTGGCTGAGCGGTGCGGA 662
Db 659 CGCGACTTTGAGAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGTTCATGAA 718
QY 663 CTCCTGGAAGGAAGATGCTTATTTGGGTACAGTTTCTTAATGGCGGCAACCCCGTGTG 722
Db 719 TCACCTGGCAGGAAGACCTGATGTTTGGCTACAGTTCTCTGAATGGCTGCAACCTGTGTT 778
QY 723 GCTGAGGCGCTCTGCTACCTTCTGCTCGCTAGTGTTCCTCCAGGACATGGA----- 776
Db 779 GATCGGCGCTGCAAGAGCTGCCGGAAGCTCCCGGTGACCAAGAGATGTTAGAGTG 838
QY 777 -----GGAACTGCGAGGCCAGCTGGGAAGAGAGCTGGAGGAGGACACACTGTTTCGAAGC 830
Db 839 CAGCTGGAGCGGAGCTCAGCTTGGAGCAGAGGTCCAGCAAGGAAACATTTTCATCGT 898
QY 831 TGACTTCTCCTGCTGGATGGATCAAGGCCAAGCTCA---TCTCTGTAGCCAGCAGCA 887
Db 899 GGACTTTGAGCTGTGGATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 958
QY 888 CCTGCTGCGCTCTAGTCACTGCTGAATTCAGCCTGATGGGAACCTTTCGCCCATGCT 947
Db 959 CTGCGCGCTCCCATCTGCTGTGTATAGAACTCTGGCCAAAGATGTGCCCATGTC 1018
QY 948 CATCAGCTCCAGCTGCCCCCGCACAGGATCCCACTCCCTCCCTTCTTCTGCTTACGGA 1007
Db 1019 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAACTTATTTCTCCCTTCGGA 1072
QY 1008 TCCCCCAATGGCTGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCCAGCTCA 1067
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QY 1068 TGAGCTGAGTCTCATCTTCTGAGGGGACACTTGTGCTGAGGTCTTGTGTGGCCAC 1127
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Db 1193 GTACCGCCAGCTGCTGCTGTGACCCCACTTTTCAAGCTGTGTGGTGGCAGCTGAGAT 1252
QY 1188 CACCTGGAATTAAGCTCGCGGCGCAGAGCTGGGCTGTCTCTGACATGGAATTTTCGA 1247
Db 1253 CACCATTTCAATCAACCAAGGCGGTGAGCAGCTCATCTGCGAGTGTGGCTCTTTTGA 1312
QY 1248 CCAGTATGAGCACTGTGGGAGGCGCAGCTGCTGCTCAAGCAAGCTGGAGCTT 1307
Db 1313 CAAGGCAACCGCCACAGGGGCGGTGGGACGTGAGATGCTGAGAGGCGCATGAAGGA 1372
QY 1308 CCTAACCTTACAGTCTCTTCTGCTCCCTCTGATGACTTGGCCGACCGGGGCTCTCTG- 1362
Db 1373 CTTGACCTATGCTCTCTCTGCTCTTCCGAGGCCATCAAGGCCCGGGGCGATGGAGCAA 1432
QY 1363 -----GGAGTGAAGTCTTCTCTATATGCCCAAGATGCGCTGCGGCTCTGGGAAATCATCTA 1418

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Db 1433 AGAAGACATCCCTACTTCTTACCGGACGACGGGCTCCTGGTGTGGAAAGCCATCAG 1492
Qy 1419 TCGGTATGTGGAAGGAATCGTGAAGTCTTCACTATAGACAGAGCTGGCTGTGAAGACGA 1478
Db 1493 GACGTTTACCGGCGGAGTGTGATGACATCTACTACGAGGGCGACCAAGTGTGGAGAGGA 1552
Qy 1479 CCAGAGCTGCAGACCTGTGTGAGAGATCACTGAAATCGGCTGCAAGGGGCCAGGA 1538
Db 1553 CCGGAGCTGCAGGACTTGTGACATGTCTACGTGTAGGATGCGGGCGGCAAGTC 1612
Qy 1539 CCGAGGTTTCTGTCTTCTTTACAGCTCGGACCAAGTTTGCCTTTTGTTCACCAATG 1598
Db 1613 CTGAGGCTTCCCAAGTCTGATGAGTCAAGAGCGGAGCAGCTGTGAGTACTGACCGTGT 1672
Qy 1599 TATCTTCACTGCACCGGCAACACGCTCTGTGACCTGGGCCAGCTGGAATGTTACTC 1658
Db 1673 GATCTTCAAGGCTTCCGCGCCAGCACCGCGGTCAACTTTCGGCCAGTACGACTGGTCTC 1732
Qy 1659 TTGGGTGCTTAATGACCTGTGACGATGCGGTGCTGCGCCGCAACCAAG---GATGC 1715
Db 1733 CTGGATCCCAATGCGCCCAACCATGCGAGCCCGCCGACGACTGCGCAAGGGCGTGT 1792
Qy 1716 AACGCTGGAACAGTGTATGCGACACTGCGCCAACTTCCACCAAGTCTTCTTCCAGATGC 1775
Db 1793 GACCATTTGACAGATCGTGGACAGCTGCGCGACGCTGCGCGCGCTCTGCTGGCATCTGG 1852
Qy 1776 CATCACTTGGCAGCTGGCAGAGCGCCAGCCGTTATGTTGGTGTGGGCCAGCATGAGGA 1835
Db 1853 TGCACTGTGGCGCTGAGCGAGTTCCAGGAAACGAGCTGTCTCGGCGATGTACCCAGA 1912
Qy 1836 GGAGTATTTTTCGGGCGCTGAGCCTAAGCTGTGCTGAAGAGTTCAGGAGGAGCTGGC 1895
Db 1913 AGAGCATTTTATCGAAGCTGTGAAGAGCATGAGCCGATGCGCCGATTCGCAAGAACCTCGA 1972
Qy 1896 TGCCCTGGATTAAGAAATTGAGATCCGGAATGCAAAAGCTGGACATGCCCTTACGAGTACT 1955
Db 1973 GGCCATTGTGAGCGTGTGCTGAGCGCAACAGAAAGAGCAGCTGCCATATTACTACTT 2032
Qy 1956 GCGGCCAGCGTGTGGAAGACAGTGTGGCATTAAGCTGCGCCACCTTTGGTTATTT 2015
Db 2033 GTCCCCAGACCGGATTCGGAACAGTGTGGCCATCTGAGCACACTGCCAGTCTCACTGTGG 2092
Qy 2016 CAGCCCCCATCACCCAGCCACCAAG 2040
Db 2093 GAAGGCCAGCTGCCCGCCAGCCAGATG 2117

RESULT 6
US-09-949-016-109
; Sequence 109, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-109
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Query Match 14.3%; Score 382.6; DB 4; Length 2497;
Best Local Similarity 52.5%; Pred. No. 4.1e-92;
Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

Qy 126 CGCAGCGGGCAAGGAGACAGAACTCAAGTGGNAGTACCGGAGTATCTGGGGCCCGCTGCT 185
Db 182 CGAGCGTGGCGGCTGGATTCATAGCAGTGAATGAGCGAGGAACTGGGCGAGATCCA 241
Qy 186 GTTGTGAAACTGCGCAAAACGCGCACTCTCTTAAGACGACGCTGTTCTGCAACTGGAT 245
Db 242 GCTGTGAGATCGAGAGCGCAAGTACTGGCTGAATGACGACTGCTGACTGAAGTACAT 301
Qy 246 CTCGTGAGGCGCCCGGAGCGGGGACAGAGTCAAGTTCCTTGTTCACGCTGGTGA 305
Db 302 CACGCTGAAGACGCGCC---CACGGGAGCTATCATCGAGTTCCTCTGCTACCGCTGATCAC 358
Qy 306 GGGCAACGGCGTCTGAGCCTGCTGAGGACGACCGCGCAGCTGTGGGCGAGGACCCCTCA 365
Db 359 CGGCGATGTCGAGGTGTCTCTGAGGATGGAGCGCCAAAGTTGGCCCGAGATGACCAAT 418
Qy 366 GGGCCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAAAGTGTGACCGGTG 425
Db 419 TCACATTTCTAAGCAACACCGAGCTAAGAACTGGAACACGCGCAAAACATATCGATG 478
Qy 426 GGGAACTGGAAGAGCGGTTAAATTCGAAATGCTGGGGCCAAACTATATGACCTCCC 485
Db 479 GATGAGTGGAAACCCCTGGCTTCCCTTGAGCATCGATGCAAAATGCCAAGAGATTTACC 538
Qy 486 TGTGATGAGCATTTCTGGAAGACAGAGAGTTCAGCTTTGAGGTTTCGCTGCCCAAGG 545
Db 539 CCGTATATCCAGTTTGTAGTGAAGAAAGAGTGAAGTTCGTAATTAATCTCCAAAGC 598
Qy 546 GCTGCGCAGCTCGCTATCAAAAGACT---CTCTAAATGTTCTGACTTGTGGAAGGATCT 602
Db 599 GATGAGAGACCTGTTTCATCAACCGCTTCATGCACATGTTCCAGTCTTCTTGAATGACTT 658
Qy 603 AGATGACTTCAACCGGATTTCTGTGTGCTCAGAGCAAGCTGGCTGAGCGGTGGCGGA 662
Db 659 CGCCGACTTTGAGAAAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGTTCATGAA 718
Qy 663 CTCCTGGAAGGAGATGCTTATTTGGGTACAGTTTCTTAATGCGCCAAACCCCGTGT 722
Db 719 TCACCTGGCAGGAGACCTGATGTTTGGCTTACAGTTTCTGAAATGGCTGCACACCTGTGTT 778
Qy 723 GCTGAGGCGCTCTGCTCACCTTCTGCTCGCTAGTGTTCCTCCCTCCAGGCAATGGA----- 776
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Qy 777 -----GGAACTGCGAGGCCAGCTGGAGAAAGAGCTGGAGGGAGGAGGACACTGTTTGAAGC 830
Db 839 CAGCCTGGAGCGGAGCTCAGCTTGGAGCAGGAGGTCCAGCAAGGGAACATTTTCATCGT 898
Qy 831 TGACTTCTCCCTGCTGGATGGATCAAGGCCAACGTC---TTCCTGTAGCCAGCAGCA 887
Db 899 GGACTTTGAGCTGCTGGATGGATCGATGCCAAACAAACAGACCCCTGTCACACTCCAGTT 958
Qy 888 CTTGGCTGCCCTCTAGTCACTGCTGAAATTTGAGCCTGATGGGAAACTCTTGCCCACTGTT 947
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Qy 948 CATCCAGCTCCAGCTGCGCCCGCACAGGATCCCAACCACTCCCTCTTTCTTGTGCTACGGA 1007
Db 1019 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAAACCTTATTTCTCTCTCTCCGGA 1072
Qy 1008 TCCCCCAATGGCTGCTTCTGCGCAAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCA 1067
Db 1073 TGCAAATACGACTGGCTTTTGGCCAAATCTGGGTGCGTTCAGTGACTTCCAGTCCA 1132
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Db 1193 GTACCCGAGCTGCTGCTGTGACCCCAATTTCAAGCTGTGTGGCACGCTGAGATT 1252
Qy 1188 CACCTTGGAAATTAACGTCCGGCCAGGACTGGGCTGTCTCTGACATGGGAATTTTGA 1247
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Qy 1248 CCAGATAATGAGCACTGTGTGGGGAGGCCACGTGACAGCTGTCTCAAGCAAGCTGGAGCCTT 1307
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Qy 1308 CTTAACTACAGCTCTCTCTGCTCCCTCATGACTTGGCGGACCGGGGGCTCTCG---- 1362
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Qy 1419 TGGTATGTGGAAGGAATCGTAGTCTCACTATATAGACAGAGTGGCTGTGAAGACGA 1478
Db 1493 GACGTTTACGGCGGAGGTGTAGACATCTACTACGAGGGCGACCAAGTGTGGAGGAGA 1552
Qy 1479 CCAGAGCTGCAGACCTGTGTGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAGGA 1538
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Qy 1539 CCGAGGGTTCTCTCTTTACAGCTCGGACAGAGTTTGCCTTTGTCCACATGTG 1598
Db 1613 CTCAGGCTTCCCAAGTCGTCAGAGCCGGAGCAGCTGTGGAGTACTGACCGTGT 1672
Qy 1599 TATCTTACCTGACCGGCAACAGCCCTCTGTGACCTGGGCGCAGCTGGATGTACTTC 1658
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Qy 1659 TTGGGTGCTTAATGACCTGACAGTGGGCTGCGCCCGCCGCAACCAAG--GATGC 1715
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Qy 1776 CATCACTTGGCAGCTGGGAGAGCGAGCCCGTATGTGGTGTGGGCGCAGCATGAGGA 1835
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Qy 1836 GGAGTATTTTTCGGGCCCTGAGCCTAAGCTGTCTGAAGAAAGTTTCAGGGAGAGTGGC 1895
Db 1913 AGAGCATTTTATCGAAGAGCCTGTGAAGGAAGCCATGGCCCGATTCGCGAAGACTCGA 1972
Qy 1896 TGCCCTGGATAAGGAATTTGAGATCCGGAATGCAAGCTGGACATGCCCTACGAGTACT 1955
Db 1973 GGCCATTTGTCAGCTGATTTGCTGAGGCGCAACAGAGAGCAGTGGCCATATTACTATT 2032
Qy 1956 GCGGCCAGCGTGTGGAAAAACAGTGTGCCATCTAAGCGTGCACCCCTTTGGTTATTT 2015
Db 2033 GTTCCCGACAGCCGATTCGGAACAGTGTGGCCATCTGAGCACACTGCCAGTCTCACTGTGG 2092
Qy 2016 CAGCCCCCATACCCAGCCCAAG 2040
Db 2093 GAAGCCAGCTGCCCGCAGCCAGT 2117

RESULT 7

US-09-061-768A-1

; Sequence 1, Application US/09061768A

; Patent No. 6204037

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; APPLICANT: BOEGLIN, WILLIAM E.

; APPLICANT: JISAKA, MITSUO

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLYING APPLICATION NUMBER: US/09/061,768A

FILING DATE: APRIL 16, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA: NONE

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 493-8000

TELEFAX: (919) 419-0383

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2685 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

US-09-061-768A-1

Query Match 12.8%; Score 342.8; DB 3; Length 2685;
Best Local Similarity 51.0%; Pred. No. 2e-81;
Matches 924; Conservative 0; Mismatches 867; Indels 21; Gaps 4;

Qy 196 CTGGCAAAACGCGACCTCTTTAAGGACGACGCGCTGTCTGCACTGGATCTCTGTGCAG 255
Db 297 CTGCCCTGTCTGGGCGCCCTGGCCCGGATGCTGCTTCTGCCCTGTGTTTCAGCTGACA 356
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Db 357 CGCGCGCGGGCGG---CCACTCTCTTCCCTGCTACAGTGGCTGGAGGGGGGGGG 413
Qy 316 GTCTGTAGCCTGCTGAAAGGACCGGCGCACTGTGGGGGAGGACCTTCAGGGCCTGTTC 375
Db 414 ACCCTGTGTCTGCAGGAGGTACAGCCAAAGGTGTCTCTGGGAGAGCCACCCCTGTGCTC 473
Qy 376 CAGAAACACCGGAGAGAGAGCTGGAAGAGAGAGAGTGTACCGGTGGGGGAACTGG 435
Db 474 CAGCAACAGCGCCAGAGAGAGCTTCAGGCCCGGCGAGAGAGTGTACAGTGGAGGCTTAC 533
Qy 436 AAGGACGGGTTAAATTTCTGAATATGCTGGGGCCAAACTATATGACCTCCCTGTGGATGAG 495
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Qy 556 CTCGCTATCAAGACTCTCTAAATGTTCTGACTTCTGCGAAGGATCTAGATGACTTCAAC 615
Db 654 ATGAAATCAAGGGGTGCTGGACCGGAGGGGCTCTGGAGAGTCTGAAATGAGATGAA 713
Qy 616 CGGATTTTCTGTTGTGGTTCAGAGCAAGCTGCTGAGCCGCTGCGGGAATCTCTCTGGAAGAA 675
Db 714 AGGATCTCAACTTCCGGAGAGAGCCCGACAGCTGAGCAGCGATTTGAGCAGCTGGCAGAG 773
Qy 676 GATGCTTTATTTGGGTACAGTCTTTTAAATGGGCGCAACCCCGTGGTGTGAGGCGCTCT 735

Db 774 GATGCTCTCTGCGCTCCAGTTCCTGAATGGTCTCAACCCCTGCTGATCGCGCTGT 833
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Db 834 CACTACTCCCAAGAAGTTCCTCCGCTCACTGATGCCATGGTGGCTCTATTGTTGGTCT 893
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Db 1014 ACCCTGCTATACAGAGCCAGGCTGGGGCGCTGC---TGCTCTCGCCATCCAGCTC 1070
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QY 1384 GCCCAAGATGCTGCGGCTCTGGGAATCATCTATCGGTATGTGGAAGGAATCGTGAGT 1443
Db 1491 CGTGATGATGGATGCAGATTTGGGGTGCAATGGAGCGCTTCTCTGAAATCATCGGT 1550
QY 1444 CTCACATATAAGACAGAGTGGCTGTGAAGACAGCCAGAGCTGACAGCTGCTGTGCGA 1503
Db 1551 ATCTACTACCAAGTATGATGCTGTCTCAAGATGACAGAGAGCTCCAGGCTGGGTCAG 1610
QY 1504 GAGATCACTGAATCGGGCTGCAAGGGGCCAGGAGCGGGTTCTGCTCTTTACAG 1563
Db 1611 GAGATCTTCTCAAGGCTTCTTAACAGAGAGCTGAGTATCCCTTCTCACTGGAG 1670
QY 1564 GCTCGGGACCAAGTTTGCCACTTTGTCAACATGATGTATTTCACTTGCACCGGCCAACAC 1623
Db 1671 ACCGGGAAGCCCTGGTGCGAGTATGTCAACATGGTGATATTCACCTGCTCAGCAAGCAT 1730
QY 1624 GCCTCTGTGACCTGGGCCAGCTGGAGTGTGATCTTTGGGTGCTGATGACCCCTGACG 1683
Db 1731 GCGGCTGTGAGTGAGGCGAGTTTGACTCTGCTGCTTGGATGGCCAACTGCGCACCCAGC 1790
QY 1684 ATGCGGCTGCCCGCCCAACCAACCAAG---ATGCAACGCTGGAGACAGTATGGGGACA 1740
Db 1791 ATGAGCTGCCACACCAACCTTCAAGGGCTGGCAACATGCGAGGGCTTCATAGCAACC 1850
QY 1741 CTGCCCAACTTCCACCAAGGCTTCTCTCCAGATGTCCATCTATTTGGCAGCTGGGACAGC 1800

Db 1851 CTCCACCTGTCAATGCCACATGTGATGTATCTCTGTTGCTGCTGAGCAAGGAG 1910
QY 1801 CAGCCCGTTATGGTGGCTGTGGCCAGCATGAGGAGGAGTATTTTCGGGGCCCTGAGCCT 1860
Db 1911 CTGGAGACCAAGGCCCTGGGACCTATCCGGATGAGCACTTCACAGAGGAGGCCCT 1970
QY 1861 AAGGCTGTCTGAAGAAGTTTCAGGAGGAGCTGGGTGCGCCCTGGATAAGGAAATTTGAGATC 1920
Db 1971 CGGCGGAGCATCGCCACCTTCCAGAGCGCCCTGGCCAGATCTCGAGGGGCATCCAGGAG 2030
QY 1921 CGGAATGCAAGCTGGACATGCCCTACGAGTACCTGCGGCCAGCTGCTGTAACACACT 1980
Db 2031 CGGAACCGGGGCTGGTGTCTGCTGCTACCTACCTAGACCTCCCTCATCGAGAACAGC 2090
QY 1981 GTGGCCATCTAA 1992
Db 2091 GHTCTCATCTAA 2102

RESULT 8
US-09-764-246-1
; Sequence 1, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-764-246-1

Query Match 12.8%; Score 342.8; DB 4; Length 2685;
Best Local Similarity 51.0%; Pred. No. 2e-81;
Matches 924; Conservative 0; Mismatches 867; Indels 21; Gaps 4;
QY 196 CTGGCAACCGCACCTCTTAAAGGACGAGCTGGTCTTGAACCTGGATCTCTGTGCGAG 255
Db 297 CTGCCCTCTGGGGCCCTCGCCCGGATGCTGTGCTGCGCTGGTTCCAGACTGACA 356

QY	256	GGCCCCGAGCGGGGACGAGGTCAGGTTCCCTTGTTTACCCTGTGGTGGAGGGCAACGGC	315
Db	357	CGCGCGCGGGCGG---CCACCTCTCTTCCCTCTACTACCACTAGTGCTGGAGGGCGGGG	413
QY	316	GTCTGTAGCCTGCCTGAAGGCACGGCCGCACCTGTGGCGAGGACCCCTCAGGGCCTGTTC	375
Db	414	ACCCTGTGTCTGCAAGGGGTACAGCAAGGTGTCTCTGGGCAGACCAACCCCTGTGTCTC	473
QY	376	CAGAAACACCGGGAAGAGAGCTCGAAGAGAGAAAGTAAGTTGTACCGGTGGGGAATCTGG	435
Db	474	CAGCAACACGCCAGGAGGAGCTTCAGSCCCGCGAGGAGATGTACCAGTGGAGGCCTTAC	533
QY	436	AAGNCGGTTAAATTCGATATATGTCTGGGCGCAAACTATATATGACTCCCTGTGTGATGAG	495
Db	534	AACCCAGGTTGGCCTCACTGCTGCGATGAAAGAAGACAGTGGAGAAGCTTGGAGCTCAATATC	593
QY	496	CGATTCTTGGGAAGACAAGAGAGTTGACTTTCAGGTTTCGTGGCCAGGGGCTGCCCGAC	555
Db	594	AAATACTCCACAGCCCAAGATGCCAACTTTTATCTCAAGCTGGCTCTGCTTTTGGCAGAG	655
QY	556	CTCGCTATCAAGAGACTCTCTAAATGTTCTTGACTTGTCTGGAAAGGATCTAGATGACTCAAC	615
Db	654	ATGAATCAAGGGGTTGCTCGACCGCAAGGGGCTCTGGAGAGTCTGATAGATGAAATGAA	713
QY	616	CGAATTTTCTGGTGTGTCGAGCAAGCTGTGCTGAGCGCTGCGGAGCTCTCTGGAAGAA	675
Db	714	AGGATCTTCAACTTCCGAGGACCCACGACGCTGAGCAGCATTTTGACACTGCGCAGGAG	773
QY	676	GATGCTTATTTGGGTACCACTTTCTTAATGGCGCAACCCGCTGGTGTCTGTAGGCGCTCT	735
Db	774	GATGCTTCTTTCGGCTCCCACTTCTGAAAGGTTCTCAACCCGTCTCTGATCCGCGCGTGT	833
QY	736	GCTCACCTTCTGCTCGGCTAGTGTTCCTCCAGGCATGGAGGAA-----CTG	783
Db	834	CACTACCTCCCAAGAACTTCCCGTCACTGATGCCATGTGTGGCTCATTTGTGGGTCTCT	893
QY	784	CAGGCCAGCTGGAGAAAGGAGCTGGAGGGAGGCACACTGTTCGAAAGCTGACTTCTCCCTG	843
Db	894	GGGACCACTTGCAGGCTGAGCTAGAGAAAGGCTCCCTGTTCTTGGTGGATCACGGCATC	953
QY	844	CTGATGGGATCAAGGCCAAGCTCATTTCTGTGTAGCCAGCAGCACTGGCTGCCCTCTTA	903
Db	954	CTCTCTGGCATCCAGACCAATGTCTTAATGGGAAGCGCGAGTTCTCTGCGGCCCCAATG	1013
QY	904	GTCAATGCTGAAATTCGACGCTGATGGGAAACTCTTTGCCCATGTGTCATTCAGCTCCAGCTG	963
Db	1014	ACCTCTGTATACAGAGCCAGGCTGGGGCGGTGC---TGCCTCTGCCCATCCAGCTC	1070
QY	964	CCCCGCAACAGGATCCCCACCACTCCCTCTTTTGTGCTACGGATCCCCCAATGGCTCGG	1023
Db	1071	AGCCAGACCCCGGCCCAACAGCCCCCATCTTCTGCCCCACTGATGACAGTGGGACTGG	1130
QY	1024	CTTCTGGCCAAATGCTGGGTGGGAGCTCTGACTTTCAGCTCCATAGACTGCGAGTCTCAT	1083
Db	1131	TTGCTGGCCAAAGACTGGGTGGCAATGCCGAGTTCTCTTCCAATGAGGCCCTCACGCAC	1190
QY	1084	CTTCTGAGGGGACACTTGATGGCTGAGTCAATTTGTTGGCCACCATGAGGTGCTGCCG	1143
Db	1191	CTGCTGCACTACACTGTCTGCCCTGAGGTCTTCAACCTGGCTACCTTGCCTGAGCTGCC	1250
QY	1144	TCGATACATCTATCTTCAAGCTTTAATTTCCCCACCTGGGATACACCTCGGAAATTAAC	1203
Db	1251	CACCTGCACCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACCTTGCACTCAAC	1310
QY	1204	GTCGGGCGCAGGACTGGGCTGGTCTCTGACATGGGAATTTTTCGACAGATAATGAGCACT	1263
Db	1311	ACACTCGCCGGGAGCTGCTTATCTGTCCAGGGCAGGTGGTGGACAGGCTCCACAGGCATC	1370
QY	1264	GGTGGGGAGGCCACGTGCGACTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGCTCC	1323
Db	1371	GGCAATGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTGGAATTTCTCTC	1430
QY	1324	TTCTGTCCCCCTGATGACTTTGGCCGACCGGGGGCTCTCTGGGAGTGAAGTCTTCTCTCTAT	1383

Db	1431	CTGTGTCTGCTGAGGATATCCGACCCGAGGAGTTGAAAGACATCCCAGGCTACTACTAC	1490
Qy	1384	GCCCAAGATCGCTCGGGCTCTCGSAAATCATCTATCGGTTATGTGGAAGMAATCGTGAGT	1443
Db	1491	CGTGATGATGGGATGCMAGATTTGGGTGCMGTGGAAACGCTTTGTCTCTGAAATCATCGGT	1550
Qy	1444	CTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGCA	1503
Db	1551	ATCTACTACCAAGTGATGAGTCTGTCCAAGATGACAGAGAGCTCCAGGCTGGGTCAGA	1610
Qy	1504	GAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCCTGTCTCTTTACAG	1563
Db	1611	GAGATCTTCTCCAAGGGCTTCTTAAACCAAGGAGAGCTCAGGTATCCCTTCTCAGCTGGAG	1670
Qy	1564	GCTCGGACACAGGTTTGGCACTTTGTTCACCATGTGATCTTTCACCTGCAACCGGCCAACAC	1623
Db	1671	ACCGGGAGAGCCCTGGTGAGTATGTCCACATGGTGATATTACCTGTCTCAGCAAGCAT	1730
Qy	1624	GCCTCTGTGCACCTGGGCCAGCTGGACTGGTACTCTTGGGTGCCTAATGCACCTGCACG	1683
Db	1731	CGGGCTGTAGTGCAGGGCAGTTTGACTCTGTGTGCTTGGATGGCCAACTGCCACCAAGC	1790
Qy	1684	ATGGGCTGCCCCGGCCACCAACCAAGG---ATGCAACGCTGGAGACAGTATGGCGACA	1740
Db	1791	ATGCAGCTGCCACCAACCCACCTCCAAAGGCTGGCAACATGCGAGGGCTTCATAGCCACC	1850
Qy	1741	CTGCCCCAATTTCAACAGAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAACGC	1800
Db	1851	CTCCCACTGTCAATGCCACATGTGATGTATCCTTGTCTCTGTGGTTGTGTAGCAAGGAG	1910
Qy	1801	CAGCCCGTTATGTGCTGTGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCCT	1860
Db	1911	CCTGGAGACAAAGGCCCTTGGGCACCTATCCGATGAGCATTTCAAGAGGAGGGCCCT	1970
Qy	1861	AAGGCTGTGCTGAAGATTGAGGAGGAGCTGGCTGCCCTGGATGAGGAAATTGATC	1920
Db	1971	CGGCGGAGCATGCCACCTTCTCAGACCGCGCTGGCCAGATCTCGAGGGGCGATCCAGGAG	2030
Qy	1921	CGGAATGCMAAGCTGGACATGCCCTTACGAGTACTTCGGGCCAGCGGTGTGGAAAAACAGT	1980
Db	2031	CGGNAACGGGGCTGGTGTGCTGCCCTACACCTACCTAGACCTCCCTCCCTCATCGNAGACAGC	2090
Qy	1981	GTGGCCATCTAA	1992
Db	2091	GTCTCACTCTAA	2102

RESULT 9

```

RES001 3
US-09-949-016-156
; Sequence 156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-156

```

Query Match 12.8%; Score 342.8; DB 4; Length 2685;
Best Local Similarity 51.0%; Pred. No. 2e-81;
Matches 924; Conservative 0; Mismatches 867; Indels 21;

Qy	196	CTGGCGAAACGGCACCCTCTTAAGGACGACGCGCTGGTTCTTGCAACTGGATCTCTGTGCAG	255
Db	297	CTGCCCCCTGTGGGGCCCCCTTGGCCCCGGATGCGCTGGTTCTGCGCGCTGGTTCCAGCTGCAC	356
Qy	256	GGCCCCGGAGCCGGGGACGAGGTCAGGTTCCCTTTGTTTACCGCTGGGTGGAGGCAACGGC	315
Db	357	CGGCGCGGGGCGG---CCACCTCTCTTCCCTGCTACAGTGGCTGGAGGGGGCGGG	413
Qy	316	GTCTGTAGCCTGCTGAAGGACCGGCGGCACCTGTGGGCGAGACCTCAGGGCCCTGTTTC	375
Db	414	ACCTGTGTCTGACGAGGGGTACAGCCAAGGTGTCTGGGCAGACCAACCCTGTGCTC	473
Qy	376	CAGNAACACCGGNAGAGAGCTGGAGAGAGAGGAAGTTGTACCGTGGGGAACATGG	435
Db	474	CAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGCAGGAGATGTACCAAGTGGAAAGCTTAC	533
Qy	436	AAGGACCGGGTTAATTTCTGAATATAGGCTGGGGCCAAACTATATGACCTCCCTGTGGATGAG	495
Db	534	AAACCAGTTGGCCTCACTGCCTGGATGAAAAGACAGTGGAGACTTGGAGCTCAATATC	593
Qy	496	CGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCCAAAGGGGCTGGCGGCAC	555
Db	594	AAATACTCCACAGCAAGAATGCCAACTTTTATCTACAAGCTGGCTCTGCTTTTTCAGAG	653
Qy	556	CTCGCTATCAAGACTCTCTAAATGTTCTGCATTTGCTGGAAGGATCTAGATGACTTCCAAC	615
Db	654	ATGAAATCAAGGGGTTGCTGGACCGCAAGGGGCTCTGGAGGAGTCTGAATGAGATGAAA	713
Qy	616	CGGATTTTCTGTTGTGTCAGAGCAAGCTGGCTGAGCGCGTGGGGACTCCTGGAAGGAA	675
Db	714	AGGATCTTCAACTTCGCGAGACCCACGAGCTGAGCACGCAATTTGAGCACTGGCAGGAG	773
Qy	676	GATGCTTATTTGGGTACCAAGTTCTTAATGGCGCCAAACCCGTGGTGTCTGAGGCGCTCT	735
Db	774	GATGCTTCTTCGCTCCCAAGTTCTCAATGGTCTCAACCTGTGCTGATCCCGCGCTGT	833
Qy	736	GCTCACCTTCTGCTCGCTAGTGTTCCTCCAGGCATGGAGGAA-----CTG	783
Db	834	CACTACCTCCCAAGAACTTCCCGTCACTGATGCCATGGTGGGCTCATTTGTTGGGTCT	893
Qy	784	CAGGCCAGCTGGAGAAAGGAGCTGGAGGGAGGCACTGTTTGGAACTGACTTCTCCCTG	843
Db	894	GGGACCAAGCTTGCAAGCTGAGCTAGAGAAAGGGCTCCCTGTTCTTTGTGTGATCAGGCATC	953
Qy	844	CTGGATGGATCAAGGCCCAACGTCATCTCTGTAGCCAGCAGCACCTGGCTGCCCTCTA	903
Db	954	CTCTCTGGCATCCAGACCAATGTCAATATGGGAAGCCGCAAGTTCTCTGGGCCCCCAATG	1013
Qy	904	GTCAATGTTGAAATTCGACGCTGATGGGAAAATCTTTGCCCATGGTCTATCCAGCTCCAGCTG	963
Db	1014	ACCTGCTATACAGAGCCCAAGGCTCGGGGCGCTGC---TGCCTCTCGGCATCCAGCTC	1070
Qy	964	CCCCGCACAGGATCCCAACACCTCCCTTTTCTTGCTACGATACCCCAATGGGCTCG	1023
Db	1071	AGCCAGACCCCCGGGCCCCAAACAGGCCCACTCTTCTGCCCCACTGATGCAAGATGGGACTGG	1130
Qy	1024	CTTCTGGGCAAAATGCTGGGTGGCAGCTCTGACTTCCAGCTCCATGAGCTGCAGTCTCAT	1083
Db	1131	TTGCTGGCCAAGACTGGGTGGCAATGCCAGATTCTCTTCCATGAGGCCCTCACGGAC	1190
Qy	1084	CTTCTGAGGGACACTTGATGGCTGAGTCAATGTTGTGGCCAACATGAGGTGCTCGCG	1143
Db	1191	CTGCTGCACTCACATCTGCTGCCTGAGTCTTCAACCTGGCTACCTCGCTCACTGCTGCC	1250
Qy	1144	TCGATACATCTATCTTCAAGCTTATAATTCGCCACCTGGCATACCCCTGGAAATTAAC	1203
Db	1251	CACTGCCACCTCTCTTCAAGCTGCTGATCCCGCACCCCGATACACCTTGCACTCAAC	1310
Qy	1204	GTCCGGGCCAGGACTGGGCTGTCTCTGACATGGGAATTTTTCGACAGATTAATGAGCACT	1263

RESULT 10

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US-09-949-016-3041
; Sequence 3041, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3041
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3041

Query Match      12.8%; Score 341.2; DB 4; Length 2674;
Best Local Similarity 50.9%; Pred. No. 5.3e-81;
Matches 923; Conservative 0; Mismatches 868; Indels 21; Gaps 4;

QY 196 CTGCGCAAAACGACCTCTTAAGACGACGCTGTTCTGCACTGGAATCTCTGTGCAG 255
Db 298 CTGCCCCCTCTGGGGCCCTTGGCCCCGCGATGCTGTTCTGCGCTGGTTCCAGCTGACA 357
QY 256 GGCCTCCGAGCGGGGACAGAGTCAGGTTCCCTTTGTTACCGCTGGGTGGAGGGCAACGGC 315
Db 358 CCGCGCGGGGGCGG---CCACCTCTCTTCCCTGCTACCACTGGCTGGAGGGGGGGG 414
QY 316 GTCTGAGCTTGGCTGAAGGACCGGCCCACTGTGGGGGAGGACCTCAGGGCCTGTTC 375
Db 415 ACCCTGTGTCTGACGAGGGGTACAGCAAGGTGTCTCTGGGCGAGACCACCACCTGTGCTC 474
QY 376 CAGAAACACCGGAGAGAGCTGGAAGAGAGAGAGAGTGTACCGGTGGGGAACCTGG 435
Db 475 CAGCAACACCGGAGAGAGCTTACAGGCCGAGGAGATGTACAGTGGAGAGGCTTAC 534
QY 436 AAGGACGGGTAAATCTGTAATATGGCTGGGGCCAACTATATGACCTCCTCTGTGATGAG 495
Db 535 AACCAGGTTGGCTCACTGCTTGGATGAAAGACAGTGGAGACTTGGAGCTCAATATC 594
QY 496 CGATTTCTGGAGAGCAAGAGAGTTGATTTGAGGTTTCGCTGCCAAGGGGCTGGCCGAC 555
Db 595 AAATACTCCACAGCCAAAGAAATGCCAACTTTATCTACAGGCTGGCTCTGTTTGCAGAG 654
QY 556 CTGCTATCAAGACTCTTAATGTTCTGACTGTGTGAAGATCTAGACTTCAAC 615
Db 655 ATGAAATCAAGGGGTGTGTCGACCGCAAGGGGCTCTGGAGGAGTCTGAATGAGATGAA 714
QY 616 CGGATTTCTGTGTGTCAGAGCAAGCTGGCTGAGCGGTGGGACCTCTCGGAAGGAA 675
Db 715 AGGATCTTCACTTCGGAGGACCCAGCAGCTGAGCAGCAATTTGAGCATTGGCAGAG 774
QY 776 GATGCTTATTTGGTACAGTTTCTTAATGCGCAACCCCGTGGTGTGAGGCGCTCT 735
Db 775 GATGCTTCTTGGCTTCCAGTCTTCTGATGATGTTCTCAACCTGTCTGATCGCGCTGT 834
QY 736 GCTCACCCTCTGCTGCTAGTGTTCCTCCAGGATGGAGAA-----CTG 783
Db 835 CACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGGTGGCTCTCAAGTGTGGGTCT 894
QY 784 CAGGCCACGCTGGAGAGGAGCTGGAGGAGGACACACTGTTCGAAAGCTGACTTCTCCCTG 843
Db 895 GGGACGAGCTTGACGCTGAGCTAGAGAGGCTCTCCTGTTCTTGGTGGATCAGGCAATC 954
QY 844 CTGGATGGGATCAAGCCCAAGCTCAATTTCTGTAGCCAGCAGCACCCTGGCTGCCCTCTA 903
Db 955 CTCTCTGGCATCCAGACCAATGTCTTAATGGAGGCTCAGTCTCTGCGGCCCAATG 1014
QY 904 GTCATGCTGAATTTGACGCTGATGGGAAATCTTTCGCCCATGGTCAATCAGCTCAGCTG 963
Db 1015 ACCCTGCTATACAGAGCCGAGGCTGCGGGCGGCTGCTGCTCTGCTGCTGCTGCTGCT 1071
QY 964 CCGCGCAGAGGATCCCAACCACTCCCTCTTTCTTCTGCTTACGATCCCGCAATGGCTGG 1023
Db 1072 AGCCAGACCCCGGCCCAAGAGCCCACTTCTTCTGCCCCACATGATGACAAAGTGGAGCTG 1131
QY 1024 CTTCTGGCCAAATGCTGGGTGGCGAGCTCTGACTTCCAGCTCCATGAGCTGAGTCTCAT 1083
Db 1132 TTGCTGGCCAAAGCCTGGGTGGCGAATGCGAGTCTCTCTTCCATGAGGCTCTCAGCAC 1191
QY 1084 CTTCTGAGGGGACACTTGTATGGCTGAGGTCATTTGTTGGGCCCAACCATGAGGTGCTGCG 1143
```

RESULT 11

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US-09-547-435-29
; Sequence 29, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
```

```

; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6592957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-29

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Query Match	12.4%	Score 332;	DB 4;	Length 3384;
Best Local Similarity	53.7%	Pred. No. 1.8e-78;		
Matches 767;	Conservative	0;	Mismatches 640;	Indels 21; Gaps 3;
Qy	589	TGCTGGAAAGGACTTAGATGACTTCAACCGGATTTTCTGGTGTGGTCAAGCAAGCTGGCT	648	
Db	1222	TCTTGGNAAAGCTGGATGACATCGAGAAATCTTCTGGTGCCATAAGACCTTCAACGACA	1281	
Qy	649	GAGCGCTGCGGGAATCCTTGGAAAGGAAGATGCCTTATTTGGGTACCAAGTTTCTTAATGGC	708	
Db	1282	AAGTATGTCAAGAGCACTGGTGTGAAGATCACTTCTTGGGTACCAAGTACCTGAATGGT	1341	
Qy	709	GCCAAACCCCTGGTGTGAGCGCTCTGCTCACCTTCTCTGCTCGCTAGTGTTCCTCCCA	768	
Db	1342	GTCAATCCCCGTATGCTTCCACTGTATCTTAGCTTGCACGAAGCTGCTGTGACCAAT	1401	
Qy	769	GGCATGG-----AGGAACTGACGGCCCGAGCTGGAGAAGGAGCTGGAGGGAGGC	816	
Db	1402	GACATGTGCCCCCTTGTCTGGGACAGACACATGCTCTGCAGACAGAGCTAGAGAGGGG	1461	
Qy	817	ACACTGTTGAAAGTGAATCTTCCCTCTGGATGGGATCAAGGCCAAGTCAATCTCTGT	876	
Db	1462	AACATCTTCTAGCGGACTACTGGATCCTGGCGAGGCCCCCACTGCTTAAACGGC	1521	
Qy	877	AGCCAGCAGACACTGGCTGCCCCCTTACTAGTCAATGCTGAAATTTGCAGCCTGATGGAAACTC	936	
Db	1522	CGCCAGCAGTACGTGGCGGCCCACTGTGCTGTGTGGCTCAGCCCCCAGGGGGCGCTG	1581	
Qy	937	TTGCCCATGTGATPCAGCTCAGCTGCCCGCGACAGAGATCCCAACACTTCCCTTTTC	996	
Db	1582	GTGCCCTTGGCCATPCACAGCTCAGCCAGCAGACCCCC-----GGGCGTGACAGCCCCATCTC	1635	
Qy	997	TTGCTACGATCCCCCAATGGCTGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGAC	1056	
Db	1636	CTGCCACTGACTCCGAATGGGACTGGCTGTGTGCCAAGAGCTGGGTGCGCACTCTGAG	1695	
Qy	1057	TTCCAGCTCCATGAGCTGCAGTCTCATCTTCTGAGGGGACACTTGTATGGCTAGGTCATT	1116	
Db	1696	TTCTGTGTGACGAAACAAACAGCACACTTCTGTGACGCAATTTGCTGTGCGAGGCTTC	1755	
Qy	1117	GTGTGGCCACCATGAGGTGCTGCGTGCATATCATCTATCTTCAAGCTTATTAATCCC	1176	
Db	1756	GCCATGCCACGCTGCGCCAGCTGCCGCTGCGCACCCCATCTACAAGCTCTTACTCCCC	1815	
Qy	1177	CACCTGCGATACACCTCGGAAATTAACGTCCGGGCCAGGACTGGGCTGGTCTCTGACATG	1236	
Db	1816	CACACTCGATACAGCTGCAGGTGAAACACCATCGCGAGGGCCACGCTGCTCAACCCCGAG	1875	
Qy	1237	GGAAATTTTCGACCAAGATAATGAGCACTGTGTGGGGAGGCCACGTGCGAGCTGCTCAAGGAA	1296	
Db	1876	GGCCTCGTGGACCAAGGTCACTGTCATCGGAGGGAAGAGCCCTCATCTACCTCATGAGCAGC	1935	
Qy	1297	GCTGGAGCTTCTTAACCTACAGCTCTCTTGTCCCCCTGATGACTTGGCCGACCGGGG	1356	
Db	1936	GGCCTGGCCCACTTCACTACACAAATTTCTGGCTTTCGGHACAGCTTGGGGCCCGCGC	1995	
Qy	1357	CTCCTGGGAGTGAAGTCTTCTCTTATGCCCAAGATCGCTTGGCTGCGGCTCTGGGAAATCATC	1416	
Db	1996	GTCTTGGCTATPCCCAACTACACTACCGAGACGACGCTGGAAGATCTGGCGGCGCAT	2055	

1417	QY	TATCGGTATGTGAAGGAATCGTAGTCTCCACTATAACAGACAGCTGCCTGTGAAGAC	1476
2056	Db	GAGAGCTTTGTCTCGAATACTGGGGCTACTATTATCCAGTGAACGCACTCTGTGCAGCAG	2115
1477	QY	GACCCAGAGCTGCAGACCTGGTGTGAGAGATACACTGAAATCGGGCTGCAAGGGGCCAG	1536
2116	Db	GATTGGAGCTGCAGGCCCTGGACTGGCGAGATTTTTTGTCTCAGCGTTCCTGGGCCGGGA	2175
1537	QY	GACCGAGGGTTTCTGTCTCTTTACAGGCTCGGGACCAGGTTTGCCACTTTGTCCACATG	1596
2176	Db	AGCTCAGGTTTCCCAAGCCGGCTGTGCACCCGAGGAGAGATGTTGAAGTTTCTCTCACTGCA	2235
1597	QY	TGTATCTTCACTGTGACACGGGCGAACACGGCTCTGTGCACTGTGGGCCAGCTGGAATCGGTAC	1656
2236	Db	ATCATCTTCAATTTGCTCTGCCAGCAGCGTGTGTCAACAGTGGGCAGCATGACTTTGGG	2295
1657	QY	TCTTGGGTGCCTAATGCACCCCTGCAGATGCGGCTGCCCGCCCAACACCAACCAAGG--AT	1713
2296	Db	GCTCTGATGCCAATGCTCCATCATCATGAGGACGCCCCACCCAGACCAAGGGGACC	2355
1714	QY	GCAACGCTCGAGACAGTGTGCGCACACTGCCCAACTTCCACCGAGCTTCTCTCCAGATG	1773
2356	Db	ACCACCTGAAGACTTACCTAGACACCTCCCTGAGTGAACATCAGCTGTAAACACCTC	2415
1774	QY	TCCATCACTTGGCAGCTGGGCAGACGCCAGCCGGTTATGGTGGCTGTGGGCCAGCATGAG	1833
2416	Db	CTCCTCTTCTGGTTGTTAGCCAAAGAACCAAGGACGAGAGGCCCTGGGCACCTACCCA	2475
1834	QY	GAGGAGTATTTTTCGGGCCCTTGAGCCTTAAGGCTGTCTGAAAGAAGTTTCAGGAGGAGCTG	1893
2476	Db	GATGAGCATTTACAGAGAGGGCCCCGAGCGGAGCATCGCCGCTTCCAGAGCCGCTG	2535
1894	QY	GCTGCTCCTGGTAAGGAAATTTGAGATCCGGAAATGCAAAAGCTGGACATGCCCTACGAGTAC	1953
2536	Db	GCCAGATCTCAAGGACATCCAGAGCGGAACCGGCTGTGGCACTGCCCTACACCTAC	2595
1954	QY	CTGCGGCCAGCGTGTGTGAAACACAGTGTGGCCATCTAAGCGTTCGCA	2011
2596	Db	CTGGACCTTCCCTCATGTAGAACAGTGTCTCCATCTAACCAACCCGCA	2643

RESULT 12

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US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-5

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Query Match	12.4%	Score 330.4	DB 4	Length 2236
Best Local Similarity	53.8%	Pred. No. 3.8e-78		
Matches 766	Conservative	0	Mismatches 641	Indels 21
Gaps	3			
Qy	589	TCGTGGAAGGATCTAGATGACTTCAACCGGATTTTCTGGTGGTTCAGAGCAAGCTTGGCT	648	
Db	259	TCCTTGAAGAAGCTTGGATGATCATGTGAGAACATCTTCTGGTGGCATTAAGACCTTTCACGACA	318	


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Qy 1057 TTCCAGCTCCATGAGCTGCACTCTCATCTTCTGAGGGGACACTTGTATGGCTGAGTCAAT 1116
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Qy 1117 GTTGTGGCCACCATGAGTGGCTGGCTGATACATCTTCTCAAGCTTATAATTCCT 1176
Db 1258 GCCATGCCACGCTGGCGCCAGCTGCGCTCTGCGACCCCCATCTACAAGCTCTTACTCCCC 1317
Qy 1177 CACTGTGATACACCTCTGGAATTTAAGCTCGGGCCAGGACTGGGTCTGTCTGTACATG 1236
Db 1318 CAACTCGATACAGCTGCAAGTGAAACACATCGGAGGCCACAGTGTCTCAACCCCGAG 1377
Qy 1237 GGAATTTTCAGCAGATAATGAGCACTGTGTGGGGAGGCCACGTGCAGCTGTCTCAAGCAA 1296
Db 1378 GGCTGTGTGACACAGGTCAAGTCCATCGGGAGGCAAGGCCCTCATCTCATGAGCAG 1437
Qy 1297 GCTGGAGCTTCTTAACCTACAGCTCTTCTGTCCCTGATGACTTGGCGGACCGGGG 1356
Db 1438 GGCTGTGCGCACTTCACTACACCAATTTCTGCTTCCGACAGCCTGGGGCCCGCGC 1497
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Db 1558 GAGAGCTTTCTCAGAAATCGTGGGCTACTATTATCCAGTGACGCATCTGTGCAGCAG 1617
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Qy 1537 GACCGAGGTTCTCTGTCTTTACAGGCTCGGACACAGGTTTGCACATTTGTCAACATG 1596
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Qy 1657 TCTTGGTGTCTAATGACCTGCAAGTGGCTGCGGCTGCGGCCCAACCCAGG---AT 1713
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Qy 1714 GCAACGCTGGAGACAGTGTGGGACACTGCCAACTTCCACAGGCTTCTCTCCAGATG 1773
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Qy 1774 TCCATCACTTGGCAGCTGGGCAGACGCCAGCCGCTTATGTGTGCTGTGGCCAGCATGAG 1833
Db 1918 CTCCTCTTCTGTGTGTAGCAAGAACCCAAAGACAGAGGCCCTCTGGGCACTACCCCA 1977
Qy 1834 GAGAGTATTTTTCGGGCCCTGAGCTTAAGGCTGTGCTGAAGATTTCAGGAGGAGCTG 1893
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Qy 1894 GCTGCCCTGGATAGGAAATTTAGATCCGGAATGCAAAAGCTGGACATGCCCTTACGAGTAC 1953
Db 2038 GCCAGATCTCAAGGGACATCCAGGAGCGGAACAGAGGTCTGGCACTGCCCTTACACCTAC 2097
Qy 1954 CTGCGGCCCAAGCGTGTGGAAACAGTGTGGCCATCTTAAGCGTGGCA 2001
Db 2098 CTGAGCCCTCCCTCTTTGAGAACAGCGTCTCCATCTTAACCAACCCCA 2145
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RESULT 14

US-09-799-451-803

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; Sequence 803, Application US/09799451
; Patent No. 6783969
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GENERAL INFORMATION:

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; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunding
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 803_
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (172)..(2304)
; US-09-799-451-803
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Query Match 12.3%; Score 327.8; DB 4; Length 2307;

Best Local Similarity 53.6%; Pred. No. 1.9e-77;

Matches 761; Conservative 0; Mismatches 637; Indels 21; Gaps 3;

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Qy 649 GAGCGGTGCGGACTCTCTGGAAGGAAGATGCTTATTTGGGTACCAGTTTCTTAATGGC 708
Db 955 AAGTATGTACAGAGCACTGGTGTGAAGATCACTTCTTTGGGTACAGTACCTGATGTT 1014
Qy 709 GCCAACCCCGTGGTGTGAGGCGCTGTGCTCACTTCTGCTGGCTAGTGTTCCTCCA 768
Db 1015 GTCATATCCGTCATGCTCCACTGCATCTCTAGCTTGGCCAGCAAGCTGTGCACCAAT 1074
Qy 769 GGCATGG-----AGGAATGCGAGGCCAGCTGGAGNAGAGAGCTGGAGGGAGGC 816
Db 1075 GACATGGTGGCCCCCTTGTCTGGGACAGGACACATGCTTCAGACAGAGTAGAGAGGGG 1134
Qy 817 ACACCTGTCGAAGCTGACTTCTCCCTGTGGATGGATCAAGGCCAAACGTCATTCTCTGT 876
Db 1135 AACATCTTCTAGCGGACTACTGGATCTCTGGCGGAGGCCCCACCACTGCTTAACGGC 1194
Qy 877 AGCCAGCAGCACTGGCTGCCCTCTCTAGTCTAGTGAATTCAGCCTGATGGGAACTC 936
Db 1195 CGCCAGCAGTACGTGGCGCCCACTGTGCTGCTGTGGCTAGCCCCCAGGGGGGCGCTG 1254
Qy 937 TTGCCCATGGTATCCAGCTCCAGCTGCCCCGACAGAGTCCCCACCACTCCCTTTTC 996
Db 1255 GTGCCCTTGGCCATCCAGCTCAGCCAGACCCCC-----GGGCGCTGACAGCCCCATCTTC 1308
Qy 997 TTGCTTACGGATCCCCCAATGGCTTCTGGCCAAATGCTGGGTGGCGAGCTCTGAC 1056
Db 1309 CTGCCCACTGACTCCGAATGGGACTGGCTGTGGCCAAAGACGTGGGTGGCACTCTGAG 1368
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QY 1369 TTCCTGGTGCAGAAACACACGCACTTCTGTGCACGATTTGCTGTGCGAGCCCTTC 1428
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QY 1117 GTTGTGGCCACCATGAGTGCCTGCGCTCGATACATCTCTATCTTCAAGCTTATAATCC 1176
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QY 1177 CACCTGCGATACACCTCGAATTAACGTCGGGCGCAGACTGGGTGCTCTCTGACATG 1236
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QY 1489 CACACTCGATACACGCTGAGTGAACACCATCGCGAGGCCACGCTGCTCAACCCGAG 1548
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QY 1237 GGAAATTTTCGACGATATGACCTGCTGGGGAGGCCACGTCGAGCTGTCAAGCA 1296
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QY 1477 GACCCAGACTCGACAGCTGTGTGAGAGATCACTGAAATCGGGCTGCAAGGGGCCAG 1536
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QY 1849 AGCTCAGGTTTCCCAAGCGGCTGTGCACTCCAGGAGAGATGTTGAAGTTCCTACTGCA 1908
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QY 1597 TGTATCTTCACTGACCGGCCAACGCGCTGTGTGACCTGGCGCAGCTGACTGCTAC 1656
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QY 1909 ATCATCTTCAATTTGCTCTGCCAGCAGCTGTGTCAACAGTGGGCGAGCATGACTTTGGG 1968
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1657 TCTTGGGTGCTTAATGCACTTGCAGATGCGGCTGCGCTGCCCGCCCAACCAAGG--AT 1713
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QY 1969 GCTGTGATGCCAATGCTCATATCATATGAGGAGGAGCCCGCCAGACCAAGGGGACC 2028
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QY 1714 GCAAGCTGGAGACAGTATGAGGACATCTGCCCACTTCCACAGGCTTCTCTCCAGATG 1773
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QY 2029 ACCACCTGAAGACTTACCTAGACACCTCTCTGAAGTGAACATCAGCTGTAAACACTC 2088
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QY 1834 GAGGAGTATTTTTCGGCCCTGAGCTAAGGCTGTGCTGAAGATTTTCAGGAGGAGCTG 1893
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2149 GATGAGCACTTTCACAGAGAGGCGCCGAGCGGAGCATGCCGCTTTCAGAGCGCCCTG 2208
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QY 1894 GCTGCGCTCGATAAGGAATGAGATCCGGAATCCAAAGCTGGACATGCCCTTACGAGTAC 1953
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QY 2209 GCCAGATCTCAAGGACATCCAGGAGCGAACCAGGCTTGGCACTGGCTTACACCTAC 2268
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QY 1954 CTGGGCGCCAGCGTGTGGAACAGTGTGGGCATCTAA 1992
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QY 2269 CTGGACCTTCCCTCATTTGAGAACAGCGTCTCCATCTAA 2307
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RESULT 15

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US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
```

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; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 2604
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-23
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Query Match 12.3%; Score 327.8; DB 4; Length 2604;
Best Local Similarity 53.6%; Pred. No. 2e-77;
Matches 761; Conservative 0; Mismatches 637; Indels 21; Gaps 3;
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QY 589 TCCTGGAAGGATCTAGATGACTTCAACCGGATTTTCTGGTGTGTGCAGAGCAAGCTGGCT 648
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QY 709 GCCAACCCGCTGCTGAGCGCTCTGCTCACTTCTTCTGCTCGCTAGTGTTCCTCTCCA 768
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QY 1312 GTCAATCCCGTCATGCTCCACTGATCTCTAGCTTGGCCAGCAAGCTGCTGTCAACAT 1371
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QY 769 GGCATGG-----AGGAATCGAGCGCCAGCTGAGAGAGAGCTGAGGAGGAGCG 816
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QY 1432 AACATCTTCTAGCGGACTTCTGGATCTGCGGAGGCCCCCACTGCTTAAACGCG 1491
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QY 877 AGCAGCAGCACTGCTGCTGCTTCTAGTCTATGCTGAAATTTGCAGCCTGATGGGAACTC 936
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QY 1492 CGCAGCAGTACGTGGCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1551
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QY 937 TTGCCCCATGCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
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QY 997 TTGCTACGGATCCCCCAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056
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QY 1606 CTGCCCCACTGACTCGAATGGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1665
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QY 1666 TTCTGTGTGACGAAACACACGCACTTCTGTGACGCACTTGTGTGCTGCTGCTGCTGCTG 1725
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QY 1117 GTTGTGGCCACCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
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QY 1726 GCCATGGCCACGCTGCGCAGCTGCGCTCTGCGCACCCCACTTCAACAGCTCTCTACTCCC 1785
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QY 1237 GGAAATTTTCGACGATATGAGCACTGCTGGTGGGAGGCCACGTCGAGCTGTCTCAAGCAA 1296
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QY 1297 GCTGGAGCTTCTTAACCTACAGCTCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1356
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QY 1906 GGCCTGGGCCACTTCACTACCAATTTCTGCTGCTTCCGAGCAGCTGCGGCGCCGCGC 1965
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QY 1357 CTCCTGGGAGTGAAGTCTTCTTATGCCCCAAGATGCTGCTGCGCTCTGCGAAATCATC 1416
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Db	1966	GTCTGGCTATCCCCAACTACCACTACCGAGACGACGGCTGAAGATCTGGGCGGCATT	2025
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Db	2026	GAGAGCTTGTCTCAGAAATCGTGGGTACTATTATCCAGTGACGCATCTGTGCAGCAG	2085
Qy	1477	GACCCAGAGCTGCAGACCTCGTGTGCAGAGATCACTGAAATCGGGGTGCAAGGGGCCAG	1536
Db	2086	GATTCGGAGCTGCAGGCTGGAAGTGGCGAGATTTTGTCTCAGGCGTTCTTGGGCGGGAA	2145
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Db	2446	GATGAGCACTTTCAGAGAGGAGGCCCGAGGGGAGCATCGCCGCTTCCAGAGCCGCTG	2505
Qy	1894	GCTGCCCTGGATAGGAAATTGAGATCCGGAATGCAAGCTGGACATGCCCTACGAGTAC	1953
Db	2506	GCCAGATCTCAAGGGACATCCAGGAGCGGAACCCAGGGTCTGGCACTGCCCTACACCTAC	2565
Qy	1954	CTGGCGCCAGCGTGGTGGAAACAGTGTGCCATCTAA	1992
Db	2566	CTGGACCTCCCTCATTTGAGAACAGCGTCTCCATCTAA	2604

Search completed: July 19, 2005, 21:31:56
Job time : 305.231 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2005, 21:40:47 ; Search time 113.625 Seconds
(without alignments)
2249.936 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLVIRVSTGASLYAGSNN.....KLDMPYEYLRPSVSVNSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3503.5	99.7	662	4	Aae00939 Human 15S
2	3503.5	99.7	662	7	Add47873 Human Pro
3	3503.5	99.7	662	8	Adj75368 Marker Ge
4	3503.5	99.7	662	8	Adq91786 Human 15S
5	3503.5	99.7	662	8	Adq37894 Human 15-
6	3494.5	99.4	684	5	AB508005 Human lip
7	2691	76.6	662	7	Add47871 Rat Prote
8	2676	76.2	663	8	Adj76170 Marker ge
9	2316	65.9	663	8	Adq39837 Human myo
10	2298.5	65.4	647	8	Adq39836 Human myo
11	2280	64.9	663	3	Adq39833 Human the
12	2280	64.9	663	3	AB24019 Arachidon
13	2230.5	63.5	632	8	Adsl1946 Human the
14	2230.5	63.5	632	8	Adsl1947 Human the
15	2230.5	63.5	632	8	Adsl1945 Human the
16	1969	56.0	399	6	Aae38235 Human enz
17	1298.5	37.0	674	5	Aae15432 Human 5-1
18	1298.5	37.0	674	6	ABU08713 Alzheim
19	1298.5	37.0	674	6	ABU89732 Protein d
20	1298.5	37.0	674	6	ABr42217 Mouse B6
21	1298.5	37.0	674	6	ABr42215 Human 5-1
22	1298.5	37.0	674	8	Adf53274 Human 5-1
23	1298.5	37.0	674	8	Adp54502 Human PRO
24	1297.5	36.9	674	6	ABr42216 Mouse CAS
25	1295.5	36.9	674	1	Aap90730 Synthetic

ALIGNMENTS

RESULT 1

AAE00939

ID AAE00939 standard; protein; 662 AA.

AC AAE00939;

DT 04-JUL-2001 (first entry)

DE Human 15S-lipoxygenase (15-Lox-1) protein.

KW Human; 15S-lipoxygenase; 15-Lox-1; non-haeme iron dioxygenase;
KW arachidonic acid; feed additive; livestock; antigen.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 340..344 /note= "Consensus sequence"

FT Binding-site 360 /note= "Iron ligand"

FT Binding-site 365 /note= "Iron ligand"

FT Region 494..498 /note= "Consensus sequence"

FT Binding-site 540 /note= "Iron ligand"

FT Binding-site 544 /note= "Iron ligand"

FT Region 546..550 /note= "Consensus sequence"

FT Binding-site 662 /note= "Iron ligand"

PN US6204037-B1.

XX 20-MAR-2001.

XX 16-APR-1998; 98US-00061768.

XX 16-APR-1998; 98US-00061768.

XX (UYVA-) UNIV VANDERBILT.

XX Brash AR, Boeglin WE, Jisaka M;

XX WPI; 2001-289517/30.

XX New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed

PT

PT additives for livestock, or as antigens for producing antibodies.
XX Disclosure; Fig 1; Sipp; English.
XX The present sequence is human 15S-lipoxygenase (15-Lox-1) protein.
CC Lipoxygenases are a structurally related family of non-haeme iron
CC dioxygenases that function in the production of fatty acid
CC hydroperoxides. 15-Lox-1 acts in the metabolism of arachidonic acid to
CC 15S-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as
CC diagnostic tools to detect normal and abnormal DNA sequences derived from
CC patient cells, for detecting and isolating other members of the
CC polypeptide family and related polypeptides from a DNA library
CC potentially containing the sequences, as primers for hybridising to
CC related sequences for amplifying those sequences or for altering native
CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives
CC for livestock and as antigens for producing antibodies
XX
SQ Sequence 662 AA;
Query Match 99.7%; Score 3503.5; DB 4; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNQVQLVLVQGHGAALGKRLWPARG-ETELKVEVPYLGSL 59
DB 1 MGLYRIRVSTGASLYAGSNQVQLVLVQGHGAALGKRLWPARGKETELKVEVPYLGSL 60
QY 60 LFVKLRKHLKDDAWFCNWIISVQSGAGDGVRFPCYRWVEGVNLSLPEGTGRTVGDDP 119
DB 61 LFVKLRKHLKDDAWFCNWIISVQSGAGDGVRFPCYRWVEGVNLSLPEGTGRTVGDDP 120
QY 120 QGLFQKHREELERKLRWGNWKGDLINWAGAKLYDLPVDERFLEDKRVDFFVSLAK 179
DB 121 QGLFQKHREELERKLRWGNWKGDLINWAGAKLYDLPVDERFLEDKRVDFFVSLAK 180
QY 180 GLADLAIKDSLNLVLTCKWDLDFNRFIFWCQSKLAERVDSWKEDALFGYFLNGANPVV 239
DB 181 GLADLAIKDSLNLVLTCKWDLDFNRFIFWCQSKLAERVDSWKEDALFGYFLNGANPVV 240
QY 240 LRRSAHLPARLVPPPGMEELQALEKELEGGTTLFEADFSLLDGIKANVILCSQQHLAAPL 299
DB 241 LRRSAHLPARLVPPPGMEELQALEKELEGGTTLFEADFSLLDGIKANVILCSQQHLAAPL 300
QY 300 VMLKLPDQKLLPMVLIQQLPRTGSPPPPLFPTDPPMAWLLAKCWRSSDFQLHQLQSH 359
DB 301 VMLKLPDQKLLPMVLIQQLPRTGSPPPPLFPTDPPMAWLLAKCWRSSDFQLHQLQSH 360
QY 360 LLRGHLMAEVIIVVATWRCPLSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
DB 361 LLRGHLMAEVIIVVATWRCPLSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGGHVQLLKQACAFITYTSFCPPDDLADRLGLGVKSSFYAQLALRLWIIYRYVEGIYS 479
DB 421 GGGGHVQLLKQACAFITYTSFCPPDDLADRLGLGVKSSFYAQLALRLWIIYRYVEGIYS 480
QY 480 LHYKTDAVKDDPELQTCREITEIGLQGAQDRGPPVSLQARDQVCHFTVMCTCTGQH 539
DB 481 LHYKTDAVKDDPELQTCREITEIGLQGAQDRGPPVSLQARDQVCHFTVMCTCTGQH 540
QY 540 ASVHLGQLDWSYVVPNAPCTMLRPPPTTKDATLETVMATLPNPHQASLQMSITWQLGRQ 599
DB 541 ASVHLGQLDWSYVVPNAPCTMLRPPPTTKDATLETVMATLPNPHQASLQMSITWQLGRQ 600
QY 600 PNMVAVGQHEEYFSGPEPKAVLKRFREELAAALDKIEIRNAKLDMPYELRPSVVNSV 659
DB 601 PNMVAVGQHEEYFSGPEPKAVLKRFREELAAALDKIEIRNAKLDMPYELRPSVVNSV 660
QY 660 AI 661
DB 661 AI 662

ADD47873
ID ADD47873 standard; protein; 662 AA.
XX
AC ADD47873;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_001131, SEQ ID NO 13569.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
DR GENBANK; NP_001131.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 662 AA;

```
QY 1 MGLYRIRVSTGASLYAGSNNOVLWLVGHQGEAALGKELMPARG-ETELKVEVPEYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNNOVLWLVGHQGEAALGKELMPARG-ETELKVEVPEYLGPL 60
QY 60 LFFVKLRKRLHLLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 LFFVKLRKRLHLLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 120
QY 120 QGLFQKHREELERKLYRWGNWKGDLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 179
Db 121 QGLFQKHREELERKLYRWGNWKGDLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 180
QY 180 GLADLAIKDSLNLVLTCKWLDLDFNRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 239
Db 181 GLADLAIKDSLNLVLTCKWLDLDFNRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGKANKVILCSQQHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGKANKVILCSQQHLAAPL 300
QY 300 VMLKLOPDGKLLPMVLIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRVSSDFQLHELQSH 359
Db 301 VMLKLOPDGKLLPMVLIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRVSSDFQLHELQSH 360
QY 360 LIRGHLMAEVIVATMRCPLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LIRGHLMAEVIVATMRCPLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGGHVQLLKQAGALFTYSSFCPPDDLDRLGLGVKSSFYAQDALRLWEIIRYRVEGIVS 479
Db 421 GGGGHVQLLKQAGALFTYSSFCPPDDLDRLGLGVKSSFYAQDALRLWEIIRYRVEGIVS 480
QY 480 LHYKTDVAVKDDPELQTCWREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTQSH 539
Db 481 LHYKTDVAVKDDPELQTCWREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTQSH 540
QY 540 ASVHLGQLDWTYSWVNPACTWRLPPTTKDQATLETVMATLNFHQAOLQMSITWOLGRQ 599
Db 541 ASVHLGQLDWTYSWVNPACTWRLPPTTKDQATLETVMATLNFHQAOLQMSITWOLGRQ 600
QY 600 PVMVAVGQHEEYFSGPSPKAVLKKFREELALDKIEIRNAKLDMPEYLRPSVVNSV 659
Db 601 PVMVAVGQHEEYFSGPSPKAVLKKFREELALDKIEIRNAKLDMPEYLRPSVVNSV 660
QY 660 AI 661
Db 661 AI 662
RESULT 3
ID ADJ75368
XX ADJ75368 standard; protein; 662 AA.
AC ADJ75368;
XX
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE Marker gene related amino acid sequence SEQ ID NO:620.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX
XX Homo sapiens.
XX
XX EPI394274-A2.
XX
XX
XX 03-MAR-2004.
XX
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
PR
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```
PR 20-MAR-2003; 2003JP-00077212.
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX Example 11; SEQ ID NO 620; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (1) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (1) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 662 AA;
```

```
Query Match 99.7%; Score 3503.5; DB 8; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNNOVLWLVGHQGEAALGKELMPARG-ETELKVEVPEYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNNOVLWLVGHQGEAALGKELMPARG-ETELKVEVPEYLGPL 60
QY 60 LFFVKLRKRLHLLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 LFFVKLRKRLHLLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 120
QY 120 QGLFQKHREELERKLYRWGNWKGDLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 179
Db 121 QGLFQKHREELERKLYRWGNWKGDLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 180
QY 180 GLADLAIKDSLNLVLTCKWLDLDFNRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 239
Db 181 GLADLAIKDSLNLVLTCKWLDLDFNRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGKANKVILCSQQHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGKANKVILCSQQHLAAPL 300
QY 300 VMLKLOPDGKLLPMVLIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRVSSDFQLHELQSH 359
```

Db 301 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 419
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 480
QY 480 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIGTGOH 539
Db 481 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIGTGOH 540
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQASLQMSITWQLGRQ 599
Db 541 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQASLQMSITWQLGRQ 600
QY 600 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 659
Db 601 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 660
QY 660 AI 661
Db 661 AI 662

RESULT 4
ADQ91786
ID ADQ91786 standard; protein; 662 AA.
XX
AC ADQ91786;
DT 07-OCT-2004 (first entry)
XX
DE Human 15S-lipoxigenase.
XX
KW lipoxigenase; iron ligand; arachidonic acid metabolism; human;
KW lipoxigenase 15-Lox-2; 15S-lipoxigenase; human.
XX
OS Homo sapiens.
XX
PN US2004137483-A1.
XX
PD 15-JUL-2004.
XX
PF 18-NOV-2003; 2003US-00716204.
XX
PR 16-APR-1998; 98US-00061768.
PR 17-JAN-2001; 2001US-00764246.
XX
PA (BRAS/) BRASH A R.
PA (BOEG/) BOEGLIN W E.
PA (JISA/) JISAKA M.
XX
PI Brash AR, Boeglin WE, Jisaka M;
XX WPI; 2004-533356/51.
DR
XX
XX New lipoxigenase nucleic acid segment comprises an isolated gene encoding
PT a lipoxigenase containing an iron ligand comprising a serine, useful for
PT arachidonic acid metabolism.
XX
PS Example 1; SEQ ID NO 25; 39pp; English.
XX
CC The invention describes a nucleic acid segment (I) comprising an isolated
CC gene encoding a lipoxigenase containing an iron ligand comprising a
CC serine, or comprises at least a 10 nucleotides long contiguous stretch of
CC the nucleic acid sequence not given in the specification (SEQ ID NO. 1)
CC or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a
CC nucleic acid segment comprising at least 10 nucleotides long contiguous
CC stretch of the nucleic acid sequence not given in the specification (SEQ
CC ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is

CC a polypeptide having the amino acid sequence Trp-Leu-Leu-Ala-Lys (SEQ ID
CC NO. 5) and Gly-Gln-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxigenase nucleic
CC acids and proteins are useful in arachidonic acid metabolism. This is the
CC amino acid sequence of human 15S-lipoxigenase used in a comparison with
CC the novel human lipoxigenase 15-Lox-2.
XX
SQ Sequence 662 AA;
Query Match 99.7%; Score 3503.5; DB 8; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVQHGGAALGKRLWPARG-ETELKVEVPYELGSL 59
Db 1 MGLYRIRVSTGASLYAGSNQVQLWLVQHGGAALGKRLWPARG-ETELKVEVPYELGSL 60
QY 60 LFVKLRKHLKDDAWFCNWLISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119
Db 61 LFVKLRKHLKDDAWFCNWLISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREELERKLYRMGNKDGILNAGAKLYDLPVDERFLEDKRVDFEVS LAK 179
Db 121 QGLFQKHREELERKLYRMGNKDGILNAGAKLYDLPVDERFLEDKRVDFEVS LAK 180
QY 180 GLADLAIKDSLNLVLTCKWDLDDFNRI FWCQSKLAERVDSWKEDALFGYQFLNGANPVV 239
Db 181 GLADLAIKDSLNLVLTCKWDLDDFNRI FWCQSKLAERVDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQALKELEGGTLPFADPSLDDGIKANVILCSQQHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQALKELEGGTLPFADPSLDDGIKANVILCSQQHLAAPL 300
QY 300 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359
Db 301 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 419
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 480
QY 480 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIGTGOH 539
Db 481 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIGTGOH 540
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQASLQMSITWQLGRQ 599
Db 541 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQASLQMSITWQLGRQ 600
QY 600 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 659
Db 601 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 660
QY 660 AI 661
Db 661 AI 662

RESULT 5
ADQ37894
ID ADQ37894 standard; protein; 662 AA.
XX
AC ADQ37894;
DT 07-OCT-2004 (first entry)
XX
DE Human 15-lipoxigenase 1 protein.
XX
KW Dry eye; 15-lipoxigenase; 15-LO; ophthalmological; gene therapy;
KW postmenopausal.

XX OS Homo sapiens.
 XX PN WO2004060274-A2.
 XX PD 22-JUL-2004.
 XX PF 17-OCT-2003; 2003WO-US033139.
 XX PR 20-DEC-2002; 2002US-0435988P.
 XX PA (ALCO-) ALCON INC.
 XX PI Yanni JM, Gamache DA, Miller ST;
 XX DR WPI; 2004-543776/52.
 XX DR N-PSDB; ADQ37893.
 XX PT Treating dry eyes in postmenopausal women comprises administering a
 PT composition comprising the 15-lipoxygenase (15-LO)-1 or 15-LO-2 gene to
 PT the ocular surface cells of the post-menopausal women with dry eyes.
 XX PS Claim 5; SEQ ID NO 2; 20pp; English.
 XX CC The invention relates to a novel method for treating dry eyes. The method
 CC comprises obtaining a composition containing the nucleotide sequence of
 CC 15-lipoxygenase (15-LO)-1 or 15-LO-2, and administering the composition
 CC to a patient suffering from dry eye under conditions such that the
 CC nucleotide sequence of 15-LO-1 or 15-LO-2 is expressed. The invention
 CC further comprises a composition for the treatment of dry eye, comprising
 CC a vector having the above nucleotide sequence and an excipient. The 15-LO
 CC compositions have ophthalmological activity and may be used in gene
 CC therapy to treat disorders. The method is useful for treating dry eyes in
 CC postmenopausal women. This sequence represents the 15-lipoxygenase 1
 CC protein of the invention.
 XX SQ Sequence 662 AA;

Query Match 99.7%; Score 3503.5; DB 8; Length 662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MGLYRIRVSTGASLYAGSNQVQLWVGQHGEEALGKELWPARG-ETELKVEVEYLGPL 59
 Db 1 MGLYRIRVSTGASLYAGSNQVQLWVGQHGEEALGKELWPARGKETELKVEVEYLGPL 60
 Qy 60 LFVKLRKHLKDDAWFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGDDP 119
 Db 61 LFVKLRKHLKDDAWFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGDDP 120
 Qy 120 QGLFQKHREELERKLYRWGNWKDGLILNAGAKLYDLVDERFLDKRVDPEVSLAK 179
 Db 121 QGLFQKHREELERKLYRWGNWKDGLILNAGAKLYDLVDERFLDKRVDPEVSLAK 180
 Qy 180 GLADLAIKDSNLVLTWCXKDDFNRIFCGQSKLAERVRDSWKEDALFGYFLNGANPVV 239
 Db 181 GLADLAIKDSNLVLTWCXKDDFNRIFCGQSKLAERVRDSWKEDALFGYFLNGANPVV 240
 Qy 240 LRRSAHLPARLVFPFGMELOAQLEKELEGTLFEADFSLLDGIKANVILCSQQHLAAPL 299
 Db 241 LRRSAHLPARLVFPFGMELOAQLEKELEGTLFEADFSLLDGIKANVILCSQQHLAAPL 300
 Qy 300 VMLKLOPKGLLPMVIOQLPRTGSPRPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359
 Db 301 VMLKLOPKGLLPMVIOQLPRTGSPRPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 360
 Qy 360 LLRGLHMAEIVVATMRCLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
 Db 361 LLRGLHMAEIVVATMRCLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420
 Qy 420 GGGGHVQLLKQAGAPLTYSFSCPPDDLDADRGLLGVKSSFYAQDALRLWEIIRYVEGIVS 479
 Db 421 GGGGHVQLLKQAGAPLTYSFSCPPDDLDADRGLLGVKSSFYAQDALRLWEIIRYVEGIVS 480

Qy 480 LHYKTDVAVKDDPELQTWCREITEIGLQGAQDRGFPVLSLOARDQVCHFTWCIETCTGQH 539
 Db 481 LHYKTDVAVKDDPELQTWCREITEIGLQGAQDRGFPVLSLOARDQVCHFTWCIETCTGQH 540
 Qy 540 ASVHLGOLDWYSWVPNAPCTMRLLPPPTTKDATTLETVMATLTPNPHQASLQMSITWOLGRQ 599
 Db 541 ASVHLGOLDWYSWVPNAPCTMRLLPPPTTKDATTLETVMATLTPNPHQASLQMSITWOLGRQ 600
 Qy 600 PMVAVGQHEEYFSGPEPKAVLKKEFEELAAALDKETIEIRNAKLDMPYELRPSVVENS 659
 Db 601 PMVAVGQHEEYFSGPEPKAVLKKEFEELAAALDKETIEIRNAKLDMPYELRPSVVENS 660
 Qy 660 AI 661
 Db 661 AI 662

RESULT 6
 ABB08005
 ID ABB08005 standard; protein; 684 AA.
 XX AC ABB08005;
 XX DT 27-AUG-2002 (first entry)
 XX DE Human lipid metabolism enzyme (LME)-5 (Id: 7484270CD1).
 XX KW Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective;
 KW nontropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;
 KW anticlerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;
 KW gene therapy; protein therapy; enzyme.
 XX OS Homo sapiens.
 XX PN WO200229036-A2.
 XX PD 11-APR-2002.
 XX PF 05-OCT-2001; 2001WO-US031302.
 XX PR 06-OCT-2000; 2000US-0238388P.
 PR 13-OCT-2000; 2000US-0240616P.
 PR 02-NOV-2000; 2000US-0245719P.
 PR 08-NOV-2000; 2000US-0247503P.
 PR 17-NOV-2000; 2000US-0249503P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX PI Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;
 PI Walia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;
 PI Lal PG, Tribouley CM;
 XX WPI; 2002-315862/35.
 DR N-PSDB; ABL60541.
 XX Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-
 PT Jakob disease.
 XX Claim 1; Page 116-118; 127pp; English.
 XX The invention relates to human lipid metabolism enzymes (LMEs) and
 CC encoding polynucleotides. The LMEs can be expressed by standard
 CC recombinant technology. The LME polypeptides, polynucleotides and
 CC modulators may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate LME expression such as cancer
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
 CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
 CC pectoris and mitral valve prolapse). The present sequence represents the
 CC human LME-5 polypeptide

QY 240 LRRSAHLPARLVFPFGMEELQAELEGGLTLEADPSLLDGIKANVILCSOOHLAAPL 299
 Db 241 LKRSTCLPARLVFPFGMEELQAELEGGLTLEADPSLLDGIKANVILCSOOHLAAPL 300
 QY 300 VMLKLPDQKLLPMVQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359
 Db 301 VMLKLPDQKLLPMVQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 360
 QY 360 LLRGLHMAEVIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 419
 Db 361 LLRGLHMAEVIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 420
 QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODALRLWEIIRYVEGIVS 479
 Db 421 GGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODALRLWEIIRYVEGIVS 480
 QY 480 LHYKTDVAVKDDPELQTCREITTEIGLOAQDGRFPVSLQARDQVCHFWTCIFCTGQH 539
 Db 481 LHYKTDVAVKDDPELQTCREITTEIGLOAQDGRFPVSLQARDQVCHFWTCIFCTGQH 540
 QY 540 ASVHLGOLDWYSVWPNAPCTWRLPPTTKDATTLETVMATLNFHQAISQMSITWOLGRRQ 599
 Db 541 SSVHLGOLDWYSVWPNAPCTWRLPPTTKDATTLETVMATLNFHQAISQMSITWOLGRRQ 600
 QY 600 PWWAVGQHEEYFSGPEKAVLKXFRELAALDKKEIRNAKLDMPYELRPSVWNSV 659
 Db 601 PWWAVGQHEEYFSGPEKAVLKXFRELAALDKKEIRNAKLDMPYELRPSVWNSV 660
 QY 660 AI 661
 Db 661 AI 662
 RESULT 8
 ID ADJ76170 standard; protein; 663 AA.
 XX ADJ76170;
 AC ADJ76170;
 DT 20-MAY-2004 (first entry)
 XX Marker gene related amino acid sequence SEQ ID NO:1422.
 DE bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX Mus musculus.
 OS EPI394274-A2.
 FN 03-MAR-2004.
 PD 04-AUG-2003; 2003EP-00254857.
 PF 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX (GENO-) GENOX RES INC.
 PA Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 PI WPI; 2004-193155/19.
 DR Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX Claim 16; SEQ ID NO 1422; 241pp; English.
 PS The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises

CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC cells (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

Sequence 663 AA;

Query Match 76.2%; Score 2676; DB 8; Length 663;
 Best Local Similarity 73.6%; Pred. No. 6.3e-268;
 Matches 488; Conservative 80; Mismatches 93; Indels 2; Gaps 2;
 QY 1 MGLYRIVSTGASLYAGSNNOVLVQGHGEAALGKRLMPAR-GETELKVEVPEYLGPL 59
 Db 1 MGVTRIVSTGDSVYAGSNNEVYLWLGQHEASLGKLFRCRNSAEAFKVDVSEYLGPL 60
 QY 60 LFVKLRKHLKDDAWFCNWIISVQGP-AGDEVFPFCYRVWVEGVNGLSLPGTGTGTGVED 118
 Db 61 LFRVQKWHYLVKEDAWFCNWIISVQGPQDSSEYTFPCYRVWVQGTSLNLPSTGTCVVED 120
 QY 119 PQGLFQKREBELEERRKLYRWGNWKGDLILNAGAKLYDLPVDFERFLEKRVDFEVSIA 178
 Db 121 SQGLFRHREBELEERSLYRWGNWKGDTILNVAATSSISDLPVDFQRFREKLEFEASV 180
 QY 179 KGLADLAIKDSLNVLTCTWKDLDDFNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPV 238
 Db 181 LGTWDVTINFPKNTVTCWKSLLDDFNRYFKSGHTKMAERVNSWKEDAFFGYQFLNGANPM 240
 QY 239 VLRRSAHLPARLVFPFGMEELQAELEGGLTLEADPSLLDGIKANVILCSOOHLAAP 298
 Db 241 VLKSTCLPARLVFPFGMEELQAELEGGLTLEADPSLLDGIKANVILCSOOHLAAP 300
 QY 299 LVMLKLPDQKLLPMVQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 358
 Db 301 LVMLKLPDQKLLPMVQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 360
 QY 359 LLRGLHMAEVIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 418
 Db 361 LLRGLHMAEVIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 420
 QY 419 TGGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODALRLWEIIRYVEGIV 478
 Db 421 TGGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODALRLWEIIRYVEGIV 480
 QY 479 SLHYKTDVAVKDDPELQTCREITTEIGLOAQDGRFPVSLQARDQVCHFWTCIFCTGQH 538
 Db 481 DLYYKTDQAVQDDYELQSWCQEIITEIGLOAQDGRFPVSLQARDQVCHFWTCIFCTGQH 540
 QY 539 HASVHLGOLDWYSVWPNAPCTWRLPPTTKDATTLETVMATLNFHQAISQMSITWOLGRR 598
 Db 541 HSSVHLGOLDWYSVWPNAPCTWRLPPTTKDATTLETVMATLNFHQAISQMSITWOLGRR 600

XX WO2004058052-A2.
 XX PD 15-JUL-2004.
 XX PF 22-DEC-2003; 2003WO-US040978.
 XX PR 20-DEC-2002; 2002US-0434778P.
 XX PR 10-MAR-2003; 2003US-0453135P.
 XX PR 30-APR-2003; 2003US-0466412P.
 XX PR 23-SEP-2003; 2003US-0504955P.
 XX PA (APPL-) APPLERA CORP.
 XX PI Cargill M, Devlin JJ, Iakoubova O;
 XX DR WPI; 2004-533949/51.
 XX DR N-PSDB; ADQ39008.
 XX PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX PS Claim 10; SEQ ID NO 1499; 145pp; English.
 XX CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX SQ Sequence 563 AA;
 Query Match 65.9%; Score 2316; DB 8; Length 663;
 Best Local Similarity 65.5%; Pred. No. 1.6e-230;
 Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;
 QY 1 MGLRIRVSTGASLYAGSNQVQLWLVGQHGAEALGKELWPARG-ETELKVEVEYLGPL 59
 DB 1 MGRYRIRVATGAWLFGSGYNRYQLWLVGTRGAELEQLRFPARGEEFDDHVAEDLGL 60
 QY 60 LPVLRKRLKDDAWFCNWLISVQPGAGDEVRPPCYRWEGNVLSPGEGTRVGGDP 119
 DB 61 QFVLRKHHVLVDWAFVCDRTVQPGACAEVAFPCYRWVQGEDILSLPEGTARLPGNA 120
 QY 120 QGLFQKREELERKLYRWGNWKGILNAGAKLYDLPVDERFLEDKRVDFEVSIAK 179
 DB 121 LDMFKHREKELKDRQYICWATWKEGLPLTIAADRKDDLPPNMFHEEKKLDFEWTLKA 180
 QY 180 GLADLAIVKSNLVTCKWDLDDFNRIFWCGSGKLAERVRDWSKEDALLFGYQFLNGANPV 239

DB 181 GALEWALKRVYVTLTLLSWNCLEDFQIFWGQKSALEAKVRQCWQDDELFSYQFLNGANPWL 240
 QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGTLTLEADPSLLDGKANKVILCSQOHLAAPL 299
 DB 241 LRRSTSLPSRLVLPSCGMEELQAQLEKELEGTLTLEADPSLLDGKANKVILCSQOHLAAPL 300
 QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359
 DB 301 VMLKMEPENGKLPQMVIOQLPRTGSPPPPLPTDPPMAWLLAKCWVRSSDFQLHELQSH 360
 QY 360 LLRGLHMAEVIVVATMRCPLPSIHPFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMST 419
 DB 361 LLNTHLVAEIVATVATMRCPLPSIHPFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMST 420
 QY 420 GGGHVQLLQOAGAFLYSYSCPPDDDLADRGLLGVKSSFYAQDALRLWEIIRYVEGIVS 479
 DB 421 GGGHVQLLQOAGAFLYSYSCPPDDDLADRGLLGVKSSFYAQDALRLWEIIRYVEGIVS 480
 QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGDRGFPVSLQARDQVCHPVTWCIFCTCGH 539
 DB 481 LFYQRDDIVKGDPLQAWCREITEIGLQAGDRGFPVSLQARDQVCHPVTWCIFCTCGH 540
 QY 540 ASVHLGQLDWYSWVNPACTMRLPPPTTK-DATLETVMATLPNFHQASLQMSITWQLGRR 598
 DB 541 AAINQGQLDWYAVNPACTMRLPPPTTKEDVTWATVWGSIPDVQACIQMAISWHLSSR 600
 QY 599 QPVMVAVQHEEYFSGPEPKAVLKFPREELALDKSIEINNAKLDMPEYELRPSVWENS 658
 DB 601 QPDMVPLGHKKEKYFSGPKKAVLNQFRTOLEKKEITARNEQLDMPYELKPSCIENS 660
 QY 659 VAI 661
 DB 661 VTI 663
 RESULT 11
 ADS10679
 ID ADS10679 standard; protein; 647 AA.
 AC ADS10679;
 DT 16-DEC-2004 (first entry)
 DE Human therapeutic protein - SEQ ID 916.
 KW antinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.
 OS Homo sapiens.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PF 30-SEP-2003; 2003WO-US030720.
 PR 02-OCT-2002; 2002US-0416186P.
 PA (NUVE-) NUVELO INC.
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y; Zhou P;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 DR WPI; 2004-668857/65.
 DR N-PSDB; ADS09995.
 PT New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anemia or cancer for promoting wound healing.
 PS Claim 20; SEQ ID NO 916; 718pp; English.
 XX

CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX
SQ Sequence 647 AA;

Query Match 65.4%; Score 2298.5; DB 8; Length 647;
Best Local Similarity 67.8%; Pred. No. 1e-228;
Matches 442; Conservative 83; Mismatches 120; Indels 7; Gaps 6;

QY 1 MGLYRIRVSTGASLYAGSNNOVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 59
Db 1 MGKYTRVATGDLGLLAGSPNLVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 60
QY 60 LFVKLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 119
Db 61 LMVKLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKREELERKLYRNKGNKDGILNMGAKLYDLPVDERFLEDKRVDPEVSLA 178
Db 121 QNLFKYRQELERKLYRNKGNKDGILNMGAKLYDLPVDERFLEDKRVDPEVSLA 180
QY 179 KGLADIKIDSLNVLTCWKDLDNFRIFWCGOSKLAERVRDSWKEDALFGYQFLNGANPV 238
Db 181 KG-DLAIKGTLDNFVCKVRLEDFKIPPHGKTVLAERVYDSWKNDAPFGYQFLNGANPV 238
QY 239 VLRSALHRLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKANKVILCSQOHLAAP 298
Db 239 LLRCSRLPACLVPPGMELOAQLEKEGTLFEADPSLIDGKANKVILCSQOHLAAP 298
QY 299 LVMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQS 358
Db 299 LVMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQS 357
QY 359 HLLRGLHMAEIVAVATMRSLPSLPIHPIKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMS 418
Db 358 HLLRGLHMAEIVAVATMRSLPSLPIHPIKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMS 417
QY 419 TGGGHVQLLKQAGFLTYSSCPDDIADRLGLGVKSSFYAQDALRLWEIIVRYVEGIV 478
Db 418 TGGGHVQLLKQAGFLTYSSCPDDIADRLGLGVKSSFYAQDALRLWEIIVRYVEGIV 476
QY 479 SLHYKTDVAKDDPELOTWCREITTEIGLQAGDORGFVPSLOARDQVCHFTVTCIFCTGQ 538
Db 477 GLFYNSDQAKDDLELAQWCREWTEGLQAGDORGFVPSLOARDQVCHFTVTCIFCTGQ 536
QY 539 HASVHLGQLDWYSWVFNAPCTMLRPLPTTKDATLETWATLPNFHQAQMSITWOLGR 598
Db 537 HASVHLGQLDWYSWVFNAPCTMLRPLPTTKDATLETWATLPNFHQAQMSITWOLGR 596
QY 599 QPVMVAVGQHEEYFSGPPKAVLKFKFRELEAALDKIEIRNAKLDMPYEYL 650
Db 597 QPVMVR-SKHEEYFSGPPKAVLKFKFRELEAALDKIEIRNAKLDMPYEYL 647

RESULT 12
AAB24019
ID AAB24019 standard; protein; 663 AA.

XX
AC AAB24019;
XX
DT 25-JAN-2001 (first entry)
XX
DE Arachidonic acid metabolism related protein sequence #653.
XX Human; biallelic marker; arachidonic acid metabolism; genotyping;
KW

KW detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
KW single nucleotide polymorphism; hybridisation assay; sequencing assay;
KW specific amplification assay; identification; ERM; 12-LO-RBM;
KW eicosanoid-related biallelic marker; 12-LO-related biallelic marker.

OS Homo sapiens.

XX WO200047771-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-IB000184.

XX 12-FEB-1999; 99US-0119917P.

XX 23-MAR-1999; 99US-00275267.

XX 07-MAY-1999; 99US-0133200P.

XX (GEST) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I;

XX WPI; 2000-571881/53.

XX N-PSDB; AAC58018.

PT Novel biallelic markers useful for detecting conditions and genotypes
associated with arachidonic acid metabolism.

PS Claim 75; Page 800-801; 802pp; English.

XX The present invention describes polynucleotides including biallelic
markers derived from genes involved in arachidonic acid metabolism and
from genomic regions flanking those genes. Methods from the present
invention may be used to select individuals for clinical trials and
predict responses to treatment with drugs. The polynucleotides may be
used in hybridisation assays, sequencing assays and specific
amplification assays for identifying an eicosanoid-related biallelic
segment of nucleotides containing an ERM. The polynucleotides are useful
in diagnostic kits. The markers may be used to detect conditions and
genotypes associated with arachidonic acid metabolism. AAC57367 to
AAC58018 and AAB24019 and AAB24020 represent sequences used in the
exemplification of the present invention

XX Sequence 663 AA;

Query Match 64.9%; Score 2280; DB 3; Length 663;
Best Local Similarity 64.7%; Pred. No. 8.e-227;
Matches 429; Conservative 92; Mismatches 140; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNNOVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 59

Db 1 MGKYTRVATGDLGLLAGSPNLVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 60

QY 60 LFVKLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 119

Db 61 QFVLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 120

QY 120 QGLFQKREELERKLYRNKGNKDGILNMGAKLYDLPVDERFLEDKRVDPEVSLA 179

Db 121 LDMFKREELERKLYRNKGNKDGILNMGAKLYDLPVDERFLEDKRVDPEVSLA 180

QY 180 GLADIKIDSLNVLTCWKDLDNFRIFWCGOSKLAERVRDSWKEDALFGYQFLNGANPV 239

Db 181 GALEMALXXVYTLSSWNCLEDFDQIFWQKSALEKRVQCDXELFSYQFLNGANPV 240

QY 240 LRSALHRLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKANKVILCSQOHLAAP 299

Db 241 LRSALHRLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKANKVILCSQOHLAAP 300

QY 300 VMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQS 359

Db 301 VMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQS 360


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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1: 632
XX FT /label= Unknown, OTHER
XX FT /note= "OTHER = In-frame STOP codon"
XX PN WO2004080148-A2.
XX PN
XX PD 23-SEP-2004.
XX PF 30-SEP-2003; 2003WO-US030720.
XX PR 02-OCT-2002; 2002US-0416186P.
XX PA (NUVE-) NUVELO INC.
XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX DR WPI: 2004-668857/65.
XX DR N-PSDB; ADS11349.
XX CC New polynucleotide, useful in preparing a composition for diagnosing or
XX FT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX FT aplastic anemia or cancer for promoting wound healing.
XX PS Example 2; SEQ ID NO 2184; 718pp; English.
XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic contig
XX CC
XX CC Sequence 632 AA;
XX CC
XX CC Query Match 63.5%; Score 2230.5; DB 8; Length 632;
XX CC Best Local Similarity 64.8%; Pred. No. 1.1e-221;
XX CC Matches 430; Conservative 80; Mismatches 119; Indels 35; Gaps 4;
XX CC
XX CC 1 MGLYRTRVSTGASLYAGSNVQVQLWLVQGHGAALGKRLWPARG-FTELKVEVPEVLGPI 59
XX CC 1 MGKYTVRVATGDLILLAGSPNLVQLVGEHGEADLGKQLPPVWVGKAEFEIDVPLHLGRL 60
XX CC
XX CC 60 LFVKLRKRHLKDDAFNCWISVQGGAGDEVRFPCYRWVGGVLSLPEGTGRTVGEDP 119
XX CC 61 LMVKLRKHVLLSLDFCKWISVQGGFTQGAFFPCYRWVQGHGIIICLPEGT----- 112
XX CC
XX CC 120 QGLFQKHREBELEBERRKLYRWGNWKGDLINMAGAKLYDLVDVERFEDKRVDFEVS LAK 179
XX CC 113 -----RWGSKWKGDLILPIAGNRQPDLPDRERFLEDKDLDFNVS LAK 153
XX CC
XX CC 180 GLADLAIKSLNVLVTCKWLDLDFNRIFWCQSKLAERVDKSWKEDALFGYQFLNGANPVV 239
XX CC 154 GLKDLAIKGTLDLDFINCKRLEDFKFI FPHGKTVLAERVVDKWNKDAFFGYQFLNGANPML 213
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XX CC 240 LRSAHLPARLVPPGMEELQALEKEGGTLFEADFSLLDGIKANVILCSQOHLAAPL 299
XX CC 214 LRCSRLPACLVLPQGMEDLKTQLEKELQNGSLFEVDLSLDGKVNVI FKKQCVAAEL 273
XX CC
XX CC 300 VMKLQPDGKLLPMVJQLQPRTGSPPPPLFLPTDPPMAWLLAKWVRSSDFQLHELQSH 359
XX CC 274 VVLKLPQDGGLLPMVJQLQPPXHGCPPLFLFSPHPEMAWLLAKTWVRSSDFQLQQLQSH 333
XX CC
XX CC 360 LLRGHLMAEVIVVATWRLCPSPHPIPKLIIPHLRYTLEINVRARTGLVSDMGIDQIMST 419
XX CC 334 LLRGHLIAEVIAVATWRLSPSLPIYKLIIPHFRYTMINTLAQSSLSVSEWGFIDLIVST 393
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QY 420 GGGGHVQLLKQAGAFITYTSFPCPPDDLADRGLLGVKSSFYAQDALLRLWEIIVR--YVEGI 477
DB 394 GSGSHVDILQRAMACLTVHSLCPCPPDDLADRGLLDVKSSFYGXDAIRLWGLISREXYVEGM 453
QY 478 VSLHYKTDVAVKDDPELQTNCREITEIGLQAGNDRGFPVLSQARDQOVCHFTVMCIPTCTG 537
DB 454 VGLFYNSDQAMKDDLELQACREMTETGLQRAQDQGFLLISLSSRAQLCHFTVMCIPTCTG 513
QY 538 QHASVHLGOLDWYSWVPNAPCTMRPLPPTTKDATLETVMATLPNPFHQASLQMSITWQLGR 597
DB 514 QHASNHLGOLDWYSWIPNGPCTMQKPPFISKDVTEKDIDVLLPNLHQARMQKTFKFLGR 573
QY 598 RQPMVAVGQHHEEYFSGPEPKAVLKPFRELAALDKIEIRNAKLDMPEYVYLRSSVVEN 657
DB 574 RQPMV-----HEEKYFSGPEFQAVLRQFQEBLASMCKEIEVRNAVILNLPCELYLXPSMVEN 628
QY 658 SVAI 661
DB 629 SVTI 632

RESULT 15
ADSI1945
ID ADSI1945 standard; protein; 632 AA.
AC ADSI1945;
XX 16-DEC-2004 (first entry)
XX Human therapeutic contig protein - SEQ ID 2182.
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FT Misc-difference 1: 632
XX FT /label= Unknown, OTHER
XX FT /note= "OTHER = In-frame STOP codon"
XX WO2004080148-A2.
XX 23-SEP-2004.
XX 30-SEP-2003; 2003WO-US030720.
XX 02-OCT-2002; 2002US-0416186P.
XX (NUVE-) NUVELO INC.
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX DR WPI: 2004-668857/65.
XX DR N-PSDB; ADS11347.
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX FT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX FT aplastic anemia or cancer for promoting wound healing.
XX PS Example 2; SEQ ID NO 2182; 718pp; English.
XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic contig
XX CC
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:41:37 ; Search time 111.649 Seconds
(without alignment)
3031.690 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLYRIRVSTGASLYAGSNN.....KLDMPYELRPSVSVNSVAI 661

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3498.5	99.6	661	1	LOX1_HUMAN	P10500 homo sapien
2	3085	87.8	662	1	LOXP_BOVIN	P27479 bos taurus
3	3054	86.9	662	1	LOXP_PIG	P16469 sus scrofa
4	2891	82.3	662	1	LOX1_RABIT	P12530 oryctolagus
5	2889	82.2	662	1	LOXP_RABIT	O19043 oryctolagus
6	2891	76.6	662	1	LOX2_RAT	O02759 rattus norv
7	2882	76.3	663	2	Q6PHB2	Q6phb2 mus musculus
8	2671	76.0	662	1	LOXL_MOUSE	P39654 mus musculus
9	2352.5	66.9	662	1	LOXE_MOUSE	P55249 mus musculus
10	2350.5	66.9	662	2	Q91YW6	Q91yw6 mus musculus
11	2312	65.8	663	2	Q6ISF8	Q6isf8 homo sapien
12	2310	65.7	662	1	LOXP_HUMAN	P18054 homo sapien
13	2258	64.3	663	2	QBBHG4	Q8bhg4 m mus muscu
14	2247	63.9	662	1	LOXP_MOUSE	P39655 mus musculus
15	1905.5	54.2	555	2	Q95103	Q95103 bos taurus
16	1442	41.0	670	2	Q7T2A9	Q7t2a9 brachydanio
17	1298.5	37.0	673	1	LOX5_MOUSE	P48999 mus musculus
18	1297.5	36.9	673	1	LOX5_HUMAN	P09917 homo sapien
19	1290	36.7	672	1	LOX5_RAT	P12527 rattus norv
20	1271	36.2	672	1	LOX5_MESAU	P31399 mesocricetu
21	1255.5	35.7	390	2	Q8C5B7	Q8c5b7 mus musculus
22	1213.5	34.5	686	2	Q6GJ24	Q6gj24 xenopus lae
23	1203.5	34.2	676	2	O81YQ2	O81yq2 homo sapien
24	1202.5	34.2	676	1	LX1B_HUMAN	O15296 homo sapien
25	1198.5	34.1	667	2	Q9XT59	Q9xt59 bos taurus
26	1184	33.7	677	1	LX1B_MOUSE	O35936 mus musculus
27	1153	32.8	711	1	LXE3_HUMAN	Q9byj1 homo sapien
28	1150	32.7	711	1	LXE3_MOUSE	Q9wv07 mus musculus
29	1143	32.5	677	2	Q8K4F2	Q8k4f2 rattus norv
30	1124	32.0	701	1	LOXR_HUMAN	O75342 homo sapien
31	1113	31.7	234	2	Q6SYC4	Q6syc4 bos taurus

32	1093	31.1	701	1	LOXR_MOUSE	O70582 mus musculus
33	947	26.9	238	2	Q64042	Q64042 rattus sp.
34	863.5	24.6	1066	1	AOSL_PLEHO	O16025 plexaura ho
35	816.5	23.2	430	2	Q9BEG3	Q9beg3 bos taurus
36	522.5	14.9	917	2	Q9CAG3	Q9cag3 arabidopsis
37	508	14.5	922	2	Q93YA9	Q93ya9 sesbania ro
38	502.5	14.3	565	2	Q82V62	Q82v62 nitrosomona
39	500.5	14.2	896	1	LX23_HORVU	Q8gm2 hordeum vul
40	498.5	14.2	133	2	Q9UQM4	Q9uqm4 homo sapien
41	497	14.1	912	2	Q9LQJ5	Q9lqj5 arabidopsis
42	497	14.1	919	2	Q9LNR3	Q9lnr3 arabidopsis
43	497	14.1	919	2	Q9SMW1	Q9smw1 arabidopsis
44	496.5	14.1	865	2	Q93W22	Q93w22 gossypium h
45	496.5	14.1	900	2	Q6X5R6	Q6x5r6 nicotiana a

ALIGNMENTS

RESULT 1
LOX1_HUMAN
ID LOX1_HUMAN STANDARD; PRT; 661 AA.
AC P16050; Q8N6R7; Q99657;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 15-lipoxygenase (EC 1.13.11.33) (Arachidonate omega-6
DE lipoxygenase) (15-LOX).
GN Name=ALOX15; Synonyms=LOG15;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=89076270; PubMed=3202857;
RA Sigal E., Craik C.S., Highland E., Grunberger D., Costello L.L.,
RA Dixon R.A.F., Nadel J.A.;
RT "Molecular cloning and primary structure of human 15-lipoxygenase.";
RL Biochem. Biophys. Res. Commun. 157:457-464(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Kritzik M.R., Zlobner A.F., Sigal E., Conrad D.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS HIS-89; LYS-102 AND GLN-204.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
FHCRRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RX MEDLINE=22382625; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.W., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human


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RESULT 2
ID LOXP BOVIN STANDARD; PRT; 662 AA.
AC P27479;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX).
GN Name=ALOX12;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tracheal epithelium;
RX MEDLINE=92170942; PubMed=1539676;
RA de Marzo N., Sloan D.L., Dicharry S., Highland E., Sigal E.;
RT "Cloning and expression of an airway epithelial 12-lipoxygenase.";
RL Am. J. Physiol. 262:L198-L207(1992).
CC - FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC - CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-
CC 12-hydroperoxycosa-5,8,10,14-tetraenoate.
CC - COFACTOR: Iron.
CC - PATHWAY: Leukotrienes biosynthesis.
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - SIMILARITY: Belongs to the lipoxygenase family.
CC - SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
DR EMBL; M81320; AAA30346.1; -.
DR EMBL; M62516; AAC41614.1; -.
DR EMBL; S96247; AAB21522.2; ALT_SEQ.
DR PIR; S32825; S32825.
DR HSP; P12530; ILOX.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase LH2.
DR InterPro; IPR001885; Mam.lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 By similarity.
FT DOMAIN 1 114 PLAT.
FT METAL 360 360 Iron (By similarity).
FT METAL 365 365 Iron (By similarity).
FT METAL 540 540 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
SQ SEQUENCE 662 AA; 74910 MW; 09C6B7BE91133E61 CRC64;
Query Match 87.8%; Score 3085; DB 1; Length 662;
Best Local Similarity 86.1%; Pred. No. 1.9e-232;
Matches 570; Conservative 48; Mismatches 42; Indels 2; Gaps 2;
QY 2 GLYRIVSTGSLYAGSNQVWLVGQHGGAALGKRLMPARG-ETELKVEYPEYLGPLL 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 1 GLYRIVSTGSSFCAGSNQVHMLVGEHGAALGWAVPARGKEVEFQVDVSEYLGRL 60
QY 61 FVKLKRHLKDDAWFCNWISVQVGASGNEFRPCYRWVEGDSGLSLPEGTGRTVDDP 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RT "Structure of the mRNA and of the gene coding for the rabbit erythroid
RL 15-lipoxygenase.";
RN Biomed. Biochim. Acta 49:S17-S24 (1990).
RP [5]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RA MEDLINE=98069648; PubMed=9406550;
RA Gillmor S.A., Villaseñor A., Fletcher R., Sigal E., Browner M.P.;
RT "The structure of mammalian 15-lipoxygenase reveals similarity to the
lipases and the determinants of substrate specificity.";
RL Nat. Struct. Biol. 4:1003-1009 (1997).
CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E)-(15S)-
CC 15-hydroperoxyicoso-5,8,11,13-tetraenoate.
CC -!- COFACTOR: Iron.
CC -!- PATHWAY: Leukotrienes biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
DR EMBL; M22617; AAA31385.1; -;
DR EMBL; M33291; AAA75014.1; -;
DR EMBL; M27214; AAB86978.1; -;
DR PIR; JQ0018; JQ0018.
DR PDB; 1LOX; X-ray; @=1-662.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.
DR InterPro; IPR001885; Mam_lipoxygenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW 3D-structure; Dioxigenase; Direct protein sequencing; Iron;
KW Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 0
FT DOMAIN 1 114 PLAT.
FT METAL 360 360 Iron.
FT METAL 365 365 Iron.
FT METAL 540 540 Iron.
FT METAL 544 544 Iron.
FT METAL 662 662 Iron.
FT CONFLICT 112 112 T -> I (in Ref. 2).
FT CONFLICT 189 189 N -> D (in Ref. 2).
FT CONFLICT 193 193 I -> V (in Ref. 2).
FT STRAND 2 9
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FT STRAND 606
FT TURN 617
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FT TURN 650
FT TURN 653
FT STRAND 657
SQ SEQUENCE 662 AA; 75178 MW; 92F99AF10E241B0A CRC64;

Query Match

82.3%; Score 2891; DB 1; Length 662;

Best Local Similarity 81.0%; Pred. No. 2.9e-217; Matches 536; Conservative 59; Mismatches 65; Indels 2; Gaps 2;			
QY	2	GLYRIRVSTGASLYAGSNNOVOLMLVGQGEALGKRLWPARG-ETELKVEVPEYLGPLL	60
Db	1	GVYRVCVSTGASLYAGSNKVELMLVGQGEVGLSCLRPTRNKBEFKVNVSKYLGSL	60
QY	61	FVKLRKRLHLLKDDAWFCNWSISVQGPAG-DEVRFPCYRWVEGNVLSLPEGTGRTVGDP	119
Db	61	FVRLKXKHPLEKEDAWFCNWSISVQALGAEDKYWFFCYRWVGVGQSLPVGTGCTVGD	120
QY	120	QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDVEVSLAK	179
Db	121	QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDVEVSLAK	180
QY	180	GLADLAIKDLSNLVTCWKDLDNFRIFWCQSKLAERVRDSKEDALFCYQFLNGANPV	239
Db	181	GLAELALKNSLILAPWKTLDNFRIFWCGRSKLARRVRDSWQEDSLFGYQFLNGANP	240
QY	240	LRRSAHLPARLVFPFGMEELQALEKELEGGTLPDPPMAWLLAKCWVRSSDQVH	299
Db	241	LRRSAHLPARLVFPFGMEELQALEKELEGGTLPDPPMAWLLAKCWVRSSDQVH	300
QY	300	VMLKLPDQDKLPMVITQOLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDQVH	359
Db	301	VMLKLPDQDKLPMVITQOLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDQVH	360
QY	360	LRRGHMAEVIVVATMRCPLPSHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIM	419
Db	361	LRRGHMAEVIVVATMRCPLPSHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIM	420
QY	420	GGGGHVQLLKQAGAFITYSSFCPPDLDLDRGLLVKSSFYAODALRLWEIIRYVEG	479
Db	421	GGGGHVQLLKQAGAFITYSSFCPPDLDLDRGLLVKSSFYAODALRLWEIIRYVEG	480
QY	480	LHYKTDAVKDDELQVTCREITEIGLQAGQGRFPVLSIQAQDVCHFTVTCI	539
Db	481	LHYKTDAVKDDELQVTCREITEIGLQAGQGRFPVLSIQAQDVCHFTVTCI	540
QY	540	ASVHLGOLDWYSVVRNAPCTMRLPPPTTKDLETATLETVMATLPHFQASLQMSIT	599
Db	541	SSIHGLQDWFVTWVNPACTMRLPPPTTKDLETATLETVMATLPHFQASLQMSIT	600
QY	600	PVAVAGQHEEYFSGPEKAVLKKEFEELALDKIEIRNAKLMDPYEYLRPSVVEN	659
Db	601	PVAVAGQHEEYFSGPEKAVLKKEFEELALDKIEIRNAKLMDPYEYLRPSVVEN	660
QY	660	AI 661	
Db	661	AI 662	
RESULT 5			
LOXP RABIT			
ID	LOXP RABIT	STANDARD;	PRT; 662 AA.
AC	O19043;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX).		
GN	Names=ALOX12;		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98263260; PubMed=9600854; DOI=10.1006/jmbi.1998.1737;		
RA	Berger M., Schwarz K., Thiele H., Reimann I., Huth A., Borngraeber S.,		
RA	Kuehn H., Thiele B.J.;		
RT	"Simultaneous expression of leukocyte-type 12-lipoxygenase and		
RT	reticulocyte-type 15-lipoxygenase in rabbits."		
RL	J. Mol. Biol. 278:935-948(1998).		

CC	-!	FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.	
CC	-!	CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-	
CC		12-hydroperoxyicoso-5,8,10,14-tetraenoate.	
CC	-!	COPACTOR: Iron.	
CC	-!	PATHWAY: Leukotrienes biosynthesis.	
CC	-!	SUBCELLULAR LOCATION: Cytoplasmic.	
CC	-!	SIMILARITY: Belongs to the lipoxygenase family.	
CC	-!	SIMILARITY: Contains 1 PLAT domain.	
CC	-!	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC		the European Bioinformatics Institute. There are no restrictions on its	
CC		use by non-profit institutions as long as its content is in no way	
CC		modified and this statement is not removed. Usage by and for commercial	
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC		or send an email to license@isb-sib.ch).	
CC		-----	
DR	EMBL;	297654; CAB10746.1; -.	
DR	HSSP;	P12530; ILOX.	
DR	InterPro;	IPR000907; Lipoxygenase.	
DR	InterPro;	IPR001024; Lipoxygenase LH2.	
DR	InterPro;	IPR001885; Mam.lipoxygenase.	
DR	InterPro;	IPR008976; PLAT_LH2.	
DR	Pfam;	PF00305; Lipoxygenase; 1.	
DR	Pfam;	PF01477; PLAT; 1.	
DR	PRINTS;	PR00087; LIPOXYGENASE.	
DR	PRINTS;	PR00467; MAMLOXYGENASE.	
DR	SMART;	SM00308; LH2; 1.	
DR	PROSITE;	PS00711; LIPOXYGENASE_1; 1.	
DR	PROSITE;	PS00881; LIPOXYGENASE_2; 1.	
DR	PROSITE;	PS00995; PLAT; 1.	
KW	Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.		
FT	INIT MET	0	By similarity.
FT	DOMAIN	1	114
FT	METAL	360	Iron (By similarity).
FT	METAL	365	Iron (By similarity).
FT	METAL	540	Iron (By similarity).
FT	METAL	662	Iron (By similarity).
FT	SEQUENCE	662 AA;	48A780ED859F013E CRC64;
Query Match 82.2%; Score 2889; DB 1; Length 662;			
Best Local Similarity 81.0%; Pred. No. 4.1e-217;			
Matches 536; Conservative 59; Mismatches 65; Indels 2; Gaps 2;			
QY	2	GLYRIRVSTGASLYAGSNNOVOLMLVGQGEALGKRLWPARG-ETELKVEVPEYLGPLL	60
Db	1	GVYRVCVSTGASLYAGSNKVELMLVGQGEVGLSCLRPTRNKBEFKVNVSKYLGSL	60
QY	61	FVKLRKRLHLLKDDAWFCNWSISVQGPAG-DEVRFPCYRWVEGNVLSLPEGTGRTVGDP	119
Db	61	FVRLKXKHPLEKEDAWFCNWSISVQALGAEDKYWFFCYRWVGVGQSLPVGTGCTVGD	120
QY	120	QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDVEVSLAK	179
Db	121	QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDVEVSLAK	180
QY	180	GLADLAIKDLSNLVTCWKDLDNFRIFWCQSKLAERVRDSKEDALFCYQFLNGANPV	239
Db	181	GLAELALKNSLILAPWKTLDNFRIFWCGRSKLARRVRDSWQEDSLFGYQFLNGANP	240
QY	240	LRRSAHLPARLVFPFGMEELQALEKELEGGTLPDPPMAWLLAKCWVRSSDQVH	299
Db	241	LRRSAHLPARLVFPFGMEELQALEKELEGGTLPDPPMAWLLAKCWVRSSDQVH	300
QY	300	VMLKLPDQDKLPMVITQOLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDQVH	359
Db	301	VMLKLPDQDKLPMVITQOLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDQVH	360
QY	360	LRRGHMAEVIVVATMRCPLPSHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIM	419
Db	361	LRRGHMAEVIVVATMRCPLPSHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIM	420
QY	420	GGGGHVQLLKQAGAFITYSSFCPPDLDLDRGLLVKSSFYAODALRLWEIIRYVEG	479


```

RESULT 7
Q6PHB2
ID AC Q6PHB2 PRELIMINARY; PRT; 663 AA.
DR PROSITE; PSS0095; PLAT; 1.
KW Dioxigenase; Oxidoreductase.
SQ SEQUENCE 663 AA; 75417 MW; 86D7AA8FD380C787 CRC64;

Query Match 76.3%; Score 2682; DB 2; Length 663;
Best Local Similarity 73.8%; Pred. No. 6.5e-201;
Matches 489; Conservative 80; Mismatches 92; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNNNOVLWVGQHGAEALGKRLWPAR-GETELKVVPEYLGPL 59
Db 1 MGVYRIRVSTGDSVYAGSNNNEVYLWLGQHGASLGKLFRCNSEAEAFKVDVSEYLGPL 60
QY 60 LFLVKLRKRLHLLKDDAWFCNWSVQGP-AGDEVRRPCYRVWVEGNGVLSPEGTGRTVGED 118
Db 61 LFLRVQKWHYLLKEDAWFCNWSVQGPQGGSEYTPFCYRWVQGTSLNLPETGCTVVED 120
QY 119 PQGLFQKREEREELERKLYRWGNWKGGLIINMAGAKLYDLDPDERFELEDKEDVEVSLA 178
Db 121 SQGLFRNHREREELERSLYRWGNWKGDTILNVAATSDLPVDQRFREKDEFEASOV 180
QY 179 KGLADLAIKDSLNVLTCKWLDLDDFNRIFCWGOSKLAERVDSWKEDALFGYQFLNGANPV 238
Db 181 LGTMDTVINFPKNTVTCWKSLLDDFNYSKSGHTKMAERVNSWKEDAFFGYQFLNGANPM 240
QY 239 VLRRSAHLPARLVPPPGMEELQAQLEKELEGTLFEADFLSLDGIKANVILCSQQHLAAP 298
Db 241 VLKRSTCLPARLVPPPGMEKLAQALDEELKKGTLFEADFFLLDGIKANVILCSQQYLAAP 300
QY 299 LVMLKLQDQKLLPMVIOLOLPRTCSPPLPLPTDPPMAMLLAKCWVRSSDFOLHELQS 358
Db 301 LVMLKLQDQKLLPITAIQLELPKTSPPPIPTDPPMDMLLAKCWVRSSDLQLHELQA 360
QY 359 HLLRGLHMAEVIVVATMRCPLSIHPIFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMS 418
Db 361 HLLRGLHVAEFAVATMRCPLSVHVFVKLLVPHLLYTWEINVRASDLISERGFDDKMS 420
QY 419 TGGGHVQLLKQAGAPLYTSVSPDDADRLGLLVKVSFYAQDALRLWEIYRYVEGV 478
Db 421 TGGGHVQLLKQAGAPLYTSVSPDDADRLGLLVKVSFYAQDALRLWEIYRYVEGV 480
QY 479 SLHYKTDVAVKDDPHLOTWCREITIGLQAGDQDGFVVSLOARDQVCHVTWCIFCTGQ 538
Db 481 DLYKTDQAVDDYELQSWCQBITEIGLQAGDQDGFVVSLOARDQVCHVTWCIFCTGQ 540
QY 539 HASVHLGOLDWYSWVNPACTMRLPPTTKDATLETWATLFPNHFQASLQNSITWOLGRR 598
Db 541 HSSIHLGLQDWFYVWNPACTMRLPPTTKDATMEKLMATLFPNQTQIINWVWMLGRR 600
QY 599 QPVMVAVGQHEEYFSGPEPKAVLKFKFREELAAALDKEIEIRNAKLDMPEYLRPSVENS 658
Db 601 QAVMVPLGQHSBEHFPNPEAKAVLKFKFREELAAALDKEIEIRNKSLLDIPVEYLRPSLVENS 660
QY 659 VAI 661
Db 661 VAI 663

RESULT 8
LOXL_MOUSE
ID LOXL_MOUSE STANDARD; PRT; 662 AA.
AC P39654;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase, leukocyte-type (EC 1.13.11.31) (12-LOX).
GN Name=Alox12; Synonyms=Alox15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and ICR; TISSUE=Spleen;

SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3, and FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zerbey B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Gialakos U., Smallick D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: Iron (By similarity).
CC -1- SIMILARITY: Belongs to the lipoxygenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; BC056625.1; -.
DR EMBL; BC081546; AAH81546.1; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006691; P:leukotriene metabolism; IEA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.
DR InterPro; IPR001885; Mam_lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGNASE.
DR PRINTS; PR00467; MAMLIPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_P5; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00711; LIPOXYGNASE_1; 1.
DR PROSITE; PS00081; LIPOXYGNASE_2; 1.

```

RX MEDLINE=94245713; PubMed=8188678;
 RA Chen X.-S., Kurre U., Jenkins N.A., Copeland N.G., Funk C.D.;
 RT "cDNA cloning, expression, mutagenesis of C-terminal isoleucine,
 RT genomic structure, and chromosomal localizations of murine 12-
 RT lipoxigenases.";
 RN J. Biol. Chem. 269:13979-13987(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=95110857; PubMed=7811740; DOI=10.1016/0005-2760(94)00199-9;
 RA Freire-Moar J., Alavi-Nassab A., Ng M., Mulkins M., Sigal E.;
 RT "Cloning and characterization of a murine macrophage lipoxigenase.";
 RL Biochim. Biophys. Acta 1254:112-116(1995).
 CC -!- FUNCTION: Oxigenase and 14,15-leukotriene A4 synthase activity.
 CC Converts arachidonic acid to 12(S)-hydro(pero)xyoctadecadienoic
 CC acid (12-HETE) and 15-hydro(pero)xyoctadecadienoic acid in a 3:1
 CC ratio. Converts as well linoleic acid to 13-hydro-
 CC (pero)xyoctadecadienoic acid.
 CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-
 CC 12-hydroperoxyoctadecadienoic acid.
 CC -!- COFACTOR: Iron.
 CC -!- PATHWAY: Leukotrienes biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Found in pituitary and pineal glands as well
 CC as leukocytes, kidney, aorta and small intestine.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
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 CC -----
 DR EMBL; U04331; AAA20658.1; -;
 DR EMBL; L34570; AAA64930.1; -;
 DR PIR; B54075; B54075.
 DR HSSP; P12530; ILOX.
 DR MGD; MGI:87997; Alox15.
 DR InterPro; IPR000907; Lipoxigenase.
 DR InterPro; IPR001024; Lipoxigenase_LH2.
 DR InterPro; IPR001885; Mam_lipoxigenase.
 DR Pfam; PF00305; Lipoxigenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR PRINTS; PR00467; MAMLIPOXYGENASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS50095; PLAT; 1.
 KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
 FT INIT_MET 0
 FT DOMAIN 1 114
 FT METAL 360 360 Iron (By similarity).
 FT METAL 365 365 Iron (By similarity).
 FT METAL 540 540 Iron (By similarity).
 FT METAL 662 662 Iron (By similarity).
 FT CONFLICT 36 36 K -> N (in Ref. 2).
 FT CONFLICT 118 118 E -> Q (in Ref. 2).
 FT CONFLICT 396 396 T -> N (in Ref. 2).
 SQ SEQUENCE 662 AA; 75313 MW; 5C94965B30767C2C CRC64;
 Query Match 76.0%; Score 2671; DB 1; Length 662;
 Best Local Similarity 73.6%; Pred. No. 4.7e-200;
 Matches 487; Conservative 80; Mismatches 93; Indels 2; Gaps 2;
 OY 2 GLYIRVSTGSLVAGSNVQVQLVWGQGAALGKRLWPAR-GTELEKVRPEVYLGPLL 60
 DB 1 GYIRVSTGSLVAGSNVNEVYLVWGQGAALGKRLWPAR-GTELEKVRPEVYLGPLL 60
 OY 61 FVLRKRHLKDDAWFCNWIISVQVQPG-AGDEVRFPCYRWVEGNGVLSLPEGTGRTVGBDP 119

Db 61 FVRVQKHYLKEDAWFCNWIISVQVQPGQGSYTFPCYRWVQGTSLNLPSTGCTVVEDS 120
 OY 120 QGLFQKREEREEERKLYRWGNWKDGLILNMACAKLYDLVPDRFLDKRVDFFVSLAK 179
 Db 121 QGLFNRHREEREEERKLYRWGNWKDGLILNVAATSISDLVPDQRFREDKLEFEASQVL 180
 OY 180 GLADLAIKDSLNVLTCKWDLDDNRIFWCQSKLAERVRDSWKEDALFGYQFLANGANPVV 239
 Db 181 GTMDTVINFPKQNTVTCWKSDDFNYPKSGHTKWAERVRNSWKEDAFGYQFLANGANPVV 240
 OY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGFTLEADPFLSDGKANKANVILCSQQHLAAPL 299
 Db 241 LKRSTCLPARLVFPFGMEKLAQDLDEELKGTLEADPFLSDGKANKANVILCSQQYLAAPL 300
 OY 300 VMLKLPDQKLLPMVIQLPRTGSPPPPLPLPTDPPMAWLLAKCWVRSSPQLHQLSH 359
 Db 301 VMLKLPDQQLPLTAIQLELPKGTSTPPPIFTPLDPPMDWLLAKCWVRSSDQLHQLQAH 360
 OY 360 LLRGHLMAEVIVVATMRCCLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIPQIMST 419
 Db 361 LLRGHLVAEVFAVATMRCCLPSVHFVFKLLVPHLLYTWEINVRASDLISERGFDPKVMST 420
 OY 420 GGGGHVOLLKQAGAFLLTVSSFCPPDDDLADRGLLGVKSSFYAODALRLWEIYRYVEGIVS 479
 Db 421 GGGHLLDLKQAGAFLLTVSSLCPPDDDLAERGLDITCFYKADALQMLQVWNRVYVGMFD 480
 OY 480 LHYKTDVAVKDDPBLQTCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCICTCTQGH 539
 Db 481 LYYKTDQAVQDDYELQSWCQBEITEIGLQGAQDRGFPVSLQSAQAACHFTICTCTCTA 540
 OY 540 ASVHLGQLDVYVWVNPAPCTMRLPPPTTKATLETVMATLNFHQASLQMSITWOLGRRQ 599
 Db 541 SSIHLGQLDVYVWVNPAPCTMRLPPPTTKATLETVMATLNFHQASLQMSITWOLGRRQ 600
 OY 600 PMYAVAGQHEEYVSGPEPKAVLKKFREELAAALDKIEIRNAKLDMPVEYLRPSVWNSV 659
 Db 601 AMVPLQGHSEHPNPNPEAKAVLKKFREELAAALDKIEIRNAKLDMPVEYLRPSVWNSV 660
 OY 660 AI 661
 Db 661 AI 662
 RESULT 9
 LOXE_MOUSE STANDARD; PRT; 662 AA.
 ID LOXE_MOUSE
 AC P55249;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Arachidonate 12-lipoxigenase, epidermal-type (EC 1.13.11.31) (12-LOX).
 GN Name=Alox12e; Synonyms=Alox12-ps2, Alox2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6 X 129/Sv; TISSUE=Epidermis;
 RX MEDLINE=96394429; PubMed=8798535; DOI=10.1074/jbc.271.38.23338;
 RA Funk C.D., Keeney D.S., Olliv E.H., Boeglin W.E., Brash A.R.;
 RT "Functional expression and cellular localization of a mouse epidermal
 RT lipoxigenase.";
 RL J. Biol. Chem. 271:23338-23344(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv; TISSUE=Epidermis;
 RX MEDLINE=96085100; PubMed=7492614; DOI=10.1016/0005-2760(95)00158-9;
 RA van Dijk K.W., Stoketee K., Havekes L., Frants R., Hofker M.;
 RT "Genomic and cDNA cloning of a novel mouse lipoxigenase gene.";
 RL Biochim. Biophys. Acta 1259:4-8(1995).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=skin;
 RX MEDLINE=97118602; PubMed=9037187; DOI=10.1016/S0014-5793(96)01517-7;
 RA Kinzig A., Fuerstenberger G., Mueller F., Vogel S., Mueller-Decker K.,
 RA Mincheva A., Lichten P., Marks F., Krieg P.;
 RT "Murine epidermal lipoxigenase (Aloxe) encodes a 12-lipoxygenase
 isoform.";
 RL FEBS Lett. 402:162-166(1997).
 CC - CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z) - (12S) -
 CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.
 CC
 CC - COFACTOR: Iron.
 CC
 CC - PATHWAY: Leukotrienes biosynthesis.
 CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC - TISSUE SPECIFICITY: Epidermal.
 CC - SIMILARITY: Belongs to the lipoxygenase family.
 CC - SIMILARITY: Contains 1 PLAT domain.
 CC - CAUTION: Was originally thought to be an arachidonate 8-
 CC lipoxygenase and was called LOX8.
 CC
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 CC
 CC -----
 DR EMBL; U19200; AAC52869.1; -
 DR EMBL; U24181; AAC52324.1; -
 DR EMBL; X99252; CAA67625.1; -
 DR HSSP; P12530; ILOX.
 DR MGD; MGI:1274790; Aloxi2e.
 DR InterPro; IPR000907; Lipoxygenase.
 DR InterPro; IPR001024; Lipoxygenase LH2.
 DR InterPro; IPR001885; Mam_lipoxygenase.
 DR Pfam; PF00305; Lipoxygenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR PRINTS; PR00467; MAMLIPOXGNASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS50095; PLAT; 1.
 KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
 FT DOMAIN 2 114
 FT METAL 360 360 Iron (By similarity).
 FT METAL 365 365 Iron (By similarity).
 FT METAL 540 540 Iron (By similarity).
 FT METAL 662 662 Iron (By similarity).
 FT CONFLICT 619 619 P -> A (in Ref. 2).
 SQ SEQUENCE 662 AA; 75455 MW; D67768415BE988F7 CRC64;
 Query Match 66.9%; Score 2352.5; DB 1; Length 662;
 Best Local Similarity 66.5%; Pred. No. 3.9e-175;
 Matches 438; Conservative 97; Mismatches 123; Indels 1; Gaps 1;
 QY 4 YRIVSTGASLVAGSNVQVLVGVGHGAALCKRLWPARG-ETELKVEVPYVGLPLFV 62
 Db 4 YKILVATGVSFVAGSANLVHLVGVGHGAALCKRLWPARG-ETELKVEVPYVGLPLFV 63
 QY 63 KLKRHLKDDAWFCNWNISVQVGGAGDEVRFPCCYRWVGVNGVLSLEPGTGTVEGDPQGL 122
 Db 64 KLKRQKGLLSDWFCFSITVQVGGTQGEAFFPCYSWVQKETICTETGALKVTDQNL 123
 QY 123 FQKHREELERKLVWGNWCKGLILNAGAKLYDLVDERLEPKRVDVFEVSLAKGLA 182
 Db 124 FRKYREQLERNRVYRWGSWKEGLILPAGSTERDLPRNQRFMKDKLDFSLSLKELK 183
 QY 183 DLIAKDLNVLTCWKDLNFRIFWCGQSKLABRVDKSWKEDALFGYQFLNGANPVVLR 242
 Db 184 NFAIKGTDLFVSVRQKLEIDYQVFPHTKTALPERVGSWKEDALFGYQFLNGANPMLLR 243
 QY 243 SAHLPARLVFPQGMEEBLOAQLEKELEGGTLFEADFSLLDGIKANVILCSQQLAAPLVML 302

Db 244 SMRLPARLVLPQGMEDVOTQLEKELKAGSLFEVDFSLDGVKPNIIIFKQYVTPAPLVML 303
 QY 303 KLPDGGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAMLLAKWVRSSDFQLHLOSHLIR 362
 Db 304 KLPDGRLLPMVIOQLPRTGSPPPPLFLPTDPPMAMLLAKWVRSSDFQLHLOSHLIR 363
 QY 363 GHLMAEVIIVATMRCPLPSIHFIPKLIIPHLYTYLEINVRARTGLVSDMGIDPQIMSTGGG 422
 Db 364 GHLMAEVIIVATMRCPLPSIHFIPKLIIPHLYTYLEINVRARTGLVSDMGIDPQIMSTGGG 423
 QY 423 GHVOLLKOAGAFPLTVSSPCPDDADRLGLGVKSSFYAQDALRLWEIIRYVVEGIVSLHY 482
 Db 424 GHVDILQRTATSLYRSPCPDDADRLGLGVKSSLYAQDALRLWEIIRYVVEGIVSLHY 483
 QY 483 KTDVAVKDDPELQVWCVRETEIGLQAGDRGFPVLSQARDQVCHFTVTCIFCTCQHASTV 542
 Db 484 RSDTDVKEDPELQVWCVRETEIGLQAGDRGFPVLSQARDQVCHFTVTCIFCTCQHASTV 543
 QY 543 HLGQLDWTSVNPACTWRLPPPTTKDATLETWATLENFHOASLOMSTWOLGRQPV 602
 Db 544 HLGQLDWTSVNPACTWRLPPPTTKDATLETWATLENFHOASLOMSTWOLGRQPV 603
 QY 603 VAVGQHEEYSGPEPKAVLKFKFEELAAALDKHEIRNAKLDMPYELRPSVVENSAI 661
 Db 604 VALGQHEEYSGPEPKAVLKFKFEELAAALDKHEIRNAKLDMPYELRPSVVENSAI 662
 RESULT 10
 QY1YW6 PRELIMINARY; PRT; 662 AA.
 ID QY1YW6
 AC QY1YW6;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
 DE Arachidonate lipoxygenase, epidermal.
 GN Name=Aloxi2e;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalski U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RA	Strausberg R.-
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC	-I- COFACTOR: Iron (by similarity).
CC	-I- SIMILARITY: Belongs to the lipoygenase family.
CC	-I- SIMILARITY: Contains 1 PLAT domain.
DR	EMBL; BC013751; AAH13751.1; -.
DR	EMBL; BC051047; AAHS1047.1; -.
DR	HSSP; P12530; ILLOX
DR	MGI; MGI:1274790; Alox12e.
DR	GO; GO:0005506; F:iron ion binding; IEA.
DR	GO; GO:0016165; F:lipoygenase activity; IEA.
DR	GO; GO:0016491; F:oxygenoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	GO; GO:0006691; P:leukotriene metabolism; IEA.
DR	Pfam; PF00305; Lipoygenase; 1.
DR	Pfam; PF01477; PLAT; 1.
DR	PRINTS; PR00087; LIPOXYGENASE.
DR	PRINTS; PR00467; MAMLPOXGNASE.
DR	SMART; SM00308; LH2; 1.
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR	PROSITE; PS50095; PLAT; 1.
KW	Dioxygenase; Oxidoreductase.
SQ	SEQUENCE 662 AA; 75473 MW; 831C03803D3745D CRC64;

Query Match	66.9%; Score 2350.5; DB 2; Length
Best Local Similarity	66.6%; Pred.No.5.7e-175;
Matches 439; Conservative 95; Mismatches 124; Indels	
QY	4 YRIVSTGASLYAGSNNOVLMLVGHOGHGAALGKRLWPARG-ETELUK
DB	4 YKILVATGDSVPFAGSANLVHLVLVGEHADLGQLRPILGRKTELE
QY	63 KLRKRHLKKDAWFNCNWTLSVQGFGADGVRRPCYRWVEGNGVLSLEPE
DB	64 KLRKQGLLDSDWFCKSITVQPGTQGEAFFPCYSWVGKETICLTETEL
QY	123 FOXHREBLEERRKLRYGNWKDGILLINMAGAKLYDLVDDEPLEDK
DB	124 FRKYREQLENRRNYRWGSWEKGILLPTAGSTERDLPRNQRMFKOK
QY	183 DLAIKDSLNVLTCWKDLDDFNRIFWCGQSCLAERVDSWKEDALFGY
DB	184 NFAIKGTDLFVSRVKLEDYQKVFFHTKTALPERVSGSKWDALFGY
QY	243 SAHLPARLVFPFGMEELQAOLKELEGTVLPFADFSLLDGIKANVILI
DB	244 SMRLPARLVLPFGMEDLOTQLSEKLKAGSLFEVDFSLLDGVKNIIIII
QY	303 KLDPGKLLPMVIQLPLRTGSPPLFLTPDPMPMAWLAKCWVRSS
DB	304 KLQPDGRLLPMVIQLQPRHGCPPLFLFPSPPMAWLAKIIVWRSS
QY	363 GHLMAEIVVATMRCLPSIHPIFKLIIPHLYRTLEINVNRARTGLVSDSD
DB	364 GHLMAEIVSVATMRSLPSLHPYKLLAPHFRYTMETLARNNLVSE
QY	423 GHVQLLKQAGAFPTYSSFCPPDDLADRGLLVKSSSYAQDALRLWEI
DB	424 GHVDILQRATSCLYRSFCPPDDLADRGLLVKSSLYAQDALRLWEI
QY	483 KTDVAVKDDPELOTWCRETTETIGLAGOARDGGPVSIQARDOVCHFVT
DB	484 RSDTDDVKEDPELQVWCREVTEVGLIGAQRGGPLSLAESRAELCRFVA
QY	543 HLGQLDWTSWPNAPCTMRLPPPTTKDTALETVMATLPNFHQASLQNLQ
DB	544 HLGQLDWTAWIPNGECTWPKPPIISKDVTERDIVDSLPLCQARMQDI
QY	603 VAVGOHEEYESGPBPBKAVALKKFRBELAALDKIEIRNAKLONMPYEY
DB	604 VALGQHEEYESGSRDVLKQIQBELATMDKEIEVRNASLDLPYEYEV

RESULT 11

Q61Sf8	PRELIMINARY;	PRT;	663 AA.
AC	Q61Sf8;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Arachidonate 12-lipoxygenase.		
GN	Name=ALOX12;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PCR rescued clones;		
RC	MDLJNE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Felting F.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Morley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Vallajon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PCR rescued clones;		
RA	Director MGC Project;		
RA	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.		
CC	-1- COFACTOR: Iron (by similarity).		
CC	-1- SIMILARITY: Belongs to the lipoxygenase family.		
CC	-1- SIMILARITY: Contains 1 PLAT domain.		
DR	EMBL; BC069557; AAH69557.1; ..		
DR	GO; GO:0005829; C:cytosol; ISS.		
DR	GO; GO:0004522; P:arachidonate 12-lipoxygenase activity; ISS.		
DR	GO; GO:0004574; P:hexoxilin-epoxide hydrolase activity; ISS.		
DR	GO; GO:0047977; P:potassium channel inhibitor activity; ISS.		
DR	GO; GO:0019870; P:potassium channel inhibitor activity; ISS.		
DR	GO; GO:0019369; P:arachidonic acid metabolism; ISS.		
DR	GO; GO:0046456; P:icosanoid biosynthesis; ISS.		
DR	GO; GO:0045794; P:negative regulation of cell volume; ISS.		
DR	GO; GO:0008284; P:positive regulation of cell proliferation; ISS.		
DR	GO; GO:0042391; P:regulation of membrane potential; ISS.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR000907; Lipoxygenase.		
DR	InterPro; IPR001024; Lipoxygenase_LH2.		
DR	InterPro; IPR001885; Mam_lipoxygenase.		
DR	Pfam; PF00305; Lipoxygenase; 1.		
DR	Pfam; PF01477; PLAT; 1.		
DR	PRINTS; PR00087; LIPOXYGENASE.		
DR	PRINTS; PR00467; MAMLIPOXYGENASE.		
DR	SMART; SM00308; LH2; 1.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.		
DR	PROSITE; PS00081; LIPOXYGENASE_1; UNKNOWN_1.		
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.		
DR	PROSITE; PS00095; PLAT; 1.		
DR	Dioxygenase; Oxidoreductase..		
SK	SEQUENCE 663 AA; 75721 MW; 3957350F62D4C9E7 CRC64;		
Query Match	65.8%; Score 2312; DB 2; Length 663;		

Query Match

Best Local Similarity 65.3%; Pred. No. 5.8e-172; Matches 433; Conservative 94; Mismatches 134; Indels 2; Gaps 2;	
QY 1	MGLYRTRVSTGASLVAGSNVQVLVGVGHGAALCKRLWPARG-ETELKRVPEVLGPL 59
DB 1	MGRYRIRVATGAWLFGSGSYNRVQLMLVGTGRGAELQLRPARGEEEDHVDADLGLL 60
QY 60	LFVKLRKRLHLLKDDAWFCNWIISVQSGAGDEVRFPYCRWVEGNVLSLPEGTGRTVGDP 119
DB 61	QFVLRKRWLVDDAWFCDFRITVQSGCAEAVAFPCYRWVQGEDILSLPEGTARLPGDNA 120
QY 120	QGLFQKHREELERKLYRWGNWKGCLINWAGAKLYDLVDPERPLEDKRVDFEVS LAK 179
DB 121	LDMFQKHREKELKROQIYCWATWKEGLEPLTIAADRKDDLFPNMRPHEEKRLDFEWTLKA 180
QY 180	GLADLAIKDSLNVLTCKWLDLDFNRFWCGSKLAERVDSKEDALFGYQFLNGANPVV 239
DB 181	GALEWALKRVYLLSNWNCLEDQDFQWQKALAEKVRQWDDLELFSYQFLNGANPML 240
QY 240	LRRSAHLPARLVFPFGMEELQALEKELEGGTLFEADFSLLDGIKANVILCSQOHLAAPL 299
DB 241	LRRSTSLPSRLVLPSCMEELRAQLEKELQNGLSFEADFILLDGI PANVIRGEKQVLAAPL 300
QY 300	VMLKLPDQKLLPMVJLOLPRTGSPDPPLFLPTDPPMAWLLAKWVRSSDFOLHELQSH 359
DB 301	VMLKMEPNKLPQPMVJQIOPPNPSSPTTLFLPSDPLAWLLAKSWVRNSDFQLHEIQYH 360
QY 360	LRGLHMAEIVVATWRCPLSPHPIKLIJPHRYLTLEINVRATGLVSDMGIFDQIMST 419
DB 361	LUNTHLVAEIVATWRCPLGULHPIKFLPHIRYLTLEINVRATGLVSDMGIFDQIMST 420
QY 420	GGGGHVQLLKQAGAFITYSSFCPPDDLADRLGLGVKSSFYAQAALRLWELIIRYVEGIVS 479
DB 421	GGGGHVQLLRRAAQLTYCSLCPDDDLADRLGLGVKSSFYAQAALRLWELIIRYVEGIVH 480
QY 480	LHYKTDVAVKDDELQWTCREITEIGLQAGDRGPPVSVLSQARDQVCHFTVTCIQTGQH 539
DB 481	LFYQRDDIVKGPDELQWTCREITEIGLQAGDRGPPVSVLSQARDQVCHFTVTCIQTGQH 540
QY 540	ASVHLGQLDWYSVNPVNACTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWOLGR 598
DB 541	AALNQQLDQWYAWVNPACTMRLPPPTTKEDVTMTVMSGLSPDVQACLQMSLWHLRR 600
QY 599	QPMVAVGQHEEYFSGPPKAVLKFBELAAALDKKEIRNAKLDMPEYELRPSVENS 658
DB 601	QPMVFLGHKHKYFSGPRKPAVLNQFRITDLEKLEKEITARNQDLQWPEYELKPSCIENS 660
QY 659	VAI 661
DB 661	VTI 663
RESULT 12	
LOXP_HUMAN STANDARD; PRT; 662 AA.	
ID	AC P18054; O95569;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX)
DE	[Platelet-type lipoxygenase 12].
GN	Name=ALOX12; Synonyms=LOG12;
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90332636; PubMed=2377602;
RA	Funk C.D., Furci L., Fitzgerald G.A.;
RT	"Molecular cloning, primary structure, and expression of the human
RT	platelet/erythrocyte cell 12-lipoxygenase.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:5638-5642(1990).
[2]	
RN	SEQUENCE FROM N.A., AND VARIANTS ARG-260 AND ASN-321.
RX	MEDLINE=91017529; PubMed=2217179;
RA	Izumi T., Hoshiko S., Raadmark O., Samuelsson B.;
RT	"Cloning of the cDNA for human 12-lipoxygenase.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:7477-7481(1990).
[3]	
RN	SEQUENCE FROM N.A.
RX	MEDLINE=91058562; PubMed=2244907;
RA	Yoshimoto T., Yamamoto Y., Arakawa T., Suzuki H., Yamamoto S.,
RA	Yokoyama C., Tanabe T., Toh H.;
RT	"Molecular cloning and expression of human arachidonate 12-
RT	lipoxygenase.";
RL	Biochem. Biophys. Res. Commun. 172:1230-1235(1990).
[4]	
RN	SEQUENCE FROM N.A., AND VARIANTS ARG-260; ASN-321 AND HIS-429.
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA	Rajkumar N., Yi Q., Nickerson D.A.;
RT	"SeattlesNPS, NHLBI HL6682 program for genomic applications, UW-
RT	PHRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[5]	
RN	SEQUENCE OF 1-111 FROM N.A.
RX	MEDLINE=93077582; PubMed=1447217;
RA	Yoshimoto T., Arakawa T., Hada T., Yamamoto S., Takahashi E.;
RT	"Structure and chromosomal localization of human arachidonate 12-
RT	lipoxygenase gene.";
RL	J. Biol. Chem. 267:24805-24809(1992).
[6]	
RN	SEQUENCE OF 1-44 FROM N.A.
RX	MEDLINE=92237289; PubMed=1570320;
RA	Funk C.D., Funk L.B., Fitzgerald G.A., Samuelsson B.;
RT	"Characterization of human 12-lipoxygenase genes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:3962-3966(1992).
[7]	
RN	SEQUENCE OF 339-426 FROM N.A.
RC	TISSUE=Skin;
RX	MEDLINE=94136572; PubMed=8304420;
RA	Hussein H., Shornick L.P., Shannon V.R., Wilson J.D., Funk C.D.,
RA	Pentland A.P., Holtzman M.J.;
RT	"Epidermis contains platelet-type 12-lipoxygenase that is
RT	overexpressed in germinal layer keratinocytes in psoriasis.";
RL	Am. J. Physiol. 266:C243-C253(1994).
CC	- FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC	- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-
CC	12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC	- COFACTOR: Iron.
CC	- PATHWAY: Leukotrienes biosynthesis.
CC	- SUBCELLULAR LOCATION: Cytoplasmic.
CC	- SIMILARITY: Belongs to the lipoxygenase family.
CC	- SIMILARITY: Contains 1 PLAT domain.

CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).

DR	EMBL; M35418; AAA60056.1; -
DR	EMBL; M58704; AAA59523.1; -
DR	EMBL; M62982; AAA51533.1; -
DR	EMBL; AY527817; AAS00094.1; -
DR	EMBL; D12638; BAA02162.1; -
DR	EMBL; M87004; AAA51587.1; -
DR	EMBL; S68587; AAD14020.1; -
DR	PIR; A38283; A38283.
DR	HSSP; P12530; ILOX.
DR	Genew; HGNC:429; ALOX12.
DR	MIM; 152391; -
DR	GO; GO:0004052; F:arachidonate 12-lipoxygenase activity; TAS.
DR	GO; GO:0006631; P:fatty acid metabolism; TAS.

```

DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR001885; Mam lipoxigenase.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLPXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase;
KW Polymorphism.
FT INIT_MET 0
FT DOMAIN 1 113 PLAT.
FT METAL 359 359 Iron (By similarity).
FT METAL 364 364 Iron (By similarity).
FT METAL 539 539 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
FT VARIANT 260 260 Q -> R.
FT VARIANT 297 297 /FTID=VAR_018743.
FT VARIANT 321 321 /FTID=VAR_004279.
FT VARIANT 321 321 S -> N.
FT VARIANT 429 429 /FTID=VAR_018744.
FT VARIANT 429 429 R -> H.
FT CONFLICT 188 191 /FTID=VAR_018745.
FT CONFLICT 344 344 RVTY -> PCLH (in Ref. 3).
FT CONFLICT 388 388 S -> C (in Ref. 3).
FT CONFLICT 388 388 L -> P (in Ref. 1).
FT SEQUENCE 662 AA; 75535 MW; B7FFDCFC66F8CFB CRC64;

Query Match
Best Local Similarity 65.7%; Score 2310; DB 1; Length 662;
Matches 433; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

QY 2 GLYRIVSTGSLYAGSNQVLWLVGQHGALGRLWPARG-BTELKVEVPEYLGPLL 60
DB 1 GRYRIVATGAWLFGSSYRVLWLVGTRGAELELRPARGEEEDFHDVAEDLGLLQ 60
QY 61 FVLRKRHLKDDAFWCFNWSVQGGAGDEVRFPCYRWVGVNGLSLPEGTGRTVGEDPQ 120
DB 61 FVLRKRHLWVDVAFWCFNWSVQGGAGCAEVFPYRWVQGGEDILSLPEGTARLPEDNAL 120
QY 121 GLFQKHREELERKLYRWGKNDGLILNAGAKLYLDLPVDERFLEDRKVDVFEVSLAKG 180
DB 121 DMFQKHREKELKDRQIYCWATKESGLPLTIAADRKDDLPPNMRFHEKRLDFEWTLKAG 180
QY 181 LADLAIKDSLNLVLTCKDLDDPNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPVVL 240
DB 181 ALEMAKRVYTLSSWNCLEDFDQIFWQKGSALAEKVRQCQDDLELFSYQFLNGANPMLL 240
QY 241 RRSALHPARLVPPGMELELOALEKELGGTLFEADFSLLDGIKANVILCSQOHLAAPLV 300
DB 241 RRSTSLPRLVLPFGMELELOALEKELQNGSLFEADFIILLDGIIPANVIRGKQYLAAPLV 300
QY 301 MLKLPQDGKGLPMVLTQLQPLRTGSPPLPLFTDPPMAWLAKVWRSDSFOLHQLSHL 360
DB 301 MLKMEPNGKLPWVLTQIPSPSSPTPLFTLPSDPLAWLLAKSVWRNSDQLHQLHQL 360
QY 361 LRGHMAEVIVVATVWRLPSIHPKLIPIHLRYTLINVRARTGLVSDMGIFDQIMSTG 420
DB 361 LNTHLVAEIVATVWRLPGLHPFKLIPIHLRYTMEINTRARTQLISDGGIFDKAVSTG 420
QY 421 CGGHVQLLKQAGAFITYSSFCPPDDIADRLGLLVKSSFYAQDALRLWIIYRYVEGIVSL 480
DB 421 CGGHVQLLRRAAAQULTYCSLCPDDIADRLGLLVKSSFYAQDALRLWIIYRYVEGIVHL 480
QY 481 HYKTDVAVKDDPELQTCREITEIGLQAGQDRGFPVSLQARDQVCFHVTWICTCTGQHA 540
DB 481 FYQRDDIVKGDPELQAWCREITEVGLCQQRDRGFPVFSQSQQLCFHVTWICTCTAQA 540
QY 541 SVHLQGLDWYSWVPNAPCTMRLPPPTTK-DATLETVMATLPNFHOASLQMSITWOLGRRQ 599

```

RESULT 13

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Q8BHG4 PRELIMINARY; PRT; 663 AA.
AC Q8BHG4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus adult female vagina cDNA, RIKEN full-length enriched
DE library, clone:9930022G08 product:arachidonate 12-lipoxygenase, full
DE insert sequence (Mus musculus 2 days pregnant adult female ovary cDNA,
DE RIKEN full-length enriched library, clone:E330011M05
DE product:arachidonate 12-lipoxygenase, full insert sequence).
GN Name=Alox12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN [5]

```

Genome Res. 10:1757-1771 (2000).	QY	1	MGLYRIRVSTGASLYAGSNQVQLWLVQHGGAALGKRLMPARG-EYELKVEYVEPYLGPL	59
[6]	Db	1	MGRYRVRVVTGAWLFSGSLNLRVLRWLVGHEHREAKLEQLRPARGKEEEDFDVDPEDLGPL	60
RC STRAIN=C57BL/6J; TISSUE=Vagina;	QY	60	LFVKLRKRHLKDDAWFCNWLISVQPGAGDEVRRPCYRWVEGNGVLSPUEGTGRTVGBDP	119
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	Db	61	QFVKLUHQHTVDDDAWFCNLTIVQPGTSAEAVPCYRWVQEGILSPGEGTARLAGDNA	120
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	QY	120	QGLFKHREELERKLYRWGNKWDGLILNMAGAKLYDLFVDFRFLDKRVDVEFSLAK	179
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,	Db	121	LDVFKYREKELKERQYQYCNATWKEGLPQTIAADCKDDLPPNMRFEHEKRLDFEWTLKA	180
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,	QY	180	GLADIADKSLNVLFCWKDLDDFNRFVCGGSKLAERVRDSWKEDALFGYFLNGANPVV	239
RA Katoh H., Kawai J., Kojima Y., Itoh M., Kondo S., Konno H., Kouda M., Koya S.,	Db	181	GVLEMLKRVYTLRLSRWNHLEDFDQIFWQKQSALEKQVQWEDLFGYFLNGANPML	240
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	QY	240	LRSALHPLARLVFPPEMEOLEQALEGGTFLFEADFLDGLDKANVILCSQQHAAAPL	299
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	Db	241	LRRSTSLPSRLVLPSPMBELQALEKLNKLSLFEADFLDGLDIPANVIRGEPOYLAAPL	300
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,	QY	300	VMLKLPQDCKLIPMWIQLQLPRTGSPPPPLFLPTDPPMAWLLAKWVRSSDFQLHELOSH	359
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,	Db	301	VMLRWDPCGKLLPMAIQPPNPSPATLFLPDPPLAWLLAKTIWVNSDFQLQELQFH	360
RA Satoh A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,	QY	360	LIRGHLMAEVIVVATMRCPLPSIHPFKULIIPHLRYTLEINVRARTGLVSDMGIFQIMST	419
RA Tegawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,	Db	361	LNTHLVAEIVAVATMRCPLPGLHPLFILLVPHIRYTMETNRSRTQLISDGGIFDQVWST	420
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	QY	420	GGGHVOLLKQAGALTYSSCPDDADRGLLGVKSSFYAQDALRLWEIIVRYVEGIVS	479
CC - - SIMILARITY: Belongs to the lipoxigenase family.	Db	421	GGGHVOLLKQAGALTYSSCPDDADRGLLGVKSSFYAQDALRLWEIIVRYVEGIVS	480
CC - - SIMILARITY: Contains 1 PLAT domain.	QY	480	LHYKTDVAVKDDPELQTCWREITIGLQAGDORGPVPSLOARDQVCHPVTMTCTCTGQH	539
DR EMBL; AK036898; BAC29629.1; -;	Db	481	LFYQSDDIVRGDEPQLQACREITEVGLCHAQDRGFVSQSRQALCHFLTWCVTCTAQH	540
DR HSSP; P12530; I10X.	QY	540	ASVHLGQLDWYSWVPNAPCTMRLPPPTTK-DATLETVMATLPNFHQSLOWSITWQLGRR	598
DR MGD; MGI:87998; C.cytosol; ISS.	Db	541	AAINQQLDQWYGVNAPCTMRMPPTSKODVTMETVMSGLPDVQKACLQMTIWHLGR	600
DR GO; GO:0005829; C.cytosol; ISS.	QY	599	QPMWAVGQHESEYSGPEPKAVLKFEELAAALDKETEIRNAKLDMEYVLRSSVENS	658
DR GO; GO:0004052; Pharachidonate 12-lipoxygenase activity; ISS.	Db	601	QPDWPLGHHTKEYFSDPRTKAVLSQFQADLNLNKEITARNEQDLDPLEYLKPISRIENS	660
DR GO; GO:0047977; F:hexoilin-epoxide hydrolase activity; ISS.	QY	659	VAI 661	
DR GO; GO:0019870; F:potassium channel inhibitor activity; ISS.	Db	661	ITI 663	
DR GO; GO:0006916; P:anti-apoptosis; IMP.	RESULT 14			
DR GO; GO:0019369; P:arachidonic acid metabolism; ISS.	LOXP MOUSE			
DR GO; GO:0019395; P:fatty acid oxidation; ISS.	ID	LOXP_MOUSE	STANDARD;	PRT; 662 AA.
DR GO; GO:0046456; P:icosanoid biosynthesis; ISS.	AC	P39655;		
DR GO; GO:0045794; P:negative regulation of cell volume; ISS.	DT	01-FEB-1995 (Rel. 31, Created)		
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; ISS.	DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DR GO; GO:0030307; P:positive regulation of cell growth; ISS.	DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DR GO; GO:0008284; P:positive regulation of cell proliferation; IMP.	DE	Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX)		
DR GO; GO:0042391; P:regulation of membrane potential; ISS.	DE	(Platelet-type lipoxigenase 12).		
DR GO; GO:0042554; P:superoxide release; ISS.	GN	Name=Allox12; Synonyms=Allox12p;		
DR InterPro; IPR003006; Ig_MHC.	OS	Mus musculus (Mouse).		
DR InterPro; IPR000907; Lipoxigenase.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DR InterPro; IPR001024; Lipoxigenase_LH2.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
DR Pfam; PF01477; PLAT; 1.	OX	NCBI_TaxID=10090;		
DR PRINTS; PR00087; LIPOXYGNASE.	RN	[1]		
DR PRINTS; PR00467; MAMLIPOXGNASE.	RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ILE-662.		
DR SMART; SM00308; LH2; 1.	RC	STRAIN=C57BL/6, and ICR; TISSUE=Spleen;		
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	RX	MEDLINE=94245713; PubMed=818678;		
DR PROSITE; PS00081; LIPOXYGNASE_2; 1.	RA	Chen X.-S., Kurie U., Jenkins N.A., Copeland N.G., Funk C.D.;		
DR PROSITE; PS50095; PLAT; 1.	RT	"cDNA cloning, expression, mutagenesis of C-terminal isoleucine,		
DR DIOXYGNASE; Oxidoreductase.	RT	genomic structure, and chromosomal localizations of murine 12-		
DR DIOXYGNASE; Oxidoreductase.	RL	J. Biol. Chem. 269:13979-13987 (1994).		
DR DIOXYGNASE; Oxidoreductase.	RN	[2]		

RP SEQUENCE FROM N.A.
RA MEDLINE=96052410; PubMed=7576099;
RA Kriegl P., Kinzig A., Rees-Loschke M., Vogel S., Vanlandingham B.,
RA Stephan M., Lehmann W.D., Marks F., Furstemberger G.;
RT "12-lipoxygenase isoenzymes in mouse skin tumor development."; Mol. Carcinog. 14:118-129(1995).
RN [3]
RP SEQUENCE OF 125-217 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95312654; PubMed=7792391; DOI=10.1016/0090-6980(94)00005-H;
RA Hagnan W., Gao X., Zacharek A., Wojciechowski L.A., Honn K.V.;
RT "12-lipoxygenase in Lewis lung carcinoma cells: molecular identity, intracellular distribution of activity and protein, and Ca(2+)-dependent translocation from cytosol to membranes."; Prostaglandins 49:49-62(1995).
RL Prostaglandins 49:49-62(1995).
CC - FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC - CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC - COFACTOR: Iron.
CC - PATHWAY: Leukotriene biosynthesis.
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - TISSUE SPECIFICITY: Found primarily in platelets and in microsomal and cytosolic fractions of the epidermis.
CC - SIMILARITY: Belongs to the lipoxygenase family.
CC - SIMILARITY: Contains 1 PLAT domain.

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DR EMBL; U04334; AAA20659.1; -
DR EMBL; S80446; AAB36013.1; -
DR EMBL; S77511; AAB34667.1; -
DR PIR; A54075; A54075.
DR HSP; P12530; ILOX.
DR MGD; MGI:87998; Alox12.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.
DR InterPro; IPR001885; Mam_lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; FALSE_NEG.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS0095; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 0 By similarity.
FT DOMAIN 1 113 PLAT.
FT METAL 359 359 Iron (By similarity).
FT METAL 364 364 Iron (By similarity).
FT METAL 539 539 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
FT MUTAGEN 662 662 I->D,R,K,G: Loss of activity.
FT MUTAGEN 662 662 I->S,N: Little activity (8-15%).
FT MUTAGEN 662 662 I->V: Nearly full activity.
FT CONFLICT 2 2 A -> R (in Ref. 2).
SQ SEQUENCE 662 AA; 75214 MW; ACS62C1EDC5049B5 CRC64;

Query Match 63.9%; Score 2247; DB 1; Length 662;
Best Local Similarity 63.3%; Pred. No. 7.1e-167;
Matches 419; Conservative 96; Mismatches 145; Indels 2; Gaps 2;
QY 2 GUYRVRVSTGASLYAGSNNOVLWVGHGAEALGRLWPARG-ETELKVEVYLGPLL 60
DB 1 GAYRVRVSTGAWLFGSLMLVRLWLVGHRRAKLELQRLPARGKEEFDFPDGLGPLL 60
QY 61 FVKLRKRLKDDAWFCNWIISVQGPCAGDEVFPFCYRWVWEGNGLSLPEGTGRTVGDPQ 120

Db 61 FVKLRKQHTVDDAWFCNLTIVQPGTSAEAVFCYRWVWEGNGLSLPEGARLAGDNAL 120
QY 121 GLFQKHREELERKLYRWGNWKGILNMGAKLYDLVDPDERFLEDKRVDFEVLAKG 180
Db 121 DVFKYREKELKERQQTVCWATWKEGLPQTIAADCKDDLPPNMFHEEKRLDFEWTLKAG 180
QY 181 LADLAIKDSLNLVTCWKDLDFNRIFWCGQSKLAERVDSWKEDALFCYQFOLNGANPVVL 240
Db 181 VLENGLRVYVTLRSWNHLEDFQIFMGQKSALEKVKHCWOEDLFGYQFOLNGANPMLL 240
QY 241 RRSAPHLPARLVFPFPCMBEELQALEKELEGGTLFADFSLLDGIIKANVILCSQOHLAAPLV 300
Db 241 RRSLSLPSRLVLPFGMELOLQALEKELKNGSLFEADFIILDGIPANVIRGEPOYLAAPLV 300
QY 301 MLKLQDPGKLPVMIQQLPRGSPPPPLFLPTDPPMAWLAKCWRRSSDFQLHELOSHL 360
Db 301 MLRMDPGKLLPMAIQIOPPNPSPAPTLFLPSPDPLAWLLAKIWRNSDFQLQLPFL 360
QY 361 LRGHMAEVIIVATMRCCLPSHPHFKLIIPLRLTLEINVRARTGLVSDMGIFDQIMSTG 420
Db 361 LNTHLVAEVIIVATMRCCLPGHPIFKLVPHIRYVTEINTRTQLISDGGIFDQVWSTG 420
QY 421 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALKRLWELIIVRYVGVISL 480
Db 421 GGGHVQLLTRAVALIYHSLCPPDDLANRGLRIPSAIYARDALQWETARYVKGWHL 480
QY 481 HYKTDVAVKDDPELQTCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCICTGQHA 540
Db 481 FYQSDDIVRGDPELQAMCREITEVGLCHAQDRGFPVSPQSRALQCHFLTMCVFTCTAQA 540
QY 541 SVHLQGLDWSVWPNAPCTMLPPTTK-DATLETVMATLNFHQASLOMSITWOLGRRQ 599
Db 541 AINQGLDWSVWPNAPCTMRMPPTSKDDVTMETVMGSLPDVQKACIQMTITWHLGLIQ 600
QY 600 PMVAVGQHEEYFSGPEPKAVLKKEREELAAALDKEIEIRNAKLDMPYEYLRPSVVSNSV 659
Db 601 PMVPLGHHTKEKYPSPDRTKAVLSQFQADLONLEKEITARNEQLDLPYEYLRPSVVSNSV 660
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Db 661 TI 662

RESULT 15
Q95103 PRELIMINARY; PRT; 555 AA.
AC Q95103;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 12-lipoxygenase (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea;
RA Hornsten L.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC - COFACTOR: Iron (By similarity).
CC - SIMILARITY: Belongs to the lipoxygenase family.
CC EMBL; Y08829; CAA70062.1; -.
DR HSRP; P12530; ILOX.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0004052; F:arachidonate 12-lipoxygenase activity; ISS.
DR GO; GO:0047977; F:hexoxilin-epoxide hydrolase activity; ISS.
DR GO; GO:0019870; F:potassium channel inhibitor activity; ISS.
DR GO; GO:0019369; P:arachidonic acid metabolism; ISS.
DR GO; GO:0046456; P:icosanoid biosynthesis; ISS.
DR GO; GO:0045794; P:negative regulation of cell volume; ISS.

DR	GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
DR	GO; GO:0042391; P:regulation of membrane potential; ISS.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR000907; Lipoxigenase.
DR	InterPro; IPR001885; Mam_lipoxigenase.
DR	InterPro; IPR001005; Myb_DNA_binding.
DR	Pfam; PF00305; Lipoxigenase; 1.
DR	PRINTS; PR00087; LIPOXYGENASE.
DR	PRINTS; PR00467; MAMLOXGNASE.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR	PROSITE; PS00711; LIPOXYGENASE_1; UNKNOWN_1.
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR	PROSITE; PS00037; MYB_1; UNKNOWN_1.
KW	Dioxygenase; Oxidoreductase.
FT	NON_TER 1
FT	NON_TER 555 555
SQ	SEQUENCE 555 AA; 63266 MW; A030B187117D3AC CRC64;
Query Match 54.2%; Score 1905.5; DB 2; Length 555;	
Best Local Similarity 63.7%; Pred. No. 2.9e-140;	
Matches 352; Conservative 81; Mismatches 119; Indels 1; Gaps 1;	
QY	102 NGVLSLPEGTGRTVGEDPQGLFQKHREELERKRLYRWGNKDGILINMAGAKLYDLIPV 161
DB	1 DGVLCLEPRTARLAGNNAIDVFQRHREKELKERHKIYRWATWKGLPLTIAAGSEDDLLPA 60
QY	162 DERFLEDEKRVDFSVSLAKGLADLAIDKSLNVLTCWKDLDDFNRIFWCGOSKLAERVDSW 221
DB	61 NRRFHEEKRLDFEWTLKAGTLEMLKRVYTLSSWTSLEDFDLIFWGQKSPLAERKHQCV 120
QY	222 KEDALFGYQFLNGANPVVLRSAHLPARLVFPFGMBEELQAQLEKELEGGTLFEADFSLLD 281
DB	121 RODELFQYQFLNGANPMLRRCTSLTRLVPSGMBEELRAQLERELQNGSLFEADFILLD 180
QY	282 GIKANVILCSQQHAAPIVMLKLQDPGKULPMVLIQLPRTGSPPPPLFLPTDPPMALL 341
DB	181 GIPANVIRGEKQYLAAPVMLKMDPSKLLPMVIQIQPPSPISPTPPPLFLPSDPPFLAWLL 240
QY	342 AKCWVRSSDFQLHELQSHLLRHMAEVIWATMRCLPSIHPIFKLIIPHLYTLEINVR 401
DB	241 AKTWVRNSDFQLHQLQYHLNTHLLAEVIAVATMRCLPGLHPVFKLLMPHIYTWETNR 300
QY	402 ARTGLVSDMGIFDQIMSTGGGHVQLLKQAGAFLYTSFSCPDDDLADRGLLGVKGSFYAQ 461
DB	301 ARTQLISDGGIFDKAVSTGGGHVHLRRALQAQLTYRSLCPLDLLADRELLGTPGALYAC 360
QY	462 DALRLWEIIRYRVEGIVSLHYKTDVAVKDDPELQWCREITEIGLQGAQDRGPPVSLQAR 521
DB	361 DALRLWEITARVYVEGIVHLFYHGDDVYVKGDPPELQAWCREITEVGLPQAQERGFPVFSQ 420
QY	522 DOVCHFTWTCIFTCTGSHASVHLGQLDWTYSWVFNAPCTMRLPPPTTK-DATLETVMATLP 580
DB	421 NQLCHEFTWCFTCTAQHGAINGQGDWYAWVFNAPCTMRMPPTTKEDVTWATVWGSLLP 480
QY	581 NFHQASLQMSITWQLGRRQPMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKKEIERN 640
DB	481 DVRQACLQMAITWHLGRRQPMVPLGHHKEKYFSDPKAKSVLNQFQTDLENLEREITARN 540
QY	641 AKLDMPEYILRPS 653
DB	541 EQLDLPEYELKPS 553

Search completed: July 18, 2005, 22:01:11
Job time : 115.649 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:49:42 ; Search time 27.6652 Seconds
(without alignments)
2298.893 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLRIRVSTGASLYAGSNN.....KLDMPYELRPSVENSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3503.5	99.7	662	1	A31349	arachidonate 15-lipo
2	3090	87.9	663	2	S32825	arachidonate 12-li
3	3060	87.1	663	1	A35087	arachidonate 12-li
4	2896	82.4	663	1	QJ0018	arachidonate 15-li
5	2696	76.7	663	2	S30051	arachidonate 12-li
6	2692	76.6	663	2	I52462	arachidonate 12-li
7	2676	76.2	663	1	B54075	arachidonate 12-li
8	2312	65.8	663	1	A38283	arachidonate 12-li
9	2252	64.1	663	1	A54075	arachidonate 12-li
10	1299.5	37.0	674	2	I49479	arachidonate 5-lip
11	1298.5	37.0	674	1	DAU042	arachidonate 5-lip
12	1270	36.1	670	1	A30882	arachidonate 5-lip
13	947	26.9	238	2	I56977	arachidonate 12-li
14	863.5	24.6	1066	2	T30903	arachidonate 8-lip
15	522.5	14.9	917	2	B96699	probable lipoxigen
16	490.5	14.0	896	2	T07408	lipoxigenase (EC 1
17	490.5	14.0	914	2	T07065	probable lipoxigen
18	489.5	13.9	862	2	S57964	lipoxigenase (EC 1
19	487.5	13.9	908	2	T07409	lipoxigenase (EC 1
20	484.5	13.8	926	2	E96749	probable lipoxigen
21	483	13.7	865	2	T11852	lipoxigenase (EC 1
22	482	13.7	899	2	T11578	probable lipoxigen
23	478	13.6	858	2	T12142	lipoxigenase (EC 1
24	477.5	13.6	862	2	T07775	lipoxigenase (EC 1
25	476.5	13.6	899	2	T07062	probable lipoxigen
26	475	13.5	859	2	T06339	lipoxigenase (EC 1
27	474	13.5	859	2	T06352	lipoxigenase (EC 1
28	472.5	13.4	862	2	S22153	lipoxigenase (EC 1
29	470	13.4	859	2	T06429	lipoxigenase (EC 1

30	470	13.4	876	2	T07101	lipoxigenase (EC 1
31	470	13.4	896	2	J02391	lipoxigenase (EC 1
32	467.5	13.3	866	2	T06454	probable lipoxigen
33	466	13.3	857	2	S01864	lipoxigenase (EC 1
34	460	13.1	861	2	S44940	lipoxigenase (EC 1
35	459.5	13.1	864	1	S07075	lipoxigenase (EC 1
36	456.5	13.0	861	1	S01142	lipoxigenase (EC 1
37	454.5	12.9	876	2	T05943	probable lipoxigen
38	453.5	12.9	877	2	T10085	lipoxigenase (EC 1
39	448.5	12.8	862	2	T05941	lipoxigenase (EC 1
40	448	12.7	868	2	T06827	lipoxigenase (EC 1
41	445.5	12.7	859	1	J02267	lipoxigenase (EC 1
42	445.5	12.7	864	2	T05945	lipoxigenase (EC 1
43	445.5	12.7	864	2	S13381	lipoxigenase (EC 1
44	442	12.6	865	1	DASYLI	lipoxigenase (EC 1
45	439	12.5	856	2	T06596	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

A31349

arachidonate 15-lipoxygenase (EC 1.13.11.33) - human

N:Alternate names: arachidonate omega-6 lipoxigenase

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence revision 07-Feb-1997 #text change 09-Jul-2004

C:Accession: A31349; A28192; S19625; S19577; A61164; B61164

R:Signal, E.; Craik, C.S.; Highland, E.; Grunberger, D.; Costello, L.L.; Dixon, R.A.F.; Nadel, J.A.

Biochem. Biophys. Res. Commun. 157, 457-464, 1988

A:Title: Molecular cloning and primary structure of human 15-lipoxygenase.

A:Reference number: A31349; MUID:89076270; PMID:3202857

A:Accession: A31349

A:Molecule type: mRNA

A:Residues: 1-662 <SIG>

A:Cross-references: UNIPROT:P16050; GB:M23892; NID:g187190; PIDN:AAA36182.1; PID:g307135

A:Experimental source: reticulocyte

R:Signal, E.; Grunberger, D.; Craik, C.S.; Caughey, G.H.; Nadel, J.A.

J. Biol. Chem. 263, 5328-5332, 1988

A:Title: Arachidonate 15-lipoxygenase (omega-6 lipoxigenase) from human leukocytes. Purifi

A:Reference number: A28192; MUID:88186828; PMID:3356688

A:Accession: A28192

A:Molecule type: protein

A:Residues: 3-16 <SI2>

A:Experimental source: leukocyte

R:izumi, T.; Radmark, O.; Joernvall, H.; Samuelsson, B.

Eur. J. Biochem. 202, 1231-1238, 1991

A:Title: Purification of two forms of arachidonate 15-lipoxygenase from human leukocytes.

A:Reference number: S19577; MUID:92111501; PMID:1662607

A:Accession: S19625

A:Molecule type: protein

A:Residues: 'X', 3-4, 'X', 6, 'X', 8-22; 38-45; 157-162, 'XX', 165-168; 627-631 <IZU>

A:Accession: S19577

A:Molecule type: protein

A:Residues: 'X', 3-25; 27-31 <IZ1>

A:Note: there appear to be distinct chromatographic forms, at least one each from reticul

resor

R:izumi, T.; Radmark, O.; Samuelsson, B.

Adv. Prostaglandin Thromboxane Leukotriene Res. 21, 101-104, 1990

A:Title: Purification of 15-lipoxygenase from human leukocytes, evidence for the presence

A:Reference number: A61164

A:Accession: A61164

A:Molecule type: protein

A:Residues: 'X', 3-4, 'X', 6, 'X', 8-12, 'X', 14-19, 'T', 21-22 <IZ2>

A:Experimental source: leukocyte

A:Accession: B61164

A:Molecule type: protein

A:Residues: 'X', 3-25; 27-31 <IZ3>

A:Experimental source: leukocyte

C:Genetics:

A:Gene: GDB:ALOX15

A:Cross-references: GDB:l32454

A:Map position: 17pter-17qter

C:Function:
A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,11Z,13E)-(15S)-15-h
A:Pathway: leukotriene biosynthesis
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidore
F:360,365,540,544,662/Binding site: iron (His, His, His, His, His, Ile) #status predicted

Query Match 99.7%; Score 3503.5; DB 1; Length 662;
Best Local Similarity 99.8%; Pred. No. 6e-279; Mismatches 0; Indels 1; Gaps 1;
Matches 661; Conservative 0;

QY	1	MGLYRIRVSTGASLYAGSNQVQLMWVGQGEAALGKRLWPARG-ETELKVEVPEYLGPL	59
DB	1	MGLYRIRVSTGASLYAGSNQVQLMWVGQGEAALGKRLWPARGKETELKVEVPEYLGPL	60
QY	60	LFVKLRKRLHLLKDDAWFCNWSVQGCAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP	119
DB	61	LFVKLRKRLHLLKDDAWFCNWSVQGCAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP	120
QY	120	QGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRVDVFLSLAK	179
DB	121	QGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRVDVFLSLAK	180
QY	180	GLADLAIKDSLNVLTCKWDLDDFNRIFCWCGSKLAERVRDSWKEDALFGYQFLNGANPV	239
DB	181	GLADLAIKDSLNVLTCKWDLDDFNRIFCWCGSKLAERVRDSWKEDALFGYQFLNGANPV	240
QY	240	LRRSAHLPARLVPPPGMEELQAELEKEGGLTFEADFSLLDGIKANVILCSQQHLAAPL	299
DB	241	LRRSAHLPARLVPPPGMEELQAELEKEGGLTFEADFSLLDGIKANVILCSQQHLAAPL	300
QY	300	VMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH	359
DB	301	VMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH	360
QY	360	LLRGHLMAEVIIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST	419
DB	361	LLRGHLMAEVIIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST	420
QY	420	GGGGHVLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIIRYVVEGIVS	479
DB	421	GGGGHVLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIIRYVVEGIVS	480
QY	480	LHYKTDVAVKDDPELQTCREITEIGLOAQDRGFVSLQARDQVCHFTVTCICTGQH	539
DB	481	LHYKTDVAVKDDPELQTCREITEIGLOAQDRGFVSLQARDQVCHFTVTCICTGQH	540
QY	540	ASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ	599
DB	541	ASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ	600
QY	600	PVMVAVGOHEEYFSGPEPKAVLKKFREELAAADKEIEIRNAKLDMPYEYLRPSVVENS	659
DB	601	PVMVAVGOHEEYFSGPEPKAVLKKFREELAAADKEIEIRNAKLDMPYEYLRPSVVENS	660
QY	660	AI 661	
DB	661	AI 662	

RESULT 2
S32825
arachidonate 12-lipoxygenase (EC 1.13.11.31), tracheal - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S32825; S77975; A56770
R:De Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.
Am. J. Physiol. 262, L198-L207, 1992
A:Title: Cloning and expression of an airway epithelial 12-lipoxygenase.
A:Reference number: A56770; PMID:92170942; PMID:1539676
A:Contents: tracheal epithelium
A:Accession: S32825
A:Molecule type: mRNA

A:Residues: 1-663 <ACC>
A:Cross-references: UNIPROT:P27479; EMBL:S96247; NID:G246172; PIDN:AAB21522.1; PID:G2461;
A>Note: in the authors' translation residues 441-460 do not match the nucleotide sequence
A:Note: sequence extracted from NCBI backbone (NCBIN:96247)
R:De Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.
submitted to the EMBL Data Library, December 1993
A:Reference number: S77975
A:Accession: S77975
A:Molecule type: mRNA
A:Residues: 1-440, 'GLIGVKSSFY', 441-450, 461-663 <DEM>
A:Cross-references: EMBL:S96247
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: leukotriene biosynthesis; oxidoreductase

QY	1	MGLYRIRVSTGASLYAGSNQVQLMWVGQGEAALGKRLWPARG-ETELKVEVPEYLGPL	59
DB	1	MGLYRIRVSTGSSFCAGSNQVHLWVGEGEALGWAVRPARGKEVEFQVDVSEYLGRL	60
QY	60	LFVKLRKRLHLLKDDAWFCNWSVQGCAGDEVRFPCYRWVEGNGVLSLPEGTGTVGED	118
DB	61	LFVKLRKRLHLLSDDAWFCNWSVQGCAGSNEFRFPYRWVEGNGVLSLPEGTGTVDD	120
QY	119	PGQLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRVDVFEVSLA	178
DB	121	PGQLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRVDVFEVSLA	180
QY	179	KGLADLAIKDSLNVLTCKWDLDDFNRIFCWCGSKLAERVRDSWKEDALFGYQFLNGANPV	238
DB	181	KGLADLAIKDSLNVLTCKWDLDDFNRIFCWCGSKLAERVRDSWKEDALFGYQFLNGTNP	240
QY	239	VLRSAHLPARLVPPPGMEELQAELEKEGGLTFEADFSLLDGIKANVILCSQQHLAAP	298
DB	241	LLRRSVLPARLEFPFGMGELQAELEKEGGLTFEADFSLLMGIKANVILCTQYVAAP	300
QY	299	LVMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQ	358
DB	301	LVMLKLPDQDKLLPMVLIQOLPHKGSPPPPPLFLPTDPPMTWLLAKCWRSSDFQLHEL	360
QY	359	HLRGHLMAEVIIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIM	418
DB	361	HLRGHLVAEVIIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIM	420
QY	419	TGGGHVQLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIIRYVVEGIV	478
DB	421	TGGGHVQLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIIRYVVEGIV	480
QY	479	SLHYKTDVAVKDDPELQTCREITEIGLOAQDRGFVSLQARDQVCHFTVTCICTGQ	538
DB	481	SLHYKTDVAVKDDPELQTCREITEIGLOAQDRGFVSLQARDQVCHFTVTCICTGQ	540
QY	539	HASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGR	598
DB	541	HSSVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGR	600
QY	599	QVMVAVGOHEEYFSGPEPKAVLKKFREELAAADKEIEIRNAKLDMPYEYLRPSVVENS	658
DB	601	QVIMVAVGOHEEYFSGPEPKAVLKKFREELAAADKEIEIRNAKLDMPYEYLRPSVVENS	660
QY	659	VAI 661	
DB	661	VAI 663	

RESULT 3
A35087
arachidonate 12-lipoxygenase (EC 1.13.11.31) - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A35087

R; Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.; Tanabe, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 2142-2146, 1990
A; Title: Cloning and sequence analysis of the cDNA for arachidonate 12-lipoxygenase of *Rattus norvegicus*
A; Reference number: A35087; MUID: 90192763; PMID: 2315307
A; Accession: A35087
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-663 <YOS>
A; Cross-references: UNIPROT: P15469; GB: M31417
C; Superfamily: arachidonate 5-lipoxygenase
C; Keywords: oxidoreductase

Query Match	87.1%	Score 3060	DB 1	Length 663
Best Local Similarity	86.1%	Pred. No. 1.4e-242		
Matches 571	Conservative 40	Mismatches 50	Indels 2	Gaps 2
Qy	1	MGLYRIRVSTGASLYAGSNNOVLWVQHGCEAALGKRLWPARG-ETELKEVPEYVGLPL	59	
Db	1	MGLYRVRVSTGSSFYAGSQNVQWLWVQHGCEAALGWLCLRPARGKETFSVDVSEYLGPL	60	
Qy	60	LFVKLRKRHLTKDDAWFCNWTISVQPGA-GDEVRFPCYVRWVEGVNGVLSPEGTGRTVGED	118	
Db	61	LFVKLRKRHLTKDDAWFCNWTISVQPGANGDEFRPCYVRWVEGDRILLSPEGTARTVDD	120	
Qy	119	POGLFQKHREBELERRKLYRWGNWVKGLILNMAKALYDLPVDERFLEDKRVDPEVSLA	178	
Db	121	POGLFKKHREBELAERRKLYRWGNWVKGLILNIASTGTHDLPVDERFLEDKRIDFEASLA	180	
Qy	179	KGLADLAIKOSLNLVTCWKOLDDEFNRIFWCQSQAERVRDSWKEDALFGYQFLNGANPV	238	
Db	181	KGLADLAVKOSLNLVWMSNLSNFRIFWCQSQAERVRDSWKEDALFGYQFLNGTNP	240	
Qy	239	VLRRSAHLPARLVFPFGMEELQAQLEKELEGTTLFEADFSLLDGIKANVILCSQHLLAAP	298	
Db	241	LLRHSVELPARLKFPPGMEELQAQLEKELQGTTLFEADFSLLDGIKANVILCSQYLAVP	300	
Qy	299	LVMLKLQPDGKLLPMWTLQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRRSSDFQHLHQ	358	
Db	301	LVMLKLQPDGKLLPMWTLQOLPREGSPPLPLFLPTDPPMWLLAKCWRRSSDFQHLHLS	360	
Qy	359	HLLRGHLMAEVIVATWRCULPSIHPIFKLLIPLHRYLTLEINVRARTGLVSDMGIFDOIMS	418	
Db	361	HLLRGHLMAEVIAVATWRCULPSIHPIFKLLIPLHRYTLEINVRARGLVSDGLFDQVVS	420	
Qy	419	TGGGGHVQLLKAQCAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWEIYYRYVEGIV	478	
Db	421	TGGGGHVELLRRAAALLTYSSFCPPDDLADRGLLGVSSFYAQDALRLWEIYRYVEGIV	480	
Qy	479	SLHYKTDAVKDDPELQWCREITETIGLQAGQDRGFPVSLQARQVCHFTVMCTICTGQ	538	
Db	481	SLHYKTDESVKEDPELQAWCREFTETIGLQAGQDRGFPVSLQSKQELCHFTVMCTICTGQ	540	
Qy	539	HASVHLGOLDWYSWVPNAPCTMRPLPPPTTKDATLETWATLPNPHQASLQMSITWQJGRR	598	
Db	541	HSSNHLGOLDWYTWVPNAPCTMRPLPPPTTKDATLETWATLPNPHQASLQMSITWQJGRC	600	
Qy	599	QPVMVAVQGHHEEYFSGPEPKAVLTKFREELAAALDKBEIARNKALDMPYELRPSVYVENS	658	
Db	601	QPTMVALQGHHEEYFSGGPKAVLTKFREELAAALDKDIEVRNKAALPYELRPSVYVENS	660	
Qy	659	VAI	661	
Db	661	VAI	663	

```

RESULT 4
JQ0018
arachidonate 15-lipoxygenase (EC 1.13.11.13), erythroid-specific - rabbit
N;Alternate names: carotene oxidase; lipoxidase
N;Contains: lipoxygenase peptides
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ0018; A61060; A27327; A61568; JCI513

```

R;Fleming, J.; Thiele, B.J.; Chester, J.; O'Prey, J.; Janetzki, S.; Aitken, A.; Anton, I.
Gene 79, 181-188, 1989
A;Title: The complete sequence of the rabbit erythroid cell-specific 15-lipoxygenase mRNA
A;Accession number: JQ0018; MUID:89378774; PMID:2777088
A;Accession: JQ0018
A;Molecule type: mRNA
A;Residues: 1-663 <FILE>
A;Cross-references: UNIPROT:P12530; GB:M27214; NID:G2642134; PIDN:AA886978.1; PID:gl64907
R;Thiele, B.J.; Fleming, J.; Chester, J.; O'Prey, J.; Prehn, S.; Janetzki, S.; Rapoport, R.
Biomed. Biochim. Acta 49, s17-s24, 1990
A;Title: Structure of the mRNA and of the gene coding for the rabbit erythroid 15-lipoxygenase
A;Reference number: A61060; MUID:90351403; PMID:2386503
A;Accession: A61060
A;Status: not compared with conceptual translation
A;Molecule type: mRNA; DNA
A;Residues: 2-605, 'F', 607-663 <TH1>
A;Note: nucleotide sequence is given only for intron/exon boundaries
R;Thiele, B.J.; Fleming, J.; Kasturi, K.; O'Prey, J.; Black, E.; Chester, J.; Rapoport, S.
Gene 57, 111-119, 1987
A;Title: Cloning of a rabbit erythroid-cell-specific lipoxygenase mRNA.
A;Reference number: A27327; MUID:88112854; PMID:3123326
A;Accession: A27327
A;Molecule type: mRNA
A;Residues: 1-31 <TH2>
A;Cross-references: GB:M33291
R;Thiele, B.J.; Black, E.; Fleming, J.; Nack, B.; Rapoport, S.M.; Harrison, P.R.
Biomed. Biochim. Acta 46, S120-S123, 1987
A;Title: Cloning of reticulocyte lipoxygenase mRNA.
A;Reference number: A61568; MUID:87241419; PMID:3109402
A;Accession: A61568
A;Molecule type: mRNA
A;Residues: 1-40, 'SHEH', 540-582, 'S' <TH3>
A;Note: this clone was reevaluated in reference JQ0018 and is thought to represent a clone
R;O'Prey, J.; Chester, J.; Thiele, B.J.; Janetzki, S.; Prehn, S.; Fleming, J.; Harrison, P.
Gene 84, 493-499, 1989
A;Title: The promoter structure and complete sequence of the gene encoding the rabbit ery
A;Reference number: JC1513; MUID:90128296; PMID:2612916
A;Accession: JC1513
A;Molecule type: DNA
A;Residues: 1-112, 'T', 114-189, 'N', 191-193, 'I', 195-663 <OPR>
A;Cross-references: GB:M33291; NID:G164731; PIDN:AA75014.1; PID:gl64732
C;Comment: Rabbit reticulocyte lipoxygenase plays a role in the degradation of mitochondria
C;Comment: This enzyme catalyzes the dioxygenation of polyenoic fatty acids containing at
C;Genetics:
A;Gene: 15-*lox*
A;Introns: 45/3; 114/1; 141/2; 182/2; 217/1; 270/3; 318/3; 388/3; 417/3; 474/2; 515/1; 54
C;Superfamily: arachidonate 5-lipoxygenase
C;Keywords: erythrocyte; iron; oxidoreductase

Query Match	82.4%	Score	2896	DB 1	Length	663			
Best Local Similarity	81.1%	Pred. No.	3.9e-229						
Matches	538	Conservative	57	Mismatches	66	Indels	2	Gaps	2

QY	1	MGLYRTRVSTGASLYAGSNNVQVLWLVGQHGEEAALGKRLWPARG-ETELKVEVPEYLGPL	59
DB	1	MGVYRVCVSTGASLYAGSKNKVELWLVGQHGVEFGSLRPTNKKEEFKWNYSKYLGS	60
QY	60	LFVKLRKRHLKDDAFWCNWSVQGPAG-DEVRFPCYRWVEGNGVLSLPEGGTRTGGED	118
DB	61	LFVRLRKGHFLKEDAFWCNWSVQALGAAEDKYFFCYRWVGDSQVSPVGICTTVGD	120
QY	119	PQGLFKHREHELEERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDFEVS	178
DB	121	PQGLFKHREHELEERKLYQWGSWKEGILLNVAGSKLTDLPVDERFLEDKKTIDFEAS	180
QY	179	KGHLADIARLDSNLVLCWKDLDDFNRIFWCGOSKLAEVRVDSWKEDALFGYQFLGANPV	238
DB	181	WGLAEALAKDSLNLVLAAPWKTLLDDFNRIFWCGRSKLARRVRDSWQEDSLFGYQFLGANPM	240
QY	239	VLRRSHLPAFLVFPFGMEELQALKELEGGTLFEADFSLLDGIIKANVILCSQQHAAAP	298
DB	241	LILRSVQLPAFLVFPFGMEELQALKELEKAGTLFEADFALLDNIKANVILYCCQYLAAP	300

299	Qy	LVMKLQDPGKLLPMVIOQLPRTGSSPPPLFLPTDPPMAWILAKCWRSSDFOLHELQS	358
301	Dd	: : : : : : : : : : :	360
	Dd	LVMKLQDPGKLLPMVIOQLHPKIGSSPPPLFLPTDPPMVLWLAKCWRSSDFQVHLS	
359	Qy	HLLRGHLMAEVIIVATMCRLSPHSIPIFKLIIPHLYRTELEINVARCLUSDGMGIDPOIMS	418
361	Dd	: : : : : : : : : :	420
	Dd	HLLRGHLMAEVETVATMCRLSPHVFKLIVPHURYTLEINVRRNGLVSDFGIFDOIMS	
419	Qy	TGGGGHVQLLKQAAGFLTYSSFCPPDDDLADRGLLGVKSSFYAQDALRLMEIIYRYVEGIV	478
421	Dd	: : : : : : : : : :	480
	Dd	TGGGGHVQLLKQAAGFLYRSFCPPDDLADRGLLGVSSFYAODALRLMEIISRYVOGIM	
479	Qy	SUHYKTDAVKDDPELOQTWCBEITEIGLGQAQRGFVPVSLQARDQVCHFVTMCIFCTCG	538
481	Dd	YKTDFAVRDDLELQSWCREITEIGLGQAQKGFPFSLQSVAAQACHFTVMCIFCTCG	540
	Dd	GLYKYTDEAVRDDLELQSWCREITEIGLGQAQKGFPFSLQSVAAQACHFTVMCIFCTCG	
539	Qy	HASVHLGOLDWSWPVNAPCTMRLPPTTKDATLETVMATLBNFHQASLOMSITWOLGRR	598
541	Dd	: : : : : : : : : : :	600
	Dd	HSHIHJQLQDWFTWPNAPCTMRLPPTTKDATLETVMATLBNHLOSSLOMSIWOLGRD	
599	Qy	QPVMVAVGQBEEYFSGPPEPKAVLKCFREELAAADKEIEIRNAKLMDPYEYLPSVVENS	658
601	Dd	YMPQLGHQHEYFSGPPEPAVLEKFREELAINDKEIEIVRNEKLDIPYEYLPSIVENS	660
	Dd	QPIMYPLGHQHEYFSGPPEPAVLEKFREELAINDKEIEIVRNEKLDIPYEYLPSIVENS	
659	Qy	VAI 661 	
661	Dd	VAI 663 	

RESULT 5
S30051
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S30051
R.; Watanabe, T.; Medina, J. F.; Haegsdstroem, J. Z.; Radmark, O.; Samuelsson, B.
Eur. J. Biochem. 212, 605-612, 1993
A/Title: Molecular cloning of a 12-lipoxygenase cDNA from rat brain.
A/Reference number: S30051; MUID:93185682; PMID:8444196
A/Accession: S30051
A/Molecule type: mRNA
A/Residues: 1-663 <WAT>
A/Cross-references: UNIPROT:Q02759; EMBL:L06040; NID:g205212; PIDN:AAA41532.1; PID:g205212
C/Superfamily: arachidonate 5-lipoxygenase
C/Keywords: oxidoreductase

	Query Match	76.7%;	Score 2696;	DB 1;	Length 663;
	Best Local Similarity	74.5%;	Pred. No. 9.8e-213;		
	Matches 494;	Conservative 77;	Mismatches 90;	Indels 2;	Gaps 2;
Qy	1	MGLYRIIVSTCASLYAGSNNOVLWLVGQHGEEAALGKRLMPAR-GETELKVEVPEYIGPL	59		
Db	1	MGVYRIIVSTGDSKYAGSNNEVYLWLVGQHGEEALGKLLRPCRUSEAFFKVDVSEYIGPL	60		
Qy	60	LFVLKRRHLIKDDAWFCNWMISVQGP-AGDEVRFPCYRWVEGNGVLSLPEGTGRTVGED	118		
Db	61	LFVRVQKHVYLTDDAWFCNWMISVKGPDSQSEYMFPCYRWVQGRSILSLPEGTGCTVVED	120		
Qy	119	PQGLFQKHXREBELSERKLYRWGNWKOGLILNMAGAKLYLDPVDERFLEDKRVDVFEVSLA	178		
Db	121	SQGLFRKHXREBELSERSLYRWGNWKOGLILNVAAASITSLDPVDQRFREDKRIEFAESQV	180		
Qy	179	KGLADLAIKOSLNVLTCKWOLDDENNRIFWCQSKLAERVRDSWKEDALFGVQFLNGANPV	238		
Db	181	IGVMDTVVNFPIVTVTCWKSJDDFCNCFVFKSGHTTKAERVRNWSKEDAFFGYQFLNGANPM	240		
Qy	239	VLRSALHPARLVFPFPGMEELQAQLEKELEGTTIFEADFSLDDGIKANVILCSQOHLAAP	298		
Db	241	VLKRETCGLPARLVFPFPGMEKLOAQINKELOKGTIFEADFLLDDGKANVILCSQOYLAAP	300		
Qy	299	LVMLKLQPDGKLLPMVLIQQLPRTGSSPPPLFLPTDPPMAWLLAKCWWVRSSDFOLHELQS	358		
Db	301	LVMLKLMPDGOLLPIAIOLEPKTGSYPPPTFTSDPPMDWLLAKCWWVRSSDLOLHELQA	360		

[illegible]

RESULT 6
152462
arachidonate 12-lipoxygenase (BC 1.13.11.31) - rat
C/Species: Rattus sp. (rat)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jun-1999
C/Accession: I52462
C/hada, T.; hagiya, H.; Suzuki, H.; Arakawa, T.; Nakamura, M.; Matsuda, S.; Yoshida, T.; Biochim. Biophys. Acta 1211, 221-228, 1994
A/Title: Arachidonate 12-lipoxygenase of rat pineal glands: catalytic properties and localization
A/Reference number: I52462; PMID:94162305; PMID:8117750
A/Accession: I52462
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-663 <RES>
A/Cross-references: NID:G545793; PIDN:AB30132.1; PID:G545794
C/Superfamily: arachidonate 5-lipoxygenase
C/Keywords: oxidoreductase

[illegible]

Db 361 HLLRGHLMAEVAVATMCLPSVHFVFKLLVPHLLYTWIENVRARSDDISERGFDDKMS 420
 Qy 419 TGGGGHVLKQAGAFITYSSFCPPDDLLADRGLLGVKSSFYAQAALRLWEIYYRYVEGIV 478
 Db 421 TGGGGHLLDQAGAFITYCSLCPDDLLAERGLLDIETCFYAKDALRLWQIMNRYVVGWF 480
 Qy 479 SLHYKTDVAVKDDPELOTWCEITIEIGLQAGDQGFVSLQARDQVCHFTVTCICTGQ 538
 Db 481 NLHYKTDKAVQDDYELQSWCREITDGLQAGDQGFVSLQARAQCYFITMCIPTCTAQ 540
 Qy 539 HASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 598
 Db 541 HSSVHLGOLDWYFVWPNAPCTMRLPPPTTKETATMELKMATLPNPNQSTLQINNVWLLGRR 600
 Qy 599 QPVMVAVGQHEEYFSGPEPKAVLKPFREELAALDKETIEIRNAKLDMPYELRPSVENS 658
 Db 601 QAVMVPLGQHEEHPNPEAKAVLKPFREELAALDKETIEIRNKSUDIPYEYLRPSVENS 660
 Qy 659 VAI 661
 Db 661 VAI 663

RESULT 7

B54075
 arachidonate 12-lipoxygenase (EC 1.13.11.31), leukocyte [validated] - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: B54075; I49439
 R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.
 J. Biol. Chem. 269, 13979-13987, 1994
 A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure
 A:Reference number: A54075; MUID:94245713; PMID:8188678
 A:Accession: B54075
 A:Molecule type: DNA; mRNA
 A:Residues: 1-663 <CHE>
 A:Cross-references: UNIPROT:P39654; GB:U04331; NID:9467216; PIDN:AAA20658.1; PID:9467217
 A:Experimental source: strains C57BL/6 and ICR, spleen leukocytes
 A:Note: removal or substitution of Ile-663 abolished enzyme activity
 R:Freire-Moar, J.; Alavi-Nasab, A.; Ng, M.; Mulkins, M.; Sigal, E.
 Biochim. Biophys. Acta 1254, 112-116, 1995
 A:Title: Cloning and characterization of a murine macrophage lipoxygenase.
 A:Reference number: I49439; MUID:95110857; PMID:7811740
 A:Accession: I49439
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-36, 'N', 38-118, 'Q', 120-396, 'N', 398-663 <RES>
 A:Cross-references: GB:L34570; NID:9509607; PIDN:AAA64930.1; PID:9763530
 C:Comment: A second arachidonate 12-lipoxygenase from mouse platelets is shown in (PIR:A
 C:Genetics:
 A:Map position: 11
 C:Superfamily: arachidonate 5-lipoxygenase
 C:Keywords: oxidoreductase

Query Match 76.2%; Score 2676; DB 1; Length 663;
 Best Local Similarity 73.6%; Pred. No. 4.3e-211;
 Matches 488; Conservative 80; Mismatches 93; Indels 2; Gaps 2;
 Qy 1 MGLYRIRVSTGASLYAGSNVQVLMLVGHGGAALGKRLWPAR-CETELKVEVPYILGPL 59
 Db 1 MGVIYRIRVSTGVSIVAGSNNEVYLLIGQHGASLGLFRPCRNSEAFKVDVSEYLGPL 60
 Qy 60 LFLVKLRKHLKDDAWFCNWIISVQGP-AGDVRFPYRVGEGVLSLPEGTGRTVGED 118
 Db 61 LFRVQKWHYLLKEDAWFCNWIISVQGPQGSYTFPCRWWQSTSLMDPEGTGCTVVED 120
 Qy 119 PQGLFKHREELERKLYRGNKNGKGLILNMAGAKLYDLPVDRFRLEDKRVDFEVL 178
 Db 121 SQGLFRNREELERRSIYRGNKNGKGLILNVNATSISDLFVDQRFREDKELFEASQV 180
 Qy 179 KGLADLAIKOSLNVLVTCWKDLDFNRIFWCGOSKLAERVRDSWKSDALFGYQFLNGANPV 238

Db 181 LGTMDTVINPKNTVTCKWSLDDFNYYVFKSGHTKMAERVRNSWKEDAFPGYQFLNGANPM 240
 Qy 239 VLRSASHLPARLVPPPGMEELQALEKELEGTTFEADFSLLDGIKANVILCSQOHLAAP 298
 Db 241 VLKSTCLPARLVPPPGMEKLAQLDBELKKGTLFEADFFLLDGIKANVILCSQOYLAAP 300
 Qy 299 LVMLKLPDQDKLPMVLOLQLPRTGSPPPPLFLPTDPPMALLAKCWRSSDFOLHELQS 358
 Db 301 LVMLKLPDQDGLLPIAQLLELFTKGTSTPPPLFTDPPMDWLLAKCWRSSDLQHLQ 360
 Qy 359 HLLRGHLMAEVIVVATMCLPSIHPIFKLIIPHLYTLINVRARTGLVSDMGIFDQIMS 418
 Db 361 HLLRGHLVAEVFAVATMCLPSVHFVFKLLVPHLLYTWIENVRARSDDISERGFDDKMS 420
 Qy 419 TGGGGHVLKQAGAFITYSSFCPPDDLLADRGLLGVKSSFYAQAALRLWEIYYRYVEGIV 478
 Db 421 TGGGGHLLDQAGAFITYCSLCPDDLLAERGLLDIETCFYAKDALRLWQIMNRYVVGWF 480
 Qy 479 SLHYKTDVAVKDDPELOTWCEITIEIGLQAGDQGFVSLQARDQVCHFTVTCICTGQ 538
 Db 481 DLHYKTDQAVQDDYELQSWCREITIEIGLQAGDQGFVSLQARAQCYFITMCIPTCTAQ 540
 Qy 539 HASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 598
 Db 541 HSSVHLGOLDWYFVWPNAPCTMRLPPPTTKETATMELKMATLPNPNQSTLQINNVWLLGRR 600
 Qy 599 QPVMVAVGQHEEYFSGPEPKAVLKPFREELAALDKETIEIRNAKLDMPYELRPSVENS 658
 Db 601 QAVMVPLGQHEEHPNPEAKAVLKPFREELAALDKETIEIRNKSUDIPYEYLRPSVENS 660
 Qy 659 VAI 661
 Db 661 VAI 663

RESULT 8

A38283
 arachidonate 12-lipoxygenase (EC 1.13.11.31) - human
 N:Alternate names: platelet-type 12-lipoxygenase
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1991 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C:Accession: A38283; A36246; A35953; I51906; I64836; A33091
 R:Fizumi, T.; Hoshiko, S.; Radmark, O.; Samuelsson, B.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7477-7481, 1990
 A:Title: Cloning of the cDNA for human 12-lipoxygenase.
 A:Reference number: A38283; MUID:91017529; PMID:2217179
 A:Accession: A38283
 A:Molecule type: mRNA
 A:Residues: 1-663 <IZU>
 A:Cross-references: UNIPROT:P18054; UNIPROT:Q16120; GB:M38192; GB:M38792; GB:M58704; NID:
 A:Experimental source: platelet mRNA
 A:Note: some sequence heterogeneity was found
 R:Yoshimoto, T.; Yamamoto, Y.; Arakawa, T.; Suzuki, H.; Yamamoto, S.; Yokoyama, C.; Tanai
 Biochem. Biophys. Res. Commun. 172, 1230-1235, 1990
 A:Title: Molecular cloning and expression of human arachidonate 12-lipoxygenase.
 A:Reference number: A36246; MUID:91058562; PMID:2244907
 A:Accession: A36246
 A:Molecule type: mRNA
 A:Residues: 1-188, 'PCLH', 193-260, 'Q', 262-321, 'S', 323-344, 'C', 346-663 <YOS>
 A:Cross-references: GB:M62982; NID:9177106; PIDN:AAA51533.1; PID:9177107
 R:Funk, C.D.; Fucci, L.; FitzGerald, G.A.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5638-5642, 1990
 A:Title: Molecular cloning, primary structure, and expression of the human platelet/eryt
 A:Reference number: A35953; MUID:90332636; PMID:2377602
 A:Accession: A35953
 A:Molecule type: mRNA
 A:Residues: 1-260, 'Q', 262-321, 'S', 323-388, 'P', 390-663 <FUN>
 A:Cross-references: GB:M35418; NID:9189773; PIDN:AAA60056.1; PID:9189774
 R:Hussein, H.; Shornick, L.P.; Shannon, V.R.; Wilson, J.D.; Funk, C.D.; Pentland, A.P.; I
 Am. J. Physiol. 266, C243-C253, 1994
 A:Title: Epidermis contains platelet-type 12-lipoxygenase that is overexpressed in germi
 A:Reference number: I51906; MUID:94136572; PMID:8304420
 A:Accession: I51906

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-427 <RES>

A:Cross-references: GB:S68587; NID:G545223; PIDN:AAAD14020.1; PID:G4261720

A:Experimental source: skin, epidermal cells

A:Accession: I64836

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-396, 'V', 398-427 <RES>

A:Cross-references: GB:S68588; NID:G545222; PIDN:AAAD14021.1; PID:G4261721

C:Genetics:

A:Gene: GDB:ALOX12

A:Cross-references: GDB:127547; OMIM:152391

A:Map position: 17p13.1-17p13.1

C:Function:

A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,10E,14Z)-(12S)-12-H

A:Pathway: leukotriene biosynthesis

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidon

F:360,365,540,544,663/Binding site: iron (His, His, Asn, Ile) #status predicted

Query Match 65.8%; Score 2312; DB 1; Length 663;

Best Local Similarity 65.3%; Pred. No. 3e-181;

Matches 433; Conservative 94; Mismatches 134; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLVLVGQHGAEALGKRLWPARG-ETELKVEVPEVLGPL 59

Db 1 MGRYRIRVATGAWLFGSGYNRQLMLVGTGRGAELQLRPARGEEEDHDAEDLGLL 60

QY 60 LFFVKLRKRLHKDDDAWFCNWIISVQSGAGDEVRFPCYRWVEGNVLSPEGTGRTVEDP 119

Db 61 QFVLRKXHLWVDDAWFCNRIITVQSGACAEAVFPCYRWVQGEDILSLPEGTARLPGDNA 120

QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLVDERFLEKRVDFEVSIAK 179

Db 121 LDMFQKHREELERKLYRWGNWKGILLNAGAKLYDLVDERFLEKRVDFEVSIAK 180

QY 180 GLADLAIKDSNLVLTCKWDLDDFNRIFWCGSKLAERVDSWKEDALFGYFLNGANPVV 239

Db 181 GALEMALKRVYTLSSWNCLEDFDQIFWQKSALEKVRQCHQWDELFSYQFLNGANPML 240

QY 240 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299

Db 241 LRRSTSLPSRLVLPSCMEELQAQLEKELQNGSLFEADFIILDGIKANVIRGEKQVLAAPL 300

QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359

Db 301 VMLKMEPNGKLPQMWIOIQPPNPSSPTTLFLPSPDPLAWLLAKSWVRNSDFQLHEIOYH 360

QY 360 LLRGHLMAEVIIVATWRCCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419

Db 361 LNLTHLVAEVIIVATWRCCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVQLLKOAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWELIIVRYVEGIVS 479

Db 421 GGGGHVQLLRAAAQITYCSLCPDDLADRGLLGLPGALYAHDAALRLWELIIVRYVEGIVH 480

QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGADRFPVSLQARDQVCHFTVMCIPTCTGOH 539

Db 481 LFYQRDDIVKGDPELQAWCREITEVGLCHAQDRGFPVFSQSQSLCHFLTMCVFTCTAQH 540

QY 540 ASVHLGOLDWYSWPNAPCTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWOLGRR 598

Db 541 AAINQQLDWAYVWPNAPCTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWOLGRR 600

QY 599 QPVMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKKEIIRNAKLDMPYEYLRPSVENS 658

Db 601 QPDMVPLGHKKEKYFSGPKAVLNQFRITDLEKLEKEITARNEQDLDPVEYILKPSCIENS 660

QY 659 VAI 661

Db 661 VTI 663

RESULT 9

AS4075

arachidonate 12-lipoxygenase (EC 1.13.11.31), platelet [validated] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: A54075

R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.

J. Biol. Chem. 269, 13979-13987, 1994

A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structu

A:Reference number: A54075; MUID:94245713; PMID:8188678

A:Accession: A54075

A:Molecule type: DNA; mRNA

A:Residues: 1-663 <CHE>

A:Cross-references: UNIPROT:P39655; GB:U04334; NID:G467220; PIDN:AAA20659.1; PID:G467221

A:Experimental source: strain C57BL/6, blood platelets

A:Note: removal or substitution of Ile-663 abolished enzyme activity

C:Comment: A second arachidonate 12-lipoxygenase from mouse leukocytes is shown in (PIR:1

C:Genetics:

A:Map position: 11

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: oxidoreductase

Query Match 64.1%; Score 2252; DB 1; Length 663;

Best Local Similarity 63.3%; Pred. No. 2.5e-176;

Matches 420; Conservative 96; Mismatches 145; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLVLVGQHGAEALGKRLWPARG-ETELKVEVPEVLGPL 59

Db 1 MGAYRVRVVTGAWLFGSGSLNLVRLVLVGEHREAKLEQLRPARGKEEFDFPVEDLGLP 60

QY 60 LFFVKLRKRLHKDDDAWFCNWIISVQSGAGDEVRFPCYRWVEGNVLSPEGTGRTVEDP 119

Db 61 QFVKLHKQHTVDDAWFCNLIITVQSGPTSAEAVFPCYRWVQEGILSLPEGOARLAGDNA 120

QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLVDERFLEKRVDFEVSIAK 179

Db 121 LDVFOKYREKELKQOQTYCWATWKEGLPQTIAADCKDDLPPNMRPHEKRLDFEWTAK 180

QY 180 GLADLAIKDSNLVLTCKWDLDDFNRIFWCGSKLAERVDSWKEDALFGYFLNGANPVV 239

Db 181 GYLEMGLKRVYTLSSWNLHEDFDQIFWQKSALEKVRQCHQWDELFSYQFLNGANPML 240

QY 240 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299

Db 241 LRRSTSLPSRLVLPSCMEELQAQLEKELKNGSLFEADFIILDGIKANVIRGEKQVLAAPL 300

QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359

Db 301 VMLRMDPGKLLPMAIOIQPPNPSSPAPTFLPSPDPLAWLLAKIWNVRNSDFQLQELQPH 360

QY 360 LLRGHLMAEVIIVATWRCCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419

Db 361 LNLTHLVAEVIIVATWRCCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVQLLKOAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWELIIVRYVEGIVS 479

Db 421 GGGGHVQLLTRAVALQTYHSLCPDDLANRGLLRIPSAFYARDALQLEWTVARYVKGWVH 480

QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGADRFPVSLQARDQVCHFTVMCIPTCTGOH 539

Db 481 LFYQSDDIVKGDPELQAWCREITEVGLCHAQDRGFPVFSQSRAQLCHFLTMCVFTCTAQH 540

QY 540 ASVHLGOLDWYSWPNAPCTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWOLGRR 598

Db 541 AAINQQLDWAYVWPNAPCTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWOLGRR 600

QY 599 QPVMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKKEIIRNAKLDMPYEYLRPSVENS 658

Db 601 QPDMVPLGHKKEKYFSGPKAVLNQFRITDLEKLEKEITARNEQDLDPVEYILKPSRIENS 660

QY 659 VAI 661

Db 659 VAI 661

Db 661 ITI 663

RESULT 10

I49479
arachidonate 5-lipoxygenase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49479
R:Chen, X.S.; Naumann, T.A.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.
J. Biol. Chem. 270, 17993-17999, 1995
A:Title: cDNA cloning, expression, mutagenesis, intracellular localization, and gene characterization of mouse 5-lipoxygenase
A:Reference number: A57186; MUID:95355399; PMID:7629107
A:Accession: I49479
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-674 <RES>
A:Cross-references: UNIPROT:P48999; GB:L42198; PIDN:AAC37673.1; PID:G886333
C:Genetics:
C:Superfamily: arachidonate 5-lipoxygenase

Query Match 37.0%; Score 1299.5; DB 2; Length 674;
Best Local Similarity 39.3%; Pred No. 3.3e-98;
Matches 266; Conservative 142; Mismatches 250; Indels 19; Gaps 10;
QY 1 MGLYRIRVSTGASLYAGSNQVQLVVGQHG---EAALGKRLWP--ARGETE-LKVEYPE 54
Db 1 MPSYTVTVATGQFAGTDDYIYLSLIGSAGCSEKHLDDKAFYNDFERGAVDSYDVTDE 60
QY 55 YLGPLLFFVKLRKRLHLLKDDAWFCNWI SVQPGAGDEVFPFCYRWVEGNGVSLPBGRT 114
Db 61 ELGETIYLVKIEKKRWLHDDWYLTITLKT- HGDYIEFPFCYRWITGEIVLRDGRAL 119
QY 115 VGEDPQGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLPVDERFLEDKRVDPE 174
Db 120 ARDDQIHLKHRRKELEARQYRWMEWNPFGPLSIDAKCHKDLPRDIQPDSEKGVDFV 179
QY 175 VSLAKGLADLAITKLSNLV-TCWKDLDDFNRFWCGQSKLAERVRDSWKEDALFGYQFLN 233
Db 180 LNYSKAMENLFNRFMEHFQSSMHPADFEKIFVKISNTISERVKNHQEDLMFGYQFLN 239
QY 234 GANPVVLARSALPARLVFPQWEL---QAQLEKEGGTLFPADPSLLDGIKAN-VI 288
Db 240 GCPVLIKRCTALPKPLPVTTEWVCSLERQLSLQEVEGNIFTVDYELLDDIGIDANKTD 299
QY 289 LCSQQLAALPLVWLKLPQDKLLPWVIOQLPRTGSPPPPLPLPTDPPMALLAKCWRS 348
Db 300 PCTHQLAAPICLLYKLNANKIVPIAQLN--QTGSENPIPLPTDSKYDWLLAKIWRVS 357
QY 349 SDFQLHELQSHLLRGLHMAEVIWVATMRCPLSIPIFKLIIPHLRYTLEINVRARTGLVS 408
Db 358 SDFVHQITITLRLTHLVSEVFGIAMYRLPAVHPLKLLVAHVAFITAINTKAREQLIC 417
QY 409 DMGIIDQIMSTGGGHVQLLQKAGFLYSSFCPPDDADRLGLLVKSS---FYAQDAIR 465
Db 418 EYGLDFKANATGGGHVQVQRAVDLTYSLLCFPEAIKARGMDSTEDMPFYFYRDDGLL 477
QY 466 LWEILYRVVGVTSVLYHKTDAVKDDPELOTCWCRITEITGLOGADRGPVSLQARDQVC 525
Db 478 VWEALQSFTMEVVSIIYENDQVVEQDELQDFVKDYVYVMGRKASGFPKSIKREKLVS 537
QY 526 HPVTMCITCTQCHASVHLGQLDWTSWPNAPCTMRLPPPTTKD-ATLETVMATLPNFHQ 584
Db 538 EYLTVITFASQAHAHVNGQYDWCSPINAPPTWAPPTKAGVVTIEQIVDTLPDRGR 597
QY 585 ASLQMSITWQLGRRQPMVAVGQHEEYFSGPEPKAVLKFFREELAAADKEIIRNAKLD 644
Db 598 SCWHLGAVWALSQFQENELFLGMPYEEHFIEKPVKEAMIRFRKNLEAITSVIAERNKKNK 657
QY 645 MPYEYLRVSVENSVAI 661
Db 658 LPYYLYSPDRIPNSVAI 674

RESULT 11

DAHUAL
arachidonate 5-lipoxygenase (EC 1.13.11.34) [validated] - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1989 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C:Accession: A28117; A37017; A28397; A32104; A38410
R:Dixon, R.A.F.; Jones, R.E.; Diehl, R.E.; Bennett, C.D.; Kargman, S.; Rouzer, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 416-420, 1988
A:Title: Cloning of the cDNA for human 5-lipoxygenase.
A:Reference number: A28117; MUID:88124852; PMID:3422434
A:Accession: A28117
A:Molecule type: mRNA
A:Residues: 1-674 <DI>
A:Cross-references: UNIPROT:P09917; GB:J03600; NID:g187192; PIDN:AAA36183.1; PID:g187193
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.
Adv. Prostaglandin Thromboxane Leukot. Res. 19, 466-469, 1989
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.
A:Reference number: A37017; MUID:89320027; PMID:2526519
A:Accession: A37017
A:Molecule type: mRNA
A:Residues: 1-674 <MATS>
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 26-30, 1988
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.
A:Reference number: A28397; MUID:88124804; PMID:2829172
A:Accession: A28397
A:Molecule type: mRNA
A:Residues: 1-535, 'PVGPRDGLHRLPARQRLPRVLLVLDPCAPNHASPATDCQ', 581-674 <RF1>
A:Note: parts of the sequence, including the amino end, were confirmed by protein sequencing.
A:Note: This sequence report appears to contain a frameshift error
R:Funk, C.D.; Hoshiko, S.; Matsumoto, T.; Radmark, O.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 86, 2587-2591, 1989
A:Title: Characterization of the human 5-lipoxygenase gene.
A:Reference number: A32104; MUID:89202374; PMID:2565035
A:Accession: A32104
A:Molecule type: DNA
A:Residues: 1-50 <FUN>
A:Cross-references: GB:J04520; NID:g187168; PIDN:AAA59522.1; PID:g187169
R:Hoshiko, S.; Radmark, O.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 87, 9073-9077, 1990
A:Title: Characterization of the human 5-lipoxygenase gene promoter.
A:Reference number: A38410; MUID:91067649; PMID:2251250
A:Accession: A38410
A:Molecule type: DNA
A:Residues: 1-11 <HOS>
A:Cross-references: GB:M38191
C:Comment: This calcium- and ATP-requiring enzyme catalyzes the first two steps in the biosynthesis of prostaglandins and thromboxane.
C:Genetics:
A:Gene: GDB:ALOX5
A:Cross-references: GDB:L32453; OMIM:152390
A:Map position: 10q11.2-10q11.2
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: iron; leukotriene biosynthesis; metalloprotein; oxidoreductase
F:2-674/Product: arachidonate 5-lipoxygenase #status experimental <MAT>
F:368,373,551,555,674/Binding site: iron (His, His, His, Asn, Ile) #status predicted

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QY 115 VGEDPQGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLPVDERFLEDKRVDPE 174
Db 120 ARDDQIHLKHRRKELETRQYRWMEWNPFGPLSIDAKCHKDLPRDIQPDSEKGVDFV 179

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:45:07 ; Search time 1063.87 Seconds
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15928.199 Million cell updates/sec

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Scoring table: IDENTITY NUC
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Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2644.2	99.0	2844	17	US-10-398-663-13
4	1306	48.9	2048	17	US-10-191-803-178
5	1306	48.9	2048	18	US-10-152-319A-1857
6	1021.2	38.2	2348	18	US-10-240-425-1325
7	1016.4	38.1	2368	21	US-10-741-600-671

8	1016.4	38.1	2867	21	US-10-741-600-672	Sequence 672, App
9	1015.2	38.0	2368	19	US-10-741-601-232	Sequence 232, App
10	1015.2	38.0	2867	19	US-10-741-601-233	Sequence 233, App
11	1013.6	37.9	2343	17	US-10-170-097-652	Sequence 652, App
12	1013.6	37.9	2343	21	US-10-926-684-652	Sequence 652, App
13	515.6	19.3	584	19	US-10-681-818-13	Sequence 13, Appl
14	514	19.2	584	19	US-10-681-818-12	Sequence 12, Appl
15	382.6	14.3	2420	16	US-10-240-305-15	Sequence 15, Appl
16	382.6	14.3	2484	17	US-10-191-997-91	Sequence 91, Appl
17	382.6	14.3	2484	19	US-10-283-975A-296	Sequence 296, App
18	382.6	14.3	2497	9	US-09-964-824A-543	Sequence 543, App
19	382.6	14.3	2497	9	US-09-962-832-97	Sequence 97, Appl
20	382.6	14.3	2497	9	US-09-954-456-942	Sequence 942, App
21	382.6	14.3	2497	16	US-10-240-305-13	Sequence 13, Appl
22	382.6	14.3	2497	18	US-10-641-643-1155	Sequence 1155, Ap
23	382.6	14.3	2497	19	US-10-071-411-3	Sequence 3, Appl
24	382.6	14.3	2497	20	US-10-741-292-1	Sequence 1, Appl
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26	382.6	14.3	2497	21	US-10-843-641A-3969	Sequence 3969, Ap
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31	371.4	13.9	2107	20	US-10-741-292-17	Sequence 17, Appl
32	342.8	12.8	2685	9	US-09-764-246-1	Sequence 1, Appl
33	342.8	12.8	2685	10	US-09-960-706-985	Sequence 985, App
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37	332	12.4	3320	14	US-10-175-696-22	Sequence 22, Appl
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39	332	12.4	3384	16	US-10-422-264-29	Sequence 29, Appl
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42	329.4	12.3	2136	9	US-09-862-658-3	Sequence 3, Appl
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44	329.4	12.3	2136	19	US-10-776-871-24	Sequence 24, Appl
45	327.8	12.3	2307	18	US-10-302-172-803	Sequence 803, App

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10688676A
; Publication No. US20040248794A1
; GENERAL INFORMATION:
; APPLICANT: Alcon, Inc.
; APPLICANT: Yanni, John M.
; APPLICANT: Gamache, Daniel A.
; APPLICANT: Miller, Steven T.
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo
; TITLE OF INVENTION: Activity to Ocular Surface Cells
; FILE REFERENCE: 2394 US
; CURRENT APPLICATION NUMBER: US/10/688,676A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/435,988
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2671
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-688-676A-1

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Qy 2460 CTCAGCTCTCTGAGTAGCTGGGACTACAGGCTCATGCTCATGCTGCTGCTGCTGCTGCT 2519
Db 2892 CTCAGCTCTCTGAGTAGCTGGGACTACAGGCTCATGCTCATGCTGCTGCTGCTGCTGCT 2951
Qy 2520 TTATTTTCGTGGAGCGGGCTCTCATATGTTGCTAGGCTGGAAATAGGATTTTGAACC 2579
Db 2952 TTATTTTCGTGGAGCGGGCTCTCATATGTTGCTAGGCTGGAAATAGGATTTTGAACC 3011
Qy 2580 CAATTTGATTTTAAATAATAAAGTTGTTTACGCTAAAGATGGAAGAACTAGGA 2639
Db 3012 CAATTTGATTTTAAATAATAAAGTTGTTTACGCTAAAGATGGAAGAACTAGGA 3071
Qy 2640 CTGAATTTTAAATAATAATTTGGCAAAAG 2671
Db 3072 CTGAATTTTAAATAATAATTTGGCAAAAG 3103

RESULT 3

US-10-398-663-13
; Sequence 13, Application US/10398663
; Publication No. US20040053281A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE, CORPORATION; HARLAND, Lee;
; APPLICANT: ARVIZU, Chandra S.; DAS, Debopriya;
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;
; APPLICANT: DING, Li; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; LU, Yan;
; APPLICANT: ELLIOTT, Vicki S.; THANGAVELU, Kavitha;
; APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti G.;
; APPLICANT: TRIBOULEY, Catherine M.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0250 USN
; CURRENT APPLICATION NUMBER: US/10/398,663
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/31302
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/238,388
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,616
; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 60/245,719
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/247,503
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/249,503
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053281A1 7484270CBI
US-10-398-663-13

Query Match 99.0%; Score 2644.2; DB 18; Length 2844;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2652; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	1	AAGATGGGTCTCTACCGCATCCGCTGTCCACTGGGGCTCGCTCTATGCCGGTTCCAAAC	60
DB	170	AAGATGGGTCTCTACCGCATCCGCTGTCCACTGGGGCTCGCTCTATGCCGGTTCCAAAC	229
QY	61	AACAGGTGCACTGTGCTGTGCTGCGCCAGCAGCGGGAGGCGGCTCGGGAGCGACTG	120
DB	230	AACAGGTGCACTGTGCTGTGCTGCGCCAGCAGCGGGAGGCGGCTCGGGAGCGACTG	289
QY	121	TGGCCCGCAGCGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGAGTATCTGGGGCGG	180
DB	290	TGGCCCGCAGCGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGAGTATCTGGGGCGG	349
QY	181	CTGCTGTTTGTGAAGTCTGCAAAACCGCACCTCTTAAAGGACGAGCGCTGTCTGCAAC	240
DB	350	CTGCTGTTTGTGAAGTCTGCAAAACCGCACCTCTTAAAGGACGAGCGCTGTCTGCAAC	409
QY	241	TGGATCTCTGTGCGAGGGCCCGGAGCGGGAGCGAGGTCAAGTTCCTTGTGTACCGCTGG	300
DB	410	TGGATCTCTGTGCGAGGGCCCGGAGCGGGAGCGAGGTCAAGTTCCTTGTGTACCGCTGG	469
QY	301	GTGAGGGCAACGGCGTCTGTAGCTGCTGTAAGCCACCGCGCACCTGTGGCGAGGAC	360
DB	470	GTGAGGGCAACGGCGTCTGTAGCTGCTGTAAGCCACCGCGCACCTGTGGCGAGGAC	529
QY	361	CCTCAGGGCCTGTTCCAGAAAACCGCGGAAGAGAGCTGGAAGAGAGAAAGTTGTAC	420
DB	530	CCTCAGGGCCTGTTCCAGAAAACCGCGGAAGAGAGCTGGAAGAGAGAAAGTTGTAC	589
QY	421	CGGTGGGAAACTGTGAAGAACGGGTTAATCTGAATATGGCTGGGGCCAAACTATATGAC	480
DB	590	CGGTGGGAAACTGTGAAGAACGGGTTAATCTGAATATGGCTGGGGCCAAACTATATGAC	649
QY	481	CTCCCTGTGGATGAGGATTTCTGAAGACAGAGAGTTGACTTTGAGTTTCGCTGGCC	540
DB	650	CTCCCTGTGGATGAGGATTTCTGAAGACAGAGAGTTGACTTTGAGTTTCGCTGGCC	709
QY	541	AAGGGGCTGGCGACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGAT	600
DB	710	AAGGGGCTGGCGACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGAT	769
QY	601	CTAGATGACTTCAACCGGATTTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	660
DB	770	CTAGATGACTTCAACCGGATTTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	829
QY	661	GACTCTGGAAGAGATGCTTATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
DB	830	GACTCTGGAAGAGATGCTTATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	889
QY	721	GTGCTGAGCGCTCTGCTCACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
DB	890	GTGCTGAGCGCTCTGCTCACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	949

QY	781	CTGCAGGCCAGCTGGAGAGGAGCTGGAGGAGGACACACTGTTTGAAGCTGACTTCTCC	840
DB	950	CTGCAGGCCAGCTGGAGAGGAGCTGGAGGAGGACACACTGTTTGAAGCTGACTTCTCC	1009
QY	841	CTGCTGGATGGATCAAGGCCCAACGTCATCTCTGTAGCCAGCAGCAGCTGCTGCCCT	900
DB	1010	CTGCTGGATGGATCAAGGCCCAACGTCATCTCTGTAGCCAGCAGCAGCTGCTGCCCT	1069
QY	901	CTAGTCATGCTGAAATTCGACGCTGTAGGAAACTCTTTGCCCATGGTTCATCAGCTCCAG	960
DB	1070	CTAGTCATGCTGAAATTCGACGCTGTAGGAAACTCTTTGCCCATGGTTCATCAGCTCCAG	1129
QY	961	CTGCCCGCAGCAGGATCCCAACCACTCCCTCTTTTCTGCTACGATCCCAATGGCC	1020
DB	1130	CTGCCCGCAGCAGGATCCCAACCACTCCCTCTTTTCTGCTACGATCCCAATGGCC	1189
QY	1021	TGGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGATTTCCAGCTCCATGAGTGCAGTCT	1080
DB	1190	TGGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGATTTCCAGCTCCATGAGTGCAGTCT	1249
QY	1081	CATCTTCTGAGGGACACTTGTATGGCTGAGTCAATTGTTGGCCACCACCATGAGTGCCTG	1140
DB	1250	CATCTTCTGAGGGACACTTGTATGGCTGAGTCAATTGTTGGCCACCACCATGAGTGCCTG	1309
QY	1141	CCGTGATACATCTTCAAGCTTATTAATCCCACTGCGATACACCTCTGGAAT	1200
DB	1310	CCGTGATACATCTTCAAGCTTATTAATCCCACTGCGATACACCTCTGGAAT	1369
QY	1201	AACGTCCGGGCGAGACTGGGCTGCTCTGACATGGGAAATTTTCGACAGATAATGAGC	1260
DB	1370	AACGTCCGGGCGAGACTGGGCTGCTCTGACATGGGAAATTTTCGACAGATAATGAGC	1429
QY	1261	ACTGGTGGGGAGCCAGTGCAGCTCTCAAGCAAGCTGAGGCTTCTTAACCTACAGC	1320
DB	1430	ACTGGTGGGGAGCCAGTGCAGCTCTCAAGCAAGCTGAGGCTTCTTAACCTACAGC	1489
QY	1321	TCCTTCTGTCCTGATGACTTGGCCGACCGGGGCTCTGGGAGTGAAGTCTTCTCTC	1380
DB	1490	TCCTTCTGTCCTGATGACTTGGCCGACCGGGGCTCTGGGAGTGAAGTCTTCTCTC	1549
QY	1381	TATGCCAAAGATGCGCTGCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGGAATCGTG	1440
DB	1550	TATGCCAAAGATGCGCTGCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGGAATCGTG	1609
QY	1441	AGTCTCCATATAAGACAGAGTGGCTGTGAAAGACGACCCAGAGCTCGACACCTGGTGT	1500
DB	1610	AGTCTCCATATAAGACAGAGTGGCTGTGAAAGACGACCCAGAGCTCGACACCTGGTGT	1669
QY	1501	CGAGATCACTGAAATCGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTA	1560
DB	1670	CGAGATCACTGAAATCGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTA	1729
QY	1561	CAGCTCGGGACAGGTTTGGCACTTTGTACCATGTGTATCTTCACTGCACCGGCCAA	1620
DB	1730	CAGCTCGGGTCCAGGTTTGGCACTTTGTACCATGTGTATCTTCACTGCACCGGCCAA	1789
QY	1621	CACGCTCTGTGACCTTGGGCGAGCTGAGTGTGTAATCTTGGGTGCTTAATGCACTGTC	1680
DB	1790	CACGCTCTGTGACCTTGGGCGAGCTGAGTGTGTAATCTTGGGTGCTTAATGCACTGTC	1849
QY	1681	ACGATGGGCTGCCCCCGCCCAACCAAGAGATGCAACGCTGGAGACAGTATGGCGACA	1740
DB	1850	ACGATGGGCTGCCCCCGCCCAACCAAGAGATGCAACGCTGGAGACAGTATGGCGACA	1909
QY	1741	CTGCCCAACTTCCACAGGCTTCTCCAGATGCTCACTTGGCAGCTGGCAGAGCGC	1800
DB	1910	CTGCCCAACTTCCACAGGCTTCTCCAGATGCTCACTTGGCAGCTGGCAGAGCGC	1969
QY	1801	CAGCCCGTTATGTTGGCTGTGGGCGCAGCATGAGGAGGATATTTTTCGGGCGCTGAGCT	1860
DB	1970	CAGCCCGTTATGTTGGCTGTGGGCGCAGCATGAGGAGGATATTTTTCGGGCGCTGAGCT	2029
QY	1861	AAGGCTGTGCTGAAGAAATTCAGGGAGGAGCTGGCTGCCCTGGATAGAGAAATTCAGATC	1920

Db 2030 AAGGCTGTCTGAAGAAGTTCAGGGAGGAGCTGGCTGCCCTGGATAAGGAAATTCAGATC 2089
Qy 1921 CGGAATGCAAAAGCTGACATGCCCTACGAGTACCTGCGGCCAGCGTGTGTGAAACAGT 1980
Db 2090 CGGAATGCAAAAGCTGACATGCCCTACGAGTACCTGCGGCCAGCGTGTGTGAAACAGT 2149
Qy 1981 GTGGCCATCTAAGCGTCGCGACCCCTTTGGTTATTTTTCAGCCCCCATCACCAAGCCACAAG 2040
Db 2150 GTGGCCATCTAAGCGTCGCGACCCCTTTGGTTATTTTTCAGCCCCCATCACCAAGCCACAAG 2209
Qy 2041 CTGACCCCTTGTGGTTATAGCCCTGCGCTCCCAAGTCCCAACCTTCCCAATGTCACAC 2100
Db 2210 CTGACCCCTTGTGGTTATAGCCCTGCGCTCCCAAGTCCCAACCTTCCCAATGTCACAC 2269
Qy 2101 CCTCCCTAGAGGGGACCCCTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAGA 2160
Db 2270 CCTCCCTAGAGGGGACCCCTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAGA 2329
Qy 2161 GGCACTCACCTGGGACCTTACTCTCTTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
Db 2330 GGCACTCACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2389
Qy 2221 TCT 2280
Db 2390 TCT 2449
Qy 2281 TTTCAGACTAGNATAGGGGGATATATACATATTTACTCCACACCTTTTATCAATCAAT 2340
Db 2450 TTTCAGACTAGNATAGGGGGATATATATACATATTTACTCCACACCTTTTATCAATCAAT 2509
Qy 2341 ATGATTTTTTTTGT 2400
Db 2510 ATGATTTTTTTTGT 2569
Qy 2401 GGTGCCATCACACGGCTCACTGACGCTCAGCGTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 2460
Db 2570 GGTGCCATCACACGGCTCACTGACGCTCAGCGTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 2629
Qy 2461 TCAGCCTCTGAGTACGCGGACTCAGGCTCATGCGCATCATGCGCATCATGCGCATCATGCGCAT 2520
Db 2630 TCAGCCTCTGAGTACGCGGACTCAGGCTCATGCGCATCATGCGCATCATGCGCATCATGCGCAT 2689
Qy 2521 TATTTTCGTGGAGACGGGCTCCTCATCTATGTTGCTAGGCTGGAATAGGATTTTGAACCC 2580
Db 2690 TATTTTCGTGGAGACGGGCTCCTCATCTATGTTGCTAGGCTGGAATAGGATTTTGAACCC 2749
Qy 2581 AAATTGAGTTTAAATAATAAAGTTGTTTTCGCTAAAGATGGAAGAACTAGGAC 2640
Db 2750 AACTTGAGTTTAAATAATAAAGTTGTTTTCGCTAAAGATGGAAGAACTAGGAC 2809
Qy 2641 TGAACCTATTTTAAATAATAATTTGG 2665
Db 2810 TGAGCTATTTCTAAATGAAAGTCG 2834

RESULT 4
US-10-191-803-178
; Sequence 178, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031010
US-10-191-803-178

Query Match 48.9%; Score 1306; DB 17; Length 2048;
Best Local Similarity 78.3%; Pred. No. 0; Mismatches 435; Indels 3; Gaps 1;
Matches 1580; Conservative 0;

Qy 1 AAGATGGGTCTCTACCGCATCCGCGTGTCCACTGGGGCTCTCTCTATGCCGGTTCCCAAC 60
Db 17 AAGATGGGTCTCTACCGCATCCGCGTGTCCACTGGGGCTCTCTCTATGCCGGTTCCCAAC 76
Qy 61 AACCAAGTGCAGCTGTGCTGGTCCGCCAGCACGCGGAGGCGCTCGGGAAGCGACTG 120
Db 77 AACGAGGTCTACTCTGGTGGTGGACAGCATGAGAGGCGATCTCTCGGGAAGCTGCTA 136
Qy 121 TGGCCCGCACGGGCAAGGAGACAGAACTCAAGTGGAGTACCGGAGTATCTGGGGCG 180
Db 137 CGACCTCTCGGGACTCGGAAGCAGATTTCAAGTGGATGTGTCTAGAAATACCTTGGGCCA 196
Qy 181 CTGCTGTTTGTGAACCTCGCAACCGCACCTCTTAAAGGACGACGCTGGTTCCTGCAAC 240
Db 197 CTGCTGTTTGTGAAGTGCAGAAATGGCATATATCTACGGAATGACGCTGGTTCCTGCAAC 256
Qy 241 TGGATCTCTGTGACAGGCCCCGGAGCC--GGGGACGAGGTCAAGTTCCTTTGTTACCGC 297
Db 257 TGGATTTCTGTGAAGGGCCCCGGAGACCAAGANTCAGAGTACATGTTCCCTGTTTACCGA 316
Qy 298 TGGGTGGAGGCAACGGGCTCTGAGCCTGCTGAAGCACCACCGCGCACTGTGGCGAG 357
Db 317 TGGGTTCAGGGCAGAAAGCATCTGAGCCTCTGAGGCTCTGAGGCTGACCTGACCTGGTTGAA 376
Qy 358 GACCTCTCAGGGCTCTTCCAGAAACACCGGGAAAGAGCTGGAAGAGAGAGAGAGTGG 417
Db 377 GATTCCTCAGGACTCTTCAGGAAACATAGGGAAGAGAGCTTGAAGAGAGAGAGTCTG 436
Qy 418 TACCGTGGGAAACTGGAAGGACGGGTTAATTCGAAATATGGCTGGGGCCAAACTATAT 477
Db 437 TACAGGTGGGGCAACTGGAAGGATGGCTCAATCTCTGAATGTGGCGCGCCAGTATATCT 496
Qy 478 GACCTCCCTGTGGATGAGCGATTTCTGGNAGACAGAGAGTTGACTTTTTCAGCTTCGCTG 537
Db 497 GACCTCCCTGTAGACCAACGATTTTCGAGAGGACAAAGAAATTTGAAGCTTCACAG 556
Qy 538 GCCAAGGGCTGGCCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAG 597
Db 557 GTTATAGGGTAAATGATACTGTGTCTCACTTTCCTATTAACACTGTGACCTGCTGGA 616
Qy 598 GATCTAGATGACTTCAACCGGATTTTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
Db 617 AGCCTAGATGACTTCAACTGCGTTTTTCAAGAGTGGCCATACCAAAATGGCTGAGCGGTT 676
Qy 658 CGGGAATCTTGAAGAGAGATGCTTATTTGGGTACGAGTTTCTTAATGGCCCAACCCC 717
Db 677 CGAAATCTCTGGAAGAGAGATGCTTCTTTGGGTACCAATTCCTCAATGGTGTCTAACCCC 736
Qy 718 GTGGTGTGAGGCGCTCTGCTCACCTTCTGCTCGCTAGTGTTCCTCCAGGCAATGGAG 777
Db 737 ATGGTGTGAGGCGCTCTACTTGTCTTCTGCCCGCTGTATTCCTCCAGGAAATGGAG 796
Qy 778 GAACTGCAGGCCCCAGCTGGAGAAAGGAGCTGGAGGGGACACACTGTGTCGAAGCTGACTTC 837

181 CTGCTGTTGTGAAATCTGCGCAACGGCACCTCTTAAGACGACGCGCTGTTCTGCAAC 240
197 CTGCTGTTGTAAGAGTGAGAAATGGCATATCTCACGGATGACGCTGTTCTGCAAC 256
241 TGGATCTCTGTGAGGCGCCCGGAGCC---GGGAGAGAGGTGAGTTCCTTGTACCGC 297
257 TGGATTTCTGTGAAGGGCCCGGAGACCAAGGATCAGAGTACATGTTCCTCCCTGTTACCGA 316
298 TGGGTGGGGCAACGGCGCTCTGAGCGCTGCTGAGGACCGCGGCACTGTGGCGGAG 357
317 TGGGTTTCAGGCGAGAGCATCTGAGCTCTCCCTGAGGCGACCTGGCTGCAACCGTGTGAA 376
358 GACCTTCAGGCGCTGTTCAGAAACACCGGGAAGAGCTGGAAGAGAGAGGAGTTG 417
377 GATTCTCAGGACTGTTCAGGAAACATAGGGAAGAGGACTTTGAAGAGAGGAGGAGTCTG 436
418 TACCGGTGGGAAACCTGGAAGAGCGGTTAATCTGGAATATGCTGGGGCCCAAACTATAT 477
437 TACAGGTGGGCAACTGGAAGGATGGCTCAATCTGAAATGTGGCGCGCCAGTATATCT 496
478 GACCTCCCTGTGATGAGCGATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCGGTG 537
497 GACCTCCCTGTAGACCAAGATTTGAGAGGACAAAGAAATGAAATTTGAACTTCACAG 556
538 GCCAAGGGGCTGGCCGACCTCGCTATCAAGAGCTCTCTAAATGTTCTGACTTTGCTGGAAG 597
557 GTTATAGGGGTAATGGATACTGTGTCAACTTTCCTATAAACACTGTGACCTGCTGGAAA 616
598 GATCTAGATGACTTCAACCGGATTTTCTGGTGTGAGTGTGAGAGAGCTGTGCTGAGCGCGTG 657
617 AGCCTAGATGACTTCAACTCGCTTTTCAAGAGTGGCCATACCAAAATGGCTGAGCGGGTT 676
658 CGGACTCTCTGGAAGAGATGCTTATTTGGGTACCACTTTCTTAATGCGCGCAACCCC 717
677 CGAACTCTCTGGAAGAGATGGTTCCTTTGGGTACCAATCTCTCAATGGTGTAAACCCC 736
718 GTGGTCTCAGGCGCTCTGCTCACTTCCTGCTCGCTAGTGTTCCTCCAGGCAATGGAG 777
737 ATGGTCTGAGGCTCTACTTGTCTCTGCGCGCTGGTATTCCTCCAGGAATGGAG 796
778 GAATCGAGGCCAGCTGGAAGAGAGCTGGAGGAGGACACATGTTTGAAGCTGACTTC 837
797 AAGCTACAGGCCAGCTGAACAGAGAGCTCCAGAAAGGCACTCTGTTTGAAGCGGATTC 856
838 TCCTGCTGATGGGATCAAGCCACAGTCATCTCTGTAGCAGCAGCACCTGGCTGCC 897
857 TTCCTTCTGATGGGATCAAGGCCAATGTATCTTTGTAGCAGCGTACCTGGCTGCC 916
898 CCTCTAGTCAATGCTGAAATTCAGCCCTGATGGGAAACTCTTGGCCCATGGTCAATCCAGCTC 957
917 CCTCTGTCATGCTGAAGCTGATGCTGATGGACAACTCTTGGCCCATGCCATCCAGCTT 976
958 CAGCTGCGCGGACAGGATCCCAACCACTCCCTCTTCTGCTACGGATGCCCAATG 1017
977 GAATGCCCAAAACTGGGTACTCCACCACTATTTTCAAGCCCTCGGATCCCAATG 1036
1018 GCTGCTCTCTGCGCAAAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCATGAGCTGCAG 1077
1037 GACTGCTCTCTAGCCAAATGCTGGGTCCGAGGCTCCGACTTACAGCTCCATGAGCTGCAG 1096
1078 TCTCATCTTCTGAGGGGACACTTGTAGGTGAGGTCAATTTGTTGGCCCACTGAGGTGC 1137
1097 GCTCATCTTCTGAGGGGACACTTGTAGGTGAGGTGAGCTCTTTGCTGTGGCCCACTGAGGTGC 1156
1138 CTGCGGTGATATCATCTATCTTCAAGCTTATTAATTTCCCACTGCGATACACCTGGAA 1197
1157 CTGCTTCCGTGCAACCTGTTTAAAGCTTCTAGTTCTCTCATCTGCTTTACACCATGGAA 1216
1198 ATTAAGCTCCGGGCCAGGAGTGGTCTCTGACATGGGAATTTTTCAGACAGATAATG 1257
1217 ATTAATGTCGGGCCAGGAGTACCTGATCTCAGAGAGGCTTTTTCAGCAAGGCAATG 1276
1258 AGCACTGGTGGGGAGGCCACGTCGAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTAC 1317

1277 AGCACAGGTGGGGAGGCCACCTGATCTTCTCAAGCAAGCTGGAGCCTTTCTGACCTAT 1336
1318 AGCTCCTTCTGTCCTCCCTGATGACTTTGGCCGACCGGGGGCTCCTGGGAGTGAAGTCTTCC 1377
1337 TGCTCATTTGTGTCCCTCCGATGACTTTGGCTGAGCAGACTTTGGATATCGAGACTTGC 1396
1378 TTCTATGCCCAAGATGCGCTGCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGGAATC 1437
1397 TTCTATGCTAAGAGCGCTCGGACTCTTGGCAGATCATGAATCGGTAGCTGTGGGAATG 1456
1438 GTGAGTCTCCACTATPAAGACAGACGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGG 1497
1457 TTCAATCTCCACTACAGACCGCAAAAGCTGTGCAAGACGACTATGAATGTCAGAGCTGG 1516
1498 TGTGAGAGATCACTGAATCGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCT 1557
1517 TGTGAGAGATCACTGAATTTGGTCTTCAAGGGGCCAGGACAGAGGTTTCTTACTTCT 1576
1558 TTACAGGCTCGGGACCGAGTTTGGCACTTTGTCAACATGTGTATCTTCACTTCGACCGGC 1617
1577 CTTCACTCCCGGCTCAGGCTTGTACTTTCATCACCATGTGCATCTTCACTGTCACCGCA 1636
1618 CAACACGCTCTGTGCACTTGGGCCAGCTGGACTGGTACTCTTGGGTGCTTAATGCAACC 1677
1637 CAGCACTCTTCCGTCCATCTTGGCCAGCTGGATTGGTTCTTACTGGGTTTCTTAATGCAACC 1696
1678 TGCAGATCGGCTGCGCCCGCCCAACCAAGGATCAACGCTCGAGACAGTGTATGGG 1737
1697 TGCACATCGGCTGCCACCCACCAAGGAGCAACATGGAGAGCTGATGGT 1756
1738 ACCTGCCCAACTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCGAGA 1797
1757 ACCTGCCCAACCTTAATCAGTCTACTCTCCAGATAAATGTGTTGGCTTCTGGGCGAGA 1816
1798 GCGCAGCCGTTATGGTGGCTGTGGGCCAGCATGAGGAGGATATTTTTCGGGCCCTGAG 1857
1817 GCGCAGGCTGTATGGTGGCTGCGCCCGCAGCATTCAGAGGAACACTTTTCCAAACCTGAG 1876
1858 CTTAAGGCTGTCTCAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGATGAAGAAATTTGAG 1917
1877 GCGAAGGCTGTCTGAAGAGTTTCAAGAGGAGTGGCTTGGATTTGGATTAAGAAATTTGAG 1936
1918 ATCCGGAATGCAAGCTGACATGCGCTCAAGTACTTCCGCGCCAGCGTGTGTGAAATC 1977
1937 ATTCTAATAAGAGCTTGGACATACCTTATGATGATCTGCGGCCAGCATGCTGTGAAATC 1996
1978 AGTGTGGCATCTAAGCTGCGCACCTTTTGGTTATTT 2015
1997 AGCGTGGCCATATGAGCATCCCGAGACTCTGCTTTGT 2034

RESULT 6

US-10-240-425-1325
; Sequence 1325, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1325

; LENGTH: 2348

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20040033502A1 M62982

US-10-240-425-1325

Query Match 38.2%; Score 1021.2; DB 18; Length 2348;

Best Local Similarity 69.9%; Pred. No. 7.8e-295;

Matches 1393; Conservative 0; Mismatches 598; Indels 3; Gaps 1;

QY	4	ATGGGTCTCTACCGCATCCGGCTGTCCACTGGGGCTCTCGCTCTATGCGGTTCCAAAC	63
DB	54	ATGGCCCGCTACCGCATCCGGCTGGCCACCGGGCTCGTCTCTCCGGGTCTGTACAA	113
QY	64	CAGGTGACGTGTGGCTGGCCAGCACCGCGGAGCGCGCTCGGAACGACTGG	123
DB	114	CGGTGACGTGTGGCTGGTGGGACCGCGGGAGCGGAGCTGGAGCTGCAGCTGGG	173
QY	124	CCCGCACGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCCGCTG	183
DB	174	CGGGCCGGCGAGGAGGAGTTTGTATCATGACGTTGCAGAGACTTGGGGCTCTG	233
QY	184	CTGTTTGTAACTCGGCAACCGCACCTCTCTTAAGGACGACGCTGTCTGTCAACTGG	243
DB	234	CAGTTCTGTGAGCTGCGCAAGCACCACTCTGGTGTGGACGACGCTGGTCTTCTGCGACCG	293
QY	244	ATCTCTGTGACGGCCCGGAGCCGGGACGAGTCAAGTTCCTTGTACGGCTGGGTG	303
DB	294	ATCAGGTGCAAGGGCCCTGGAGCTGCGCGAGGTGGCTTCCCGCTGTACCGCTGGGTG	353
QY	304	GAGGCAACGGGTCTCTGAGCTCTGCAAGGACCGCGCACCTGTGGCGGAGACCT	363
DB	354	CAGGCGAGGACATCTCTGAGCTCTGCCGAGGACCGCGCGCTGCCAGGAGACATGCT	413
QY	364	CAGGCTCTTCCAGAAACACCGGGAAGAGCTGTGAAGAGAGAGAAAGTTGTACCGG	423
DB	414	TTGACATGTTCCAGAACTCAGAGAAAGAACTGAAAGACAGACAGACAGATCTACTGC	473
QY	424	TGGGAATCTGGAGGAGGTTAATCTGATATGCTGTGGCTGGGCGCAACTATATGACCT	483
DB	474	TGGGCACTTGGAAAGAGGTTTACCCCTGCACCTCGCTGCAGACCGTAAGAGATGATCA	533
QY	484	CTGTGGATGACGATTTCTGGAACAAGAGAGTTGACTTTGAGTTTCGCTGGCCCAAG	543
DB	534	CTTCAATATAGATTTCTATGAGAGAGAGGCTGGACTTTGAATGACACATGAGGCA	593
QY	544	GGGCTGGCCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGATCTA	603
DB	594	GGGCTCTGGAGATGGCCCTCAACCGTGTTTACACCTCTCTGAGCTCTCGGAATGCTTA	653
QY	604	GATGATTTCAACCGGATTTCTGTGTGGTTCAGACCAAGCTGGCTGAGCGGTGGGAC	663
DB	654	GAAGACTTTGTACAGATTTCTGGGGCCAGAGAGTGGCTGGCTGGAAGGTTTGGCCAG	713
QY	664	TCCTGGAAGGAGATGCTTATTTGGGTACCAAGTTTCTTAATGGGCGCAACCCCGTGGT	723
DB	714	TGCTGGCAGGATGATGAGTTGTTGAGCTACCAAGTTCTCAATGTGGCCAAACCCCATGCTG	773
QY	724	CTGAGGCGCTCTGCTCACCTTCTGCTCGCTCTGAGTTTCCCTCCAGGATGAGGAACTG	783
DB	774	TTGAGACCTCGACCTCTCTGCGCTCCAGGCTAGTGTGCTGCGCTCGGGATGGAAGGCTT	833
QY	784	CAGGCGAGCTGGAGAGGAGCTGGAGGAGGACACACTGTTGCAAGCTGACTTCTCCCTG	843
DB	834	CAGGCTCAACTGGAGAAAGAACTTCAAGATGGTTCCTCTGTTGAGAGCTGACTTCACTCT	893
QY	844	CTGAGTGGATCAAGGCCAAAGCTCAATCTCTGTAGCAGGACGACCTGGCTGCCCTCTA	903
DB	894	CTGGATGGAATTCAGGCCAAAGTGTATCCGAGAGAGAAAGCAATACCTGGCTGCCCTCTC	953

QY	904	GTCACTGCTGAATTTGCAGCCTGATGGGAACCTCTTGCCCATGGTCTATCCAGCTCAGCTG	963
DB	954	GTTATGCTGAAGATGGAGCCCAATGGGAAGCTGCAGCCCATGGTCTATCCAGATTGAGCT	1013
QY	964	CCCGCACAGGATCCCAACACCTCCCTCTTTCTTCTACGATCCGATCCCAATGGCTGG	1023
DB	1014	CCAGCCCCAGCTCTCCAAACCAACTGTTCTCTGCTCAGACCCCACTGCTGGCTGG	1073
QY	1024	CTTCTGCCCCAAATGCTGGTGGCGAGCTGTGACTTCCAGTCTCCATGAGCTCAGTCTCAT	1083
DB	1074	CTCTGCGCCAAATGCTGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC	1133
QY	1084	CTTCTGAGGGAGACATTTGATGGCTGAGTCAATGTTGTGGCCACCATGAGTGGCTGG	1143
DB	1134	TTGCTGAACACTCACTGCTGGTGGCTGAGTCACTGCTGCGCCACCATGCGGTGCTCCA	1193
QY	1144	TCGATACATCTATCTTCAAGCTTATAATTCGCCACCTGCGATACACCTCGGAAATTAAC	1203
DB	1194	GGACTGCACCCCATCTTCAAGTCTCTGATCCCCATATCCGCTACACCATGGAAATCAAC	1253
QY	1204	GTCCGGGCCAGGACTGGGCTGCTCTGACATGGAATTTTCGACCCAGATTAATGAGCACT	1263
DB	1254	ACCGGGCCCGGACCCCAACTCATCTCAGATGGAGGAATTTTGTATAGGCAGTGAGACA	1313
QY	1264	GGTGGGGAGGCGACGTCAGCTGCTCAAGCAAGCTGGAGCTTCTTAACCTACAGCTCC	1323
DB	1314	GGTGGAGGGGGCCATGTACAGTTGCTCCGTGCGGCGGAGCTCAGCTGACCTACTGCTCC	1373
QY	1324	TTCTGTCCCTGATGACTTGGCGGACCGGGGGCTCTGGGAGTGAAGTCTTCTCTTCTAT	1383
DB	1374	CTCTGTCTCTGACGACCTGGCTGACCGGGGCTCTGTGGAGCTCCCAAGTGTCTCTAT	1433
QY	1384	GCCCAAGATGCGTGGGCTCTGGGAATCATCTATCGGTATGTGAAGGAATCGTGAGT	1443
DB	1434	GCCCATGATGCTTTACGGCTCTGGGAGATCATTCGCCAGTATGTGGAGGGATCGTCCAC	1493
QY	1444	CTCCACTATTAAGACAGAGTGGCTGTGAAGACACACCCAGAGCTGCAGACCTGTGTGCA	1503
DB	1494	CTCTTCTACCAAGGGATGACATAGTGAAGGGGACCCCTGAGCTGCAGGCTGTGTGCG	1553
QY	1504	GAGATCACTGAATTCGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTACAG	1563
DB	1554	GAGATCAGGAGTGGGGCTGTGCCAGGCCACGAGACCGAGGTTTCCCTGTCTCTTCAG	1613
QY	1564	GCTCGGACACAGGTTTCCCACTTTGTCCCATGTGTATCTTCACTGCACCGGCCAACAC	1623
DB	1614	TCCCAGAGTCAACTCTGCCATTTCTCCTCAGCATGTGCGTCTTTCAGTGCCTGCCAGAT	1673
QY	1624	GCCTCTGTGACCTGGGCGAGCTGGACTGTACTCTTTGGGTGCTTAATGACCCCTGCAAG	1683
DB	1674	GCCGCATCAACAGGGCCAGCTGGAATGCTGCTGGTGTGCTGGTCCCTTAATGCTCCATG	1733
QY	1684	ATGGGCTGCCCGCCGCAACACCAAG--GATGCAACGCTGGAGACAGATGATGCGGACA	1740
DB	1734	ATGGGATGCCCGCCCGCCAGGAGATGTGACATGTGACATGGCCACAGTATGGGTGCA	1793
QY	1741	CTGCCCAACTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGAGAGC	1800
DB	1794	CTACTGATGTCCGGCAGGCTGTCTTCAATGSCCATCTCATGSCATCTGAGTGCCTG	1853
QY	1801	CAGCCCTTATGTGGTGTGGGCGCAGCATGAGGAGGATTAATTTTCGGGCTGAGGCT	1860
DB	1854	CAGCAGACATGTGTGCTCTGGGCGACCAAGAAATAATTTCTCAGGCCCCCAAGGCC	1913
QY	1861	AAGCTGTGTGAAGATTTTCAGGGAGGCTGCTGCTCCCTGGATAAGGAATTTGAGATC	1920
DB	1914	AAAGCTGTGTAAACCAATTTCCGAAACAGATTTTGAAGAGCTAGAAAAGGAGATTACAG	1973
QY	1921	CGGAATGCAAGCTGGACATGCCCTACAGTACCTGCGGGCCAGCTGGTGGTGAAGAACT	1980
DB	1974	CGGAATGAGCACTTGACTGCCCCCTATGATATCTGAAGCCAGCTGCTGATAGAGACAGT	2033
QY	1981	GTGCCCATCTAAGC	1994

Db 2034 GTACCATTCTGAGC 2047

RESULT 7

US-10-741-600-671

; Sequence 671, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 671

; LENGTH: 2368

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-600-671

Query Match 38.1%; Score 1016.4; DB 21; Length 2368;

Best Local Similarity 69.4%; Pred. No. 2.2e-293;

Matches 1384; Conservative 8; Mismatches 599; Indels 3; Gaps 1;

QY 4 ATGGGTCCTACCGCATCCGGTGTCCACTGGGGCTCTGCTATGCGCGTTCACCAAC 63

Db 56 ATGGGCGGTACCGCATCCGGTGTGGCCACCGGGGCTTGGCTCTTCCGGGTGCTACAAAC 115

QY 64 CAGGTGCAGCTGTGGTGTGGCCAGCACGGGGAGCGCGCTCGGGAGAGCACTGTGG 123

Db 116 CGGTGCAGCTTGGTGTGGTGTGGGACGCGGGGAGCGGAGCTGAGCTGCGGTGG 175

QY 124 CCGCCACGGGGCAAGAGACAGAACTCAAGGTGGAAAGTACCGAGTATCTGGGGCGGTG 183

Db 176 CCGCGCGGGGCGAGGAGGAGGAGTTGATCATGACGTTGCAGAGACTTGGGGCTCTGTG 235

QY 184 CTGTTTGTGAACCTGCGCAACCGCACCTCTTAAAGGACGCGCTGTTTCGCAACTGG 243

Db 236 CAGTTCGTGAGGCTGCGCAAGACCACTGGTGTGGAGCGCGTGTTCGCAACCGC 295

QY 244 ATCTCTGTGCGGGCCCGGAGCGGGGACGAGGTCAAGTTCCTTGTTCACCGCTGGGTG 303

Db 296 ATCACGTGCAGGCGCTCGAGCTCGCGGAGTGGCTTCCGCTGTACCGCTGGGTG 355

QY 304 GAGGGCAACGGCTCTGAGCTGCTGCTGAAAGCACCGCGCGCACTGTGGGCGAGACCT 363

Db 356 CAGGGCGAGGACATCTGAGCTTGCCTGCGGAGGCAACCGCGCTGCGAGGACAAATGCT 415

QY 364 CAGGGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGGAGTTGTACCGG 423

Db 416 TTGGACATGTTCCAGAAAGATCAGAGAGAGGAACTGAAAGACAGACAGACATCTACTGC 475

QY 424 TGGGAAACTGGAAGACGGTTAAATCTGAATATGCTGGGGCCAAACTATATGACCTC 483

Db 476 TGGGCCACTGGAAGAGGGTTACCCCTGACCATCGCTGCAGACGTAAGGNTGATCTA 535

QY 484 CTTGTGGATGAGCAATTTCTGGAAGACAAAGAGATTTGACTTTTGTAGGTTTCGTGGCCAAAG 543

Db 536 CTTCCAAATATGAGATTTCATGAGGAGAGAGGCTGGACTTTTGAATGGACACTGAAGGCA 595

QY 544 GGGCTGGCGACTCTGCTATCAAGACTCTTAATGTTCTGACTTGTCTGGAGGATCTA 603

Db 596 GGGCTCTGAGATGGCCCTCAAACTGTTTACACCTCTGAGCTCTCGGAATGCTCTA 655

QY 604 GATGACTTCAACCGGATTTTCTGGTGTGGTTCAGAGCAAGCTGGCTGAGCGCGTGGGGAC 663

Db 656 GAAGACTTTGATCAGATCTTCTGGGCGCAGAGAGTGCCCTGGCTGAGAAGGTTGCGCAG 715

QY 664 TCCGGAAGAGATGCTTTATTTGGGTACCGATTTCTTAATGGCGCCAAACCCCGTGGTG 723

Db 716 TGCTGGCAGGATGATGATGTTGTTGAGCTACCGAGTTCCTCAATGTTGTCGAACCCCAAGCTG 775

QY 724 CTGAGGCGCTCTGCTTCACCTTCTGCTCGCTAGTGTTCCTCCAGGATGAGGAACTG 783

Db 776 TTGAGACGCTCGACCTCTCTGCCCCTCAGGCTAGTGTGCTGCTCGGGATGGAAGCTT 835

QY 784 CAGGCCACGCTGGAGAGGAGCTGGAGGGAGGACACTGTTTGGAAAGCTGACTTCTCCCTG 843

Db 836 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGGTTCCTGTTTGAAGCTGACTTCTATCCTT 895

QY 844 CTGAGTGGATCAAGGCCCAAGCTGCTCTCTGTAGCAGCAGCAGCAGCTGGCTGCCCTCTA 903

Db 896 CTGGATGAAATTCAGGCCCAAGCTGATCCGAGGAGAGAACTATCTGCTGCCCTCTC 955

QY 904 GTCATGCTGAAATTCAGCCTGATGGGAAACTCTTGGCCCATGCTCATCCAGCTCCAGCTG 963

Db 956 GTTATGCTGAGATGGAGCCCAATGGGAAGCTGAGAGCCCATGGTTCATCCAGATTGAGCT 1015

QY 964 CCCGACACAGGATCCCAACCACTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1023

Db 1016 CCCARCCCGCTCTCCAAACCCCAACTGTTCTCTGCTCTCAGACCCCTCTGCTGCTG 1075

QY 1024 CTTCTGGCCAAATGCTGGTGGGAGCTCTGACTTCCAGCTCCATGAGCTGAGCTCTCAT 1083

Db 1076 CTCCTGGCAAGTCTCTGGGTCGAAATTCAGATTTCCAACTGACGAGATCCAGTATCAC 1135

QY 1084 CTTCTGAGGGGACACTTGTGCTGAGGTCATTTGTTGGCCACCATGAGGTGCTGCTGCG 1143

Db 1136 TTGCTGAACACCACTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1195

QY 1144 TCGATACATCTTCTTCAAGCTTATAATTTCCCACTTGCATACACCTTGGAAATTAAC 1203

Db 1196 GBACTGCACCCCATCTTCAAGTTCCTGATCCCCCATATCCCGTACACCATGGAATCAAC 1255

QY 1204 GTCGGGGCAGACTGGGCTGCTCTGACATGGGAATTTTCGACAGATTAATGAGCACT 1263

Db 1256 ACCCGGGCCGAGCCAACTCATCTCAGATGGAGAAATTTTGTGAAGGCACTGAGCACA 1315

QY 1264 GTGGGGGAGGCGCTGCTCAAGCAAGCTGGAGCTTCTTAACTTACAGCTCC 1323

Db 1316 GGTGAGGGGGCCATGATACAGTTGCTCGTGGGGGGAGCTCAGCTGACCTACTGCTCC 1375

QY 1324 TTTCTGTCCTCTGATGACTTTGGCCGACCGGGGGTCTTGGGAGTGAAGTCTTCTTCTAT 1383

Db 1376 CTCTGCTCTCTGACGACTGCTGACCGGGGCTGCTGGGACTCCAGGCTGCTCTAT 1435

QY 1384 GCCCAAGATGCTGCGGCTCTGGGAATCATCTATCGTATGTTGGAAGGATCGTGAGT 1443

Db 1436 GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTTGGAGGGGATCGTCCAC 1495

QY 1444 CTCACATATAAGACAGAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGGA 1503

Db 1496 CTCCTTACBARAGGATGACATAGTGAAGGGGAGCCCTGAGCTGCAGGCTTGGTGTGG 1555

QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTAAG 1563

Db 1556 GAGATCAAGGAGTGGGCTGTGCCAGGCCAGGACCGAGGTTTCCCTGTCTCTTCCAG 1615

QY 1564 GCTCGGAGACAGGTTTGGCACTTTGTTCACCATGTGTATCTTCACTGACCGGGCCAAAC 1623

Db 1616 TCCAGAGTCAACTCTGCCATTTTCTCCCATGTGCGTCTTTCAGCTGACCTGCCAGCAT 1675

QY 1624 GCCTGTGCACTCTGGGCGAGCTGAGCTGTTGTTCTTGGGTGCTTAAATGCACTGCACTG 1683

Db 1676 GCGGCATCAACAGGGGCGAGCTGAGTGGTATGCTGGGTCCCTTAATGCTCCATGCGACA 1735

QY 1684 ATGGGCTGCCCGGCCCAACCAAG--GATGCAACGCTGGAGACAGTATGATGCGACA 1740

Db 1736 ATGGGATGCCCGGCCCAACCAAGGAGATGAGAGTGGCCACAGTATGATGGGTCA 1795

QY 1741 CTGCCCCAATCTCCACAGGCTTCTCTCAGATGTCATCATCTTGGCAGCTGGCAGAGC 1800

Db 1796 CTACCTGATGTCGGCAGGCTGTCTTCAATGGCCATCTCATGGCATTTGATGCTGCCGC 1855

Qy	1801	CAGCCCTTATGTGGCTGTGGGCCAGCATGAGGAGTATTTTTCGGGCCCTGAGCCT	1860
Db	1856	CAGCCACATGTGGCTCTGGGSCACCAAGAAAAATATTTCTCAGGCCCAAGCCC	1915
Qy	1861	AAGCTGTGCTGAAGATTTTCAGGGAGAGCTGGCTGCCCTGGATGAAGAAATTGAGATC	1920
Db	1916	AAAGCTGTGCTAAACCAATTTCCGAACAGATTTTGGAAAAAGCTRGAAGAAGAGATTACAGCC	1975
Qy	1921	CGGAATGCAAGCTGGACATGCCCTACGAGTACTCGCGGCCAGCTGGTGGGAAAAACAGT	1980
Db	1976	CGGAATGAGCAACTTGACTGSCCTATGATATCTGAAAGCCCACTGATGATGAGAACAGT	2035
Qy	1981	GTGCCCATCTAAGC	1994
Db	2016	GTCAACATCTGAGC	2049

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RESULT 8
US-10-741-600-672
; Sequence 672, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-672

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Query Match	38.1%	Score 1016.4	DB 21	Length 2867
Best Local Similarity	69.4%	Pred. No. 2.4e-293		
Matches 1384	Conservative 8	Mismatches 599	Indels 3	Gaps 1
Qy	4	ATGGGTCTCTACCGCATCCGGTGTCCACTGGGGCCTCGCTCTATGTCGGGTTCACAAAC	63	
Db	555	ATGGGCGCTACCGCATCCGGTGTGGCCACCGGGCCTGGCTCTCTCCGGTGTGTACAA	614	
Qy	64	CAGGTGCAGCTGTGGCTGGTCGCGCAGCAGGGGAGCGCGCTCGCGGAAGCGACTGTGG	123	
Db	615	CGCGTCAGCTTTGGCTTGGTCGGGACGGCGGGGAGCGGAGCTGGAGCTGCAGCTCGG	674	
Qy	124	CCGCGACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGCGCGCTG	183	
Db	675	CCSGCGGGGCGAGGAGGAGGAGTTTGATCATGACGTTGCAGAGGACTTGGGGCTCCTG	734	
Qy	184	CTGTTTGTGAACCTGGCGAAACGGCACCTCTCTAAGGACAGCGCTGGTCTTGCACTGG	243	
Db	735	CAGTTCTGTAGGCTGCGCAAGCACCACTGGCTGTGTGGACGACGCGTGGTCTTCGACCGC	794	
Qy	244	ATCTCTGTCAGGGCCCCGGGACGGGACGAGGTCAAGTTCCTTGTACCGTGGGTG	303	
Db	795	ATCACGTTGAGGGCCCTGGGAGCTGCGCGGAGTGGCTTCCCGTCTTACCGTGGGTG	854	
Qy	304	GAGGGCAACGCGTCTTGAGCTTCCTTGAGGACCGCGCGCACTGTGGGGCGAGACCT	363	
Db	855	CAGGGCAGGACATCTTGAGCTTCCCGAGGACACCGCCCTGCGCAGAGACAATGCT	914	
Qy	364	CAGGGCCTGTTTCCAGAAACACCGGGAGAAGAGCTGGAAGAGAGAAGAAAGTTGTACCGG	423	
Db	915	TTGGACATGTTCCAGAGACATCGAGAGAGGAACTGAAAGACACAGCAGACATCTACTGC	974	
Qy	424	TGGGGAACTGGAAGGACGGGTTTAATCTGTAATATGGCTGGGGCCAAACTATATGACCTC	483	
Db	975	TGGGCCACCTGGAAGGAAGGGTTACCCCTGACCATCGCTGAGACCCGTGAAGGATGATCTA	1034	

Qy	484	CTGTGATGAGCGATTTCTTGGGAAGACAAGAGAGTTGACTTTTGAAGGTTTTCGCTGGCCCAAG	543
Db	1035	CTTCCAATATGAGATTCCATGAGGAGAAGAGCGCTGGACTTTGAATGGACACTGAAGGCA	1094
Qy	544	GGGCTGCCACACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGATCTA	603
Db	1095	GGGCTCTGGAGATGGCCCTCAACRTGTTTACCCCTCTGAGCTCTGGAACTGGCCTA	1154
Qy	604	GATGACTTTCAACCGGATTTTCTGGTGTGGTCCAGAGCAAGCTGGCTGAGCCGCTGCGGGAC	663
Db	1155	GAAGACTTTGATCAGATCTTCTGGGCCAGAAAGTGCCTGGCTGAGAAGTTTGCAG	1214
Qy	664	TCCTGGAAGAAAGATGCTTTATTTGGGTACCAAGTTCTTAAATGGCGCAACCCCTGGTG	723
Db	1215	TGCTGGCAGGATGATGATGTTGTTTTCAGCTACCAAGTTCTCTCAATGGTGCACACCCCACTG	1274
Qy	724	CTGAGGGCTCTGCTCAGCTTCTCTGCTCGCTTAGTGTTCCTCCAGCGCATGGAGGAACTG	783
Db	1275	TTGAGAGCTCGACCTCTCTGCCCTCCAGGCTAGTGTGCTCCCTGCGGATGGGAAGAGCTT	1334
Qy	784	CAGGCCAGCTGGAGAAGAGCTGGAGGAGGACACACTGTTTCGAAGCTGACTTCTCCCTG	843
Db	1335	CRGGCTCMACTGAGAAAGAACTTCAGATGGTTCCTGTTTGAAGCTGACTTATCCTTT	1394
Qy	844	CTGATGGGATCAAGGCCAAAGCTCATTTCTGTAGCCAGCAGCAGCACTGGCTGCCCTCTA	903
Db	1395	CTGGATGGAATTCAGCCAAAGTGATCCGAGGAGAGAAGCAATACCTGGCTGCCCCCTC	1454
Qy	904	GTCATGCTGAATTTGAGCCCTGATGGAAACTCTTGCCCATGCTATCCAGCTCCAGCTG	963
Db	1455	GTTATGCTGAAGATGGAGCCCAATGGGAAGCTCGAGCCCATGGTCTATCCAGATTCAGCCT	1514
Qy	964	CCCGCACAGATCCCAACCACTCCCTTTTCTTGCTACGGATCCCAATGGCCTCG	1023
Db	1515	CCCAACCCAGCTCTCCAAACCCAACTGTTCTTGCCCTCAGACCCCACTTGGCTCG	1574
Qy	1024	CTTCTGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCATGAGCTGCACTCTCAT	1083
Db	1575	CTCTGSCAAGCTCTGGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC	1634
Qy	1084	CTTCTGAGGGGAACATTGATGGCTGAGGTCAATTTGTTGTGGCCACCATGAGGTGGCTGCCG	1143
Db	1635	TTGCTGAACACKACACCTGGTGGGTGAGGTATCGCTGTCCGCCCACTGCGGTGCCCTCCA	1694
Qy	1144	TCGATACATCCTATCTTCAAGCTTTAATTTCCCACTCGGATACACCTTGGAAATTAAC	1203
Db	1695	GGACTGCACCCCATCTTCAAGTTCCTGATCCCCCAATATCCGCTACACCATGGAAATCAAC	1754
Qy	1204	GTCGGGCCAGGACTGGGCTGGTCTCTGACATGGGAAATTTTCGACAGATAATGAGCACT	1263
Db	1755	ACCGGGCCCGGACCCCAACTCATCTCAGATGGAGGAATTTTGTAAAGCAGTGAGCACA	1814
Qy	1264	GGTGGGGAGGCAAGTGCAGTCTCTCAAGCAAGCTGGAGCCCTTCTTAACCTACAGTCC	1323
Db	1815	GGTGGAGGGGCCATGTACAGTTGCTCCGTGCGGCGGCGAGCTCAGCTGACCTACTGTCTCC	1874
Qy	1324	TTCTGTCCCTCTGATGACTTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCTCTCTAT	1383
Db	1875	CTCTGTCTCTCTGACGACCTTGGCTGACCGGGGGCTCTCTGGGACTCCAGGTGCTCTCTAT	1934
Qy	1384	GCCCAAGATGCGTTCGGCTCTGGGAAATCATCTATCGGTATGTGGAAAGAAATCGTAGT	1443
Db	1935	GCCCATGATGCTTTACGGCTCTGGGATCATTTGCCAGGTATGTGGAGGGATCGTCCAC	1994
Qy	1444	CTCCATATTAAGACAGAGTGGCTGTGGAAGAAGACCCAGAGCTGCAGACCTGGTGTGGA	1503
Db	1995	CTCTTCTACCARAGGGATGATAGTAGTGAAGGGGAGCCCTGAGCTGCAAGGCTGGTGTGCG	2054
Qy	1504	GAGATCACTGAATCGGCTGTCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTACAG	1563
Db	2055	GAGATCAAGAGGTGGGGCTGTGCCAGGGCCAGGACCGAGGTTTCCCTGTCTCTCTCCAG	2114
Qy	1564	GCTCGGAGCAGGTTTGGCACTTTGTTCACCATGTGTATCTTTCACCTCTGCACCGGCAACAC	1623


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QY 1384 GCCAAGATCGCTGCGCTCTGGGAAATCATCTATCGGTATGTGGAAAGAAATCGTAGT 1443
Db 1436 GCCCATGATGCTTTACGGCTCTGGGAGATCATTTCCAGGATATGTGGAGGGATCGTCCAC 1495
QY 1444 CTCACATATAGACAGAGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGTGTGCGA 1503
Db 1496 CTCCTTACCARAGGATGACATAGTGAAGGGGACCTGTAGCTGCAGGCTGTGTGTCG 1555
QY 1504 GAGATCACTGAATCGGCTGCAAGGGCCCGAGGACCGAGGCTTCTGTCTCTTTACAG 1563
Db 1556 GAGATCAGGAGGTGGGCTGTGCCAGGCCCGAGGCTTCCCTGTCTCTCTCCAG 1615
QY 1564 GCTCGGACCAAGGTTGTCATTTGTACCAATGTATCTTTCACTGCACCGGCCCAACAC 1623
Db 1616 TCCAGAGTCAACTCTGCCATTTCTCACCATGTGCGTCTTCAGTGCACCTGCCAGCAT 1675
QY 1624 GCCTGTGCACTTGGGCGAGCTGAGCTGTGACTCTTGGGTGCTTAATGCACTTGCACG 1683
Db 1676 GCGGCCATCAACGAGGCGAGCTGACTGTGTATGCTTGGGTCCCTTAATGTCTCCATGCA 1735
QY 1684 ATGCGGCTGCCGCCCAACACCAAG--GATGCAACGCTGGAGACAGTGTATGCGGACA 1740
Db 1736 ATGCGGATGCCGCCCAACACCAAGAAAGATGTGACGATGGCCACAGTGTATGGGTCA 1795
QY 1741 CTGCCCAACTTCCACCAAGCTTCTTCCAGATGTCATCATTTGCGAGCTGGGACAGCGC 1800
Db 1796 CTACCTGATGTCGGGACGCTGTCTTCAATGGCCATCTCATGGCATYTGAGTGCCTGC 1855
QY 1801 -CAGCCGTTNTGGTGTGGGCGCAGCATGAGGAGTATTTTCGGGCGCTGAGCCT 1860
Db 1856 CAGCAGACATGGTGGCTCTGGGCGACCAAGAAATAATTTCTCAGGCCCGCCAGGCC 1915
QY 1861 AAGCTGTGCTGAAGAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAAATGAGATC 1920
Db 1916 AAAGCTGTGCTTAACCAATTTGGAACAGATTTGGAAGCTTGAAGAGATTTACAGCC 1975
QY 1921 CGGAATGCAAGCTGGACATGCCCTACGAGTACCTTCGCGGCCCGAGCGTGTGGAAACAGT 1980
Db 1976 CGGAATGAGCACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 2035
QY 1981 GTGGCCATCTAAGC 1994
Db 2036 GTCCACCATCTGAGC 2049

RESULT 10
US-10-741-601-233
; Sequence 233, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS; METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-233

Query Match 38.0%; Score 1015.2; DB 19; Length 2867;
Best Local Similarity 69.4%; Pred. No. 5.6e-293;
Matches 1384; Conservative 7; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGGTCTCTACCGCATCGCGTGTCCACTGGGGGCTCGCTCTATGCGCGTTCCACACAC 63
Db 555 ATGGGCGCGTACCGCATCGCGTGTCCACCGGGGCTCGCTCTTCCCGGGTGTACACAC 614
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QY 64 CAGGTGACGTGTGGCTGTGGTCCAGCACGGGGAGCGGGCTCGGGAGAGCACTGTGG 123
Db 615 CCGTTCAGCTTTGGCTGTGGTCCGGACCGCGGGGAGCGGAGCTGGAGCTGCAGCTCGG 674
QY 124 CCGCACGGGGCAAGAGACAGACAACTCAAGGTGGAAGTACCGAGTATCTGGGGCCGCTG 183
Db 675 CCGGCGGGGCGAGGAGGAGGAGTTTGATCATGACCTTGCAGAGGACTTTGGGGCTCCTG 734
QY 184 CTGTTTGTGAAACTGCGCAACCGGCACTCTTAAAGGACGACGCTGTGTTCTGCAACTGG 243
Db 735 CAGTTCTGAGGCTGCGCAACGACCACTGGCTGTGTGACGACGCGTGTCTGCGACCGC 794
QY 244 ATCTCTGTGAGGGCCCGGAGCGGGAGCGAGTCAAGTTCCTTCTTACCGTGGGTG 303
Db 795 ATCAGGTGAGGGCCCTGGAGCTCGCGAGGTGGCTTCCCGTGTACCGTGGGTG 854
QY 304 GAGGGCAACGGCTGCTGAGCTGCTGAAAGGACACCGGCGGCACTGTGGGGGAGGACCT 363
Db 855 CAGGGCGAGACATCTTGAAGCTTGGCGGGGACCGCGGCTGCCAGGAGACATGCT 914
QY 364 CAGGGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAGGAGTGTACCGG 423
Db 915 TTGACATGTTTCCAGAAAGCATCGAGAGAAAGAACTGAAAGACAGACAGCAGATCTACTGC 974
QY 424 TGGGAACTGGAAGAGCGGTTAACTTGAATATGCTGGGCGCAAACTATATGACCTC 483
Db 975 TGGGCCACCTGGAAAGGAGGTTACCCCTGACCATGCTGAGACCGTGAAGAGTATCTA 1034
QY 484 CTTGTGATGAGCGATTTCTGGAAGACAGAGAGTGTGACTTTGAGGTTTCCTCTGCCCAAG 543
Db 1035 CTTCCAATATGATTTCCATGAGGAGAGAGCTGTGACTTTGATGGAACATGAGGCA 1094
QY 544 GGGCTGCGGACCTCGCTATCAAAGACTCTCTAAATGTTCGACTTGTGGAAGATCTA 603
Db 1095 GGGCTCTGGAGATGGCCCTCAAACTGTGTTACACCTCTCTGAGCTCTCTGGAATGCTCTA 1154
QY 604 GATGACTTCAACCGGATTTCTGTGTGTGAGAGCAAGCTGGCTGAGCGGTGGGAC 663
Db 1155 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCTGGGTGGAAGGTTTCGCCAG 1214
QY 664 TCTTGAAGGAGAGTGTCTTATTTGGGTACCACTTCTTAATGGCGCAACCCCGTGGT 723
Db 1215 TGCTGGCAGGATGATGATGTTTTCAGCTACAGTTCTCAATGTGTCACACCCATGCTG 1274
QY 724 CTGAGGCGCTCTGCTCACCTTCTGCTGCGCTAGTGTTCCTCCAGGATGAGGAACTG 783
Db 1275 TTGAGACGCTCGACCTCTCTGCGCTCAGGCTAGTGTGCTCGCTCRGGATGGAAGCTT 1334
QY 784 CAGGCCAGCTGGAGAGAGAGCTGGAGGAGGACACATGTTGGAAGCTGACTTCTCCCTG 843
Db 1335 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGGTTTCCCTGTTTGAAGCTGACTTTCATCTT 1394
QY 844 CTGATGGGATCAAGGCCCAAGCTCATTTCTGTAGCAGCAGCAGCCTGGCTGCCCTCTA 903
Db 1395 CTGATGGAATTCAGCCCAAGCTGATCCGAGGAGAGAGCAATACCTGGCTGCCCTCTC 1454
QY 904 GTCATGCTGAAATTCAGCCTGTATGGGAAACTCTTGGCCATGTGTCATCAGCTCCAGCTG 963
Db 1455 GTTATGCTGAAGTGGAGCCCAATGGGAGCTGCGAGCCCATGGTTCATCCAGATTCAGCT 1514
QY 964 CCCGCAAGATCCCAACACCTCCCTTTTCTTGTGCTAGGATCCCGCAATGGCTGG 1023
Db 1515 CCCARCCCGAGCTCTCCAAACCCCAACACTGTTCCTGCTCAGACCCCGCCACTTGGCTGG 1574
QY 1024 CTTCTGCGCAATGCTGGTGGCAGCTCTGACTTCCAGCTTCCAGCTCAGCTCTCAT 1083
Db 1575 CTCCTGGCAAGTCTCGGTCCGAAATTCAGATTTCCAACTGACGAGATCCAGTATCAC 1634
QY 1084 CTTCTGAGGGGACACTTGTATGGCTGAGGTCAATTTGTGGCCACCATGAGTGTGCTGCCG 1143
Db 1635 TTGCTGACACACACTTGGTGGCTGAGGTCACTCGTGTGCCACCATGCGGTGCTGCCA 1694
QY 1144 TCGATACATCTATCTTCAAGCTTATAATTTCCCACTGTGAGTACACCCCTGGAATTAAC 1203
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Db      1695  GGAAGTCAACCCATCTTCAAGTTCTCTGATCCCCCATATCCGCTACACCATGGAATCAAC 1754
QY      1204  GTCCGGCCAGAGCTGGCTGGTCTCTGACATCGGAATTTTCACAGATATGAGCACT 1263
Db      1755  ACCCGGCCCGGACCCCACTCATCTCAGATGAGGAAATTTTGAAGGCAATGAGACA 1814
QY      1264  GGTGGGGGAGGCCACATCGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGCTCC 1323
Db      1815  GGTGGAGGGGCCATGTACAGTTGCTCCGTGGGGCGGACGCTCAGCTGACCTACTGCTCC 1874
QY      1324  TTCTGTCCCTCGATGACTTGGCCGACCGGGGCTCTCGGAGTGAAAGTCTTCTTCTAT 1383
Db      1875  CTCTGTCTCTGACGACCTGGCTGACCGGGGCTCTCGGAGCTCCAGGTCCTCTCTAT 1934
QY      1384  GCCCAGATGCGCTGGGCTCTGGGAATCATCTATCGGTATGTGGAAGGATCGTGAGT 1443
Db      1935  GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGATCGTCCAC 1994
QY      1444  CTCACCTATAAGACAGACGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGCA 1503
Db      1995  CTCTTCTACARAGGATGACATAGTAGAGGGGACCTGAGCTGCAGGCTGGTGTGCG 2054
QY      1504  GAGATCACTGAATCGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTACAG 1563
Db      2055  GAGATCAGGAGGTGGGGCTGTGCCAGGCCCAGGACCGAGGTTTCCCTGTCTCTTCCAG 2114
QY      1564  GCTCGGGACGAGTTTGGCACTTTGTCCACTGTGTATCTTCCCTGACCGCCGCAACAC 1623
Db      2115  TCCAGAGTCAACTCTGGCAATTTCTTCAACATGTGGCTTTCACGTGCACTGCCAGCAT 2174
QY      1624  GCCTCTGTGCACCTGGGGCAGCTGGAGTGTACTCTTGGGTGCTTAATGCACCTGCACG 1683
Db      2175  GCGGCCATCAACAGGGCCAGCTGGATGCTGGTCCCTGATGCTCCATGCTCCATGCACA 2234
QY      1684  ATGCGGCTGCCCCGCCAACCAACCAAG---GATGCAACGCTGGAGACAGTATGGCGACA 1740
Db      2235  ATCGGATGCCCCCACCACCAACCAAGGAAGATGTGACGATGGCCACAGTATGGGGTCA 2294
QY      1741  CTGCCCAACTCCACAGGCTTCTCCAGATGTCCATCACTTGGCAGCTGGCGAGCGC 1800
Db      2295  CTACCTGATGTGCGGAGCGCTGTCTTCAATGGCCATCTCATGGCATTTGATGCGCGC 2354
QY      1801  CAGCCGTTATGTGTGCTGTGGGCCAGCATGAGGAGGATTTTTCGGGGCCCTGAGCCT 1860
Db      2355  CAGCCAGACATGTGTCTCTGGGCCACCAAGAAATATTTCTCAGGCCCCAGGCC 2414
QY      1861  AAGGCTGTCTGAAGAAGTTTCAGGGAGGAGCTGGCTGCCCTGGATGAAGAAATTTGAGATC 1920
Db      2415  AAAGCTGTGCTAAACCAATTCGAACAGATTTGGAAGAGCTGMAAAGAGATTACAGCC 2474
QY      1921  CGGAATGCAAGCTGACATGCCCTACGAGTACCTCGGCCCCAGCGTGTGGAACAGT 1980
Db      2475  CGGAATGACCACTTGACTGGCCCTATGAATATCTGAAGCCAGCTGYATAGAACAGT 2534
QY      1981  GTGGCCATCTAAGC 1994
Db      2535  GTCACCATCTGACC 2548
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RESULT 11

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US-10-170-097-652
; Sequence 652, Application US/10170097
; Publication No. US2003028582A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
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; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 652
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5' UTR
; LOCATION: 1..39
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..2031
; FEATURE:
; NAME/KEY: 3' UTR
; LOCATION: 2032..2343
; FEATURE:
; NAME/KEY: allele
; LOCATION: 366
; OTHER INFORMATION: 10-343-231 : deletion of C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 605
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 712
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 766
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 804
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 821
; OTHER INFORMATION: 10-347-220 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1004
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1049
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1123
; OTHER INFORMATION: 10-349-216 : deletion of CTG
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1131
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1491
; OTHER INFORMATION: 10-507-170 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1742
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OTHER INFORMATION: 10-340-112 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1760
OTHER INFORMATION: 10-340-130 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 1941
OTHER INFORMATION: 10-341-116 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 2144
OTHER INFORMATION: 10-341-319 : polymorphic base C or T
US-10-170-097-652

Query Match 37.9%; Score 1013.6; DB 17; Length 2343;

Best Local Similarity 69.2%; Pred. No. 1.5e-292;
Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGCTCTTACCGCATCCGGGTGTCCTAGTGGGCTCGCTCTATGCCGTTCCAAAC 63
DB 40 ATGGCCCGCTACCGCATCCGGGTGTCCTAGTGGGCTCGCTCTATGCCGTTCCAAAC 99
QY 64 CAGGTGCAGCTGTGGCTGCTCGGCCAGCACGCGGAGGCGGCTCGGGAAGCAGCTGTGG 123
DB 100 CCGTGCAGCTTTGGCTGCTCGGACGCGCGGAGGCGGAGCTGAGCTGAGCTGCGG 159
QY 124 CCCGACCGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCCGCTG 183
DB 160 CCGCGCGGGCGAGGAGGAGTGTGATCATGAGTTGCAGAGACTTGGGGCTCGT 219
QY 184 CTGTTGTGAAGTCTGGCAAGCGGACCTCTTAAGGACGAGCGCTGGTTCTGCAACTGG 243
DB 220 CAGTTCGTGAGCTCGCAAGCACCACCTGGCTGTGTGAGCAGCGCTGTCTGCGACCGC 279
QY 244 ATCTGTGCGGGCCCGGAGCGGGACGAGGTCAAGTTCCTTTTACCGTGGGTG 303
DB 280 ATCAGGTGCGAGGCGCTTGGAGCCTGCGGAGGTGGCTTCCCGTGTACCGCTGGGTG 339
QY 304 GAGGCAACCGGCTCTGAGCCTGCTGAAGGACCGGCGGACCTGTGGGGAGGACCT 363
DB 340 CAGGCGAGGACATCTGAGCCTGCGGAGGACCGCGCGCTCCAGGAGACATGCT 399
QY 364 CAGGCGCTGTTCCGAAGAACCGGGAAGAGCTGGAAGAGAGAGAAAGTTGTACCGG 423
DB 400 TTGACATGTTCCAGAGCTCGAGAGAGGAACTGAAGAGACAGACAGCAGATCTACTGC 459
QY 424 TGGGAACTGGAAGCGGTTAATCTGAATATGGCTGGGCGCAAACTATAGACCTC 483
DB 460 TGGGCCACTGGAAGAAAGGTTTACCCCTGACCCTGCTGAGACCGTAAGGATGATCTA 519
QY 484 CTTGTGATGAGCGATTTCTGGAAGACAGAGAGTTGACTTTGAGTTTCGCTGGCCAA 543
DB 520 CCTCCAAATATGAGATTCATGAGGAGAGAGGCTGGACTTTGATGACACTGAAGCA 579
QY 544 GGGCTGGCGGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTGTGGAAGATCTA 603
DB 580 GGGGCTCTGGAGATGGCCCTCAAAACRTGTGTTTACACCTCTCTGAGCTCTGGAATG 639
QY 604 GATGACTTCAACCGGATTTCTGGTGTGCTGAGACAGCTGGCTGAGCGGTGCGGAC 663
DB 640 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGCCTTGGCTGGAAGGTTTCGCC 699
QY 664 TCCTGGAAGGAGATGCCCTTATTTGGGTACCAAGTTTCTTAATGGGCCAAACCCCGTGGT 723
DB 700 TGCTGGCAGGATATGAGTTGTTGAGCTACCAAGTTCTCAATGGTGCCAAACCCATGCTG 759
QY 724 CTGAGCGCTCTGCTCACTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 783
DB 760 TTGAGAGCTCGACCTCTCTGCGCTCCAGGCTAGTGTGCTGCTGCTGCTGCTGCTGCT 819
QY 784 CAGGCCAGCTGGAAGGAGCTGGAGGAGGACACTGTTGGAAGCTGACTTCTCCCTG 843

DB 820 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGGTTCCTGTTTGAAGCTGACTTTCATCCTT 879
QY 844 CTGATGGGATCAAGGCCAACGTCATTTCTGTAGCAGACAGACCTGGCTGCCCTCTA 903
DB 880 CTGATGGAATTCAGGCCAACGTCATTCGAGAGAGAAAGCAATACCTGGCTGCCCTCTC 939
QY 904 GTCATGTGAATTCAGCGCTGATGGGAAACTCTTGGCCATGGTTCATCCAGCTCCAGCTG 963
DB 940 GTTATGCTGAAGATGGAGCCCAATGGGAAGCTGCAGCCCATGGTTCATCCAGATTGAGCT 999
QY 964 CCCGACAGGATCCCAACCACTTCCCTTTTTCCTTTCCTAGGATCCCAATGAGCTGG 1023
DB 1000 CCCARCCCACTCTCCAAACCCCAACTGTTCTGCTCCCTCAGACCCCSACTTGGCTGG 1059
QY 1024 CTTCTGGCCAAATGCTGGTGGCAGCTCTGACTTCCAGCTCCATGAGCTGAGCTGCTCAT 1083
DB 1060 CTCCTGGCAAGTCTCGGTCGGAATTCAGATTTCCAACTGCAGAGATCCAGTATCAC 1119
QY 1084 CTTCTGAGGGACACTTGTAGGCTGAGGTCAATGTTGGGCCACCATGAGGTGCTGCGG 1143
DB 1120 TTGCTGAACACKCACTGGTGGCTGAGGTCAATGCTGTGCGCACCATGGGTGCTCCCA 1179
QY 1144 TCGATACATCTTCTTCAAGCTTATAATTCCTCCCACTGCGATACACCTTGGAAATTAAC 1203
DB 1180 GGACTGCAACCCATCTTCAAGTTCCTGATCCCCCATATCCGCTACACCATGGAATCAAC 1239
QY 1204 GTCCGGGCGAGGATGGGCTGCTCTGACATGGGAATTTTCGACAGATTAATGAGCT 1263
DB 1240 ACCCGGCGCGGACCCAACTCATCTCAGATGAGGAATTTTGTGAAGCAGTGAAGCACA 1299
QY 1264 GGTGGGGAGGCGCAGCTGCAGCTCTCAAGCAAGCTGGAGCTTCTTAACCTACAGCTCC 1323
DB 1300 GGTGGAGGGGCGCATGTACAGTTGCTCGTCCGGCGGAGCTCAGCTGACCTACTGCTCC 1359
QY 1324 TTCTGTCCTCCCTGATGACTTGGCCGACCGGGGGCTCTCGGAGTGAAGTCTTCTTCTAT 1383
DB 1360 CTCTGCTCTCTGACAGCTGGCTGACCGGGGCTCTGAGGACTCCAGGCTGCTCTAT 1419
QY 1384 GCCAAGATGCGCTGCGGCTCTGGGAATCATCTATCGGTATGTGGAAGGAATCGTAGT 1443
DB 1420 GCCCATGATGCTTTTACGGCTCTGGGAGATCATTCGCCAGGTATGTGGAGGGATCGTCCAC 1479
QY 1444 CTCACCTATAGACAGAGTGGCTGTGAAGACACACCCAGAGCTGCAGACCTGCTGTGCA 1503
DB 1480 CTCTTCTACCARAGGAGTGAATAGTGAAGGGGACCTCTGAGCTGCAGGCTGCTGCTGG 1539
QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGCGCCAGGACCGAGGCTTCTGCTCTTTACAG 1563
DB 1540 GAGATCAGGAGGTGGGCTGTGCCAGGCCCGAGACCGAGGTTTCCCTGCTCTCTCCAG 1599
QY 1564 GCTCGGACCAAGTTTGCACCTTTGTCAACATGTGTATCTTTCACTGCACCGGCCAACAC 1623
DB 1600 TCCAGAGTCAACTCTGCCATTTCTCACCATGTGGCTCTTCACTGCACCTGCCAGAT 1659
QY 1624 GCCTGTGACCTGGGCGAGCTGGACTGTGACTCTTTGGGTGCTCTTAAGCACTGACG 1683
DB 1660 GCGCCATCAACAGGGGCGAGCTGGACTGTGTATGCTGGGTCCCTTAATGCTCAATGCA 1719
QY 1684 ATGGGCTGCCCGCCGCAACCCACCAAG--GATCAACGCTGGAGACAGTATGCGGACA 1740
DB 1720 ATGGGATGCCCGCCACCCACCCACCAAGAGATGTGAGAGGCGCACAGTATGGGTCA 1779
QY 1741 CTGCCCCAACTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGAGAGC 1800
DB 1780 CTACTGATGTCCGGCAGGCTGTCTTCAAATGSCCATCTCATGGCATCTGAGTGCAGC 1839
QY 1801 CAGCCCCGTTATGTTGGCTGTGGGCGACGATGAGGAGGATTTTTCGGGCGCTGAGCT 1860
DB 1840 CAGCCAGACATGTTGCTCTGGGCGACCAACAAAGAAAAATATTTCTCAGGCGCCCAAGCC 1899
QY 1861 AAGGCTGTGTGAAGATTTGAGGAGGAGCTGCTGCTCCCTGGATTAAGGAATTTGAGATC 1920
DB 1900 AAGCTGTGCTAAACCAATTTCCGAACAGATTTTGGAAAGCTRGAAAGAGATTTACAGCC 1959

	1921	1960	1981	2020	1980
Qy	CGGAATCGAAAGCTGGACATGCCCTTACGAGTACTCGCGGCCACAGCTGGTGGAAAACAGT		GTGCCCATCTAAGC		
Db		CGGAATGAGACAACCTGTACTGGCCCTATGGAATATCTGAAGCCCACTGCATAGAGAACAGT		GTCAACCATCTGAGC	

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RESULT 12
US-10-926--684-652
; Sequence 652, Application US/10926684
; Publication No. US20050014190A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLERIC MARKERS DERIVED FROM GENOMIC REGIONS
; TITLE OF INVENTION: CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/926,684
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/10/170,097
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 652
; LENGTH: 2343

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:	NAME/KEY:	allele
:	LOCATION:	821
:	OTHER INFORMATION:	10-347-220 : polymorphic base A or G
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1004
:	OTHER INFORMATION:	10-349-97 : polymorphic base A or G
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1049
:	OTHER INFORMATION:	10-349-142 : polymorphic base G or C
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1123
:	OTHER INFORMATION:	10-349-216 : deletion of CTG
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1131
:	OTHER INFORMATION:	10-349-224 : polymorphic base G or T
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1491
:	OTHER INFORMATION:	10-507-170 : polymorphic base A or G
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1742
:	OTHER INFORMATION:	10-340-112 : polymorphic base A or C
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1760
:	OTHER INFORMATION:	10-340-130 : polymorphic base A or T
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	1941
:	OTHER INFORMATION:	10-341-116 : polymorphic base A or G
:	FEATURE:	
:	NAME/KEY:	allele
:	LOCATION:	2144
:	OTHER INFORMATION:	10-341-319 : polymorphic base C or T
:	US-10-926-684-652	

Query Match	37.98;	Score 1013.6;	DB 21;	Length 2343;
Best Local Similarity	69.2;	Pred. No. 1.5e-232;		
Matches 1380;	Conservative 11;	Mismatches 600;	Indels 3;	Gaps 1;
Qy	4	ATGGGTCTCTACCGCATCCGCGTGCACATGGGGCCTCGCTCTATGCGGGTTCCAAACAC	63	
Db	40	ATGGCGCGCTACCGCATCCGCGTGGCCACCGGGCCTTGGCTCTCTCGGGTCGTACAC	99	
Qy	64	CAGGTGCAGCTGTGGCTGTGGCGCACACGGGGAGCGCGCTCGGGAAAGCGACTGTGG	123	
Db	100	CGCGTCAGCTTGGCTGTGGCGACGCGGGGAGCGGAGCTGGAGCTGCAGCTGCGG	159	
Qy	124	CCGCGACGGGGCAAGAGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCCGCTG	183	
Db	160	CCGCGCGGGCGAGGAGGAGGAGTTTGATCATGACGTTGCAGAGGAGCTTGGGGCTCTG	219	
Qy	184	CTGTTTGTGAACTGCGCAACGGCACTCTTTAAGGACGACGCTCGTTCTGCAACTGG	243	
Db	220	CAGTTCTGTAGGCTGCGCAAGCACACTGGCTGGTGGACGACGCTGGTCTTCGACCGC	279	
Qy	244	ATCTCTGTGAGGGCCCCGAGCGGGGACGAGGTCAAGTTCCCTTGTACCGCTGGGTG	303	
Db	280	ATCAGGTTGAGGGCCCTGGAGCTGCGCGGAGTGGCCCTCCCGTCTACCGCTGGGTG	339	
Qy	304	GAGGGCAACCGCGTCTGTAGCGCTGTGAAGGCAACCGGCCCGCACTGTGGGGCAGAACCC	363	
Db	340	CAGGGCAGGACATCTCTGAGCCTGCCCGAGGGCACCGCCCGCTGCCAGGAGACAA	399	
Qy	364	CAGGGCTGTTCAGAAACACCGGGAGAGAGAGCTGGAGAGAGAAAGGAAGTTGTACCGG	423	
Db	400	TTGGACATGTTCCAGAGACATCGAGAGAAAGGAATGAAAGACAGACAGCAGATCTAC	459	

[illegible]

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RESULT 14
US-10-681-818-12
; Sequence 12, Application US/10681818
; Publication No. US20040157240A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Scott
; APPLICANT: Tantisira, Kelan
; TITLE OF INVENTION: Diagnostic Assay and Related Products
; FILE REFERENCE: B0801.70290US00
; CURRENT APPLICATION NUMBER: US/10/681,818
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/416,969
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 374
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-818-12

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Query Match	19.2%	Score 514;	DB 19;	Length 584;
Best Local Similarity	99.6%;	Pred. No. 5.6e-143;		
Matches 514;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1812	GGTGGCTGTGGCCAGCATGAGGAGGAGTATTTTTTCGGGGCCCTCAGAGCTCAAGGCTGNGCT	1871	
Db	69	GGTGGCTGTGGCCAGCATGAGGAGGAGTATTTTTTCGGGGCCCTCAGAGCTCAAGGCTGTGCT	128	
Qy	1872	GAAGAAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATTAAGAGAAATTGAGATCCGGAATGCAAA	1931	
Db	129	GAAGAAAGTTTCAAGGAGGAGCTGGCTGCCCTGGATTAAGAGAAATTGAGATCCGGAATGCAAA	188	
Qy	1932	GCTGGA CATGCCCTTACGAGTACTCTGGGCCCCAGCGTGGTGAAACAAAGTGTGGCCATCTA	1991	
Db	189	GCTGGA CATGCCCTTACGAGTACTCTGGGCCCCAGCGTGGTGAAACAAAGTGTGGCCATCTA	248	
Qy	1992	AGCGTGCACACCTTTGGTTATTTTCAGCCCCCATCACCAAGCCACAAAGCTGACCCCTTC	2051	
Db	249	AGCGTGCACACCTTTGGTTATTTTCAGCCCCCATCACCAAGCCACAAAGCTGACCCCTTC	308	
Qy	2052	GTGCTTATAGCCCTCGCCCTCCCAAGTCCCACTCTTCCCATGTCCCAACCCCTCCCTAGAG	2111	
Db	309	GTGCTTATAGCCCTCGCCCTCCCAAGTCCCACTCTTCCCATGTCCCAACCCCTCCCTAGAG	368	
Qy	2112	GGGCACTTTTCATGGTCTCTGCAACCGAGTGAAACATATTTTACTCTTAGAGGCATCACTG	2171	
Db	369	GGGCACTTTTCATGGTCTCTGCAACCGAGTGAAACATATTTTACTCTTAGAGGCATCACTG	428	

[illegible]

Query Match	14.3%; Score 382.6; DB 16; Length 2420;
Best Local Similarity	52.5%; Pred. No. 3.5e-103;
Matches 1022; Conservative	0; Mismatches 884; Indels 39; Gaps 7;
Qy	126 CGCACGGGGCAAGGAGACAGAACTCAAAGGTGGAAGTACCGGAGTATCTGGGGCGCGTCT 185
Db	107 CGACGTGGCGCGGTGATTCATACGACGTGACTGTGGACGAGNACTGGCGGAGATCCA 166
Qy	186 GTTTGTGAACACTGGCGAAACGGCACCTCTCTTAAGGACGACGCCTGGTTCTTGCAACTGGAT 245
Db	167 GCTGGTCAGAAATCGAAGAGCGCAAGTACTGGCTGCAATGACGACTGGTACCTGAAGTACAT 226
Qy	246 CTCTGTCCAGGGCCCGGAGCCGGGGACGAGGTCAGGTTCCCTTGTTTACCGCTGGGTGGA 305
Db	227 CACGCTGAGACGCCCC---CACGGGACTACATCGAGTTCCTCTGTCTACCGCTGGATCAC 283
Qy	306 GGGCAACGGCGTCTGTAGCTGTGCTGAAGGCAACGGCCGCACGTGTGGGCGAGGACCTCTCA 365
Db	284 CGGCGATGTCGAGGTTGCTCTGAGGGATGACGCGCAAGTTGGCCCGAGATGACCAAA 343
Qy	366 GGGCTCTTCCAGAAACACCGGGAAGAGACTGGAGAGAGAAAGTTGTACCGGTG 425
Db	344 TCACATTCTCAAGCAACCCGACGTAAAGAACTTGGAAACACGGCAAAACAATATCGATG 403
Qy	426 GGGAAACTGGAAGGACGGGTTAAATTCTGAATATGGCTGGGGCCAAACTATATGACCTCCC 485
Db	404 GATGGAGTGGAAACCCCTGGCTTCCCTTTGAGCATCGATGCCAAATGCCACAAGGATTTTACC 463
Qy	486 TGTGGATGCGGATTTCTGGNACGACAGAGTTGACTTTTGAGGTTTTGCTGGCGCAAGGG 545
Db	464 CCGTGATATCCAGTTTGATAGTGAANAAGAGTGGACTTTTGTCTGAAATTACTCCAAAGC 523
Qy	546 GCTGGCCGACCTCGCTATCAAAGACT---CTCTAAATGTGTCTGACTGTCTGGAGGATCT 602

Db 524 GATGAGAACCTGTTCAATCAACCGGTTCTATGCACATGTTTCAGTCTCTCTTGGAAATGACTT 583
Qy 603 AGATGACTTCAACCGGATTTTCTGTGTGGTGCAGAGCAAGCTGGCTGAGCGCGTGCAGGGA 662
Db 584 GCGGACTTTGAGAAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGGTCATGAA 643
Qy 663 CTCCTGGAAGGAGATGCTTATTTGGGTACAGTTTCTTAATGGCGGCAACCCCGTGT 722
Db 644 TCACCTGGGAGGAGACCTGATGTTTGGCTACAGTTCTGTAATGGCTGCACCCCTGTGT 703
Qy 723 GCTGAGGCGCTCTGCTCACTTCTGCTCGCTAGTCTTCCCTCCAGGCATGGA----- 776
Db 704 GATCCGGGCTGCACAGAGCTGCCCGAGAAGCTCCGGTGAACCAAGAGATGGTAGATG 763
Qy 777 -----GGAACCTGCAGGCCAGCTGGAGAAGAGCTGGAGGAGGCACACTGTTTCGAAGC 830
Db 764 CAGCCTGGAGCGGACGCTCAGCTTGGAGCAGAGGTCCAGCAAGGAACATTTTCATGTT 823
Qy 831 TGACTTCTCCTGCTGGATGGATCAAGGCCAACTGCA-----TTCCTGTAGCCAGCAGCA 887
Db 824 GGACTTTGAGCTGCTGGATGGATCGATGCCAACAACAAACAGACCCCTGCACACTCCAGTT 883
Qy 888 CTTGGCTGCCCTCTAGTCATGCTGAATTCAGCCTGATGGGAACCTTTGGCCCATGTT 947
Db 884 CTTGGCCGCTCCCATCTGCTGTCTGTATAGAACCTGGCCCAAGATTTGCCCATTCG 943
Qy 948 CATCCAGCTCCAGCTGCCCGGCACAGGATCCCCACACTCCCTTTTCTTGGCTTACCGGA 1007
Db 944 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAACCTTATTTCTCCCTTCGGA 997
Qy 1008 TCCCCCAATGGCTGGCTTCTGGCCAAATGTGGGTGGCAGCTCTGACTTCCAGCTCCA 1067
Db 998 TGCAAAATACGACTGGCTTTTGGCCAAATCTGGGTGGCTTCCAGTGACTTCCACGTCCA 1057
Qy 1068 TGAGTGCAGTCTCATCTCTGAGGGGACACTTGATGCTGAGGTCAATTTGTTGGGCCAC 1127
Db 1058 CCAGACCAATCAACCACTTCTGCGAACACATCTGGTGTCTGAGGTTTGTGGCAITGCAAT 1117
Qy 1128 CATGAGTGCCTTCCGCTCGATACATCTTATCTTCAAGCTTATAATTCGCCACCTCGGATA 1187
Db 1118 GTACGCCAGCTGCTGCTGTGCACCCCATTTTCAAGCTGCTGGTGGCACACGTGAGATT 1177
Qy 1188 CACCTTGAAATTAAGCTCCGGGCCAGGACTGGGTCTGTCTGACATGGGAATTTTCGA 1247
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Qy 1248 CCAGATATGACACTGTTGGGGAGGCCACGTGAGCTGCTCAAGCAAGCTGGAGCCTT 1307
Db 1238 CAAGGCCAACGCCACAGGGGGCGGTGGGCACTGTCAGATGGTGCAGAGGGCCATGAAGGA 1297
Qy 1308 CTTAACTTACAGCTCTTCTGTCCCTGTATGACTTGGCCGACCGGGGCTCCTG----- 1362
Db 1298 CTTGACCTATGCTTCTGCTGTGCTTCCGAGGCCATCAAGGCCCGGGGCAATGGAGCAA 1357
Qy 1363 ----GGAGTGAAGTCTTCTTCTATGCCCAAGATCGCTCGGGCTCTCGGAAATCATCTA 1418
Db 1358 AGAAGACATCCCTACTACTTCTACCGGGAACGACGGGCTCCTGTGTGGGAAGCCATCAG 1417
Qy 1419 TCGGTATGTGAGAGAAATCGTGAGTCTCCACTATAAGACAGAGCTGGCTGTGGAAGACGA 1478
Db 1418 GACGTTCAAGCCGAGGTGGTAGACATCTACTACAGGGGCGACCAAGGGTGGTGGAGAGGA 1477
Qy 1479 CCCAGAGCTGCAGACCTGGTGTGAGAGATCACTGAATCGGGCTGCAAGGGGCCAGGA 1538
Db 1478 CCCGAGCTGCAGGACTTCTGTGAACGATGTCTACGTGTACGGCATCGGGGCCGCAAGTC 1537
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Db 1538 CTCAGGCTTCCCAAGTCCGTTCAAGAGCCGGGAGCAGCTGTCGGAGTACCTGACCGTGT 1597
Qy 1599 TATCTTCACTGCACCGGCGCAACACGCTCTGTGCACCTTGGCCGAGCTGGACTGTACTC 1658

Db 1598 GATCTTCAACCGCTCCGCCAGCAGCCGCGGTCAACTTTCGGCCAGTACGACTGGTGCTC 1657
Qy 1659 TTGGTGCCTTAATGCAACCTTGCAAGATGGGCTGCCCCCGCAACCAACCAAG----GATGC 1715
Db 1658 CTGATATCCCAATCGCCCCCAACCATGCGAGCCCGCCACCGACTGCCAAGGCGTGGT 1717
Qy 1716 AACCTCGAGACAGTGTATGGCGACACTGCCCAACTTCCACCAGGCTTCTCTCCAGATGTC 1775
Db 1718 GACCAATTGAGCAGATCTGTGGACACGCTGCCCGACCGCGGCCGCTCTGCTGGCATCTGGG 1777
Qy 1776 CATCACTTTGGCAGCTGGGCGAGACGCCAGCCCGTTATGTGTGCTGTGGGCCAGCATGAGGA 1835
Db 1778 TGCACTGTGGCGCTGAGCCAGTTTCCAGGAAACAGAGCTGTTCTTGGCATGTACCCAGA 1837
Qy 1836 GGAGTATTTTTCGGGCCCTGAGCCCTAAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTGGC 1895
Db 1838 AGAGCAATTTTATCGAAGAGCCCTGTGAAGGAAGCCATGGCCCGATTCCGCAAGAACTCGA 1897
Qy 1896 TGCCCTGGATAAGGAATTTGAGATCCGGAATGCAAGCTGGACATGCCCTACGAGTACCT 1955
Db 1898 GGCCATTTGTCAAGCTGATTGCTGAGCGCAACAGAGAAGCAGCTGCCATATTACTATT 1957
Qy 1956 GCGGCCAGCGTGTGGAATAACAGTGTGGCCATCTAAGCGTGGCCACCCCTTTGGTTATTT 2015
Db 1958 GTCCCCAGACCGGATTCGGAACAGTGTGGCATCTGAGCACATCTGAGCACACTGCCAGTCTCACTGTGG 2017
Qy 2016 CAGCCCCCATCACCCAGCCCAAG 2040
Db 2018 GAAGGCCAGCTGCCCCAGCCAGATG 2042

Search completed: July 19, 2005, 22:11:12
Job time : 1070.87 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:50:48 ; Search time 30.1353 Seconds
(without alignment)
1637.384 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLYRIRVSTGASLYAGSNN.....KLDMPYELRBSVVNSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3503.5	99.7	662	3	US-09-061-768A-25
2	3503.5	99.7	662	4	US-09-764-246-25
3	2280	64.9	663	4	US-09-641-638-653
4	2280	64.9	663	4	US-10-170-097-653
5	1298.5	37.0	674	4	US-09-949-016-5980
6	1298.5	37.0	689	4	US-09-949-016-11692
7	1203.5	34.2	679	4	US-09-949-016-8912
8	1202.5	34.2	676	3	US-09-061-768A-2
9	1202.5	34.2	676	4	US-09-764-246-2
10	1202.5	34.2	676	4	US-09-949-016-6027
11	1184	33.7	677	3	US-09-061-768A-4
12	1184	33.7	677	4	US-09-764-246-4
13	1153	32.8	711	4	US-09-547-435-2
14	1153	32.8	867	4	US-09-547-435-24
15	1124	32.0	701	3	US-09-087-727-2
16	1124	32.0	701	4	US-09-853-053-2
17	1124	32.0	701	4	US-09-949-016-6026
18	954.5	27.2	556	4	US-09-547-435-6
19	946.5	26.9	615	4	US-09-547-435-10
20	946.5	26.9	771	4	US-09-547-435-28
21	761.5	21.7	675	4	US-09-902-540-12713
22	748	21.3	460	4	US-09-547-435-12
23	704.5	20.0	489	4	US-09-547-435-4
24	704.5	20.0	645	4	US-09-547-435-26
25	580.5	16.5	291	4	US-09-547-435-14
26	548.5	15.6	582	3	US-09-413-814-83
27	506	14.4	334	4	US-09-547-435-8

28	463	13.2	857	4	US-09-751-687-17	Sequence 17, Appl
29	458.5	13.0	360	4	US-09-949-016-8911	Sequence 8911, Ap
30	456	13.0	901	4	US-09-714-767A-4	Sequence 4, Appli
31	451	12.8	864	4	US-09-810-268-3	Sequence 3, Appli
32	448.5	12.8	862	4	US-09-751-687-9	Sequence 9, Appli
33	445.5	12.7	864	4	US-09-751-687-18	Sequence 18, Appl
34	442	12.6	865	4	US-09-751-687-16	Sequence 16, Appl
35	441.5	12.6	862	4	US-09-751-687-12	Sequence 12, Appl
36	441.5	12.6	862	4	US-09-978-522-1	Sequence 1, Appli
37	439.5	12.5	859	4	US-09-978-522-3	Sequence 15, Appl
38	418.5	11.9	839	4	US-09-751-687-7	Sequence 19668, A
39	396	11.3	692	4	US-09-252-991A-19668	Sequence 20, Appl
40	374	10.6	195	4	US-09-547-435-20	Sequence 654, App
41	347.5	9.9	131	4	US-09-641-638-654	Sequence 654, App
42	347.5	9.9	131	4	US-10-170-097-654	Sequence 18, Appl
43	268.5	7.6	139	4	US-09-547-435-18	Sequence 22, Appl
44	193.5	5.5	110	4	US-09-547-435-22	Sequence 12721, A
45	167	4.8	477	4	US-09-902-540-12721	

ALIGNMENTS

RESULT 1

US-09-061-768A-25
; Sequence 25, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061.768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-061-768A-25

Query Match 99.7%; Score 3503.5; DB 3; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGLYRIRVSTGASLYAGSNNQVLWVQHGAEALGKRLWPARG-ETELKVEVPYGLPL 59

Db 1 MGLYRIRVSTGASLYAGSNQVQLWLVQGHGAALGKRLWPARGKETELKVEVPYLGPL 60
QY 60 LFKLRKRHLKDDAWFCNWSIQVQPGAGDEVRFPCYRWVEGNVLSLPEGTGRTVGEDP 119
Db 61 LFKLRKRHLKDDAWFCNWSIQVQPGAGDEVRFPCYRWVEGNVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREELERERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 179
Db 121 QGLFQKHREELERERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 180
QY 180 GLADLAIKDSNLVLTCKWLDLDFNRFWCQGSQKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GLADLAIKDSNLVLTCKWLDLDFNRFWCQGSQKLAERVRDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 300
QY 300 VMLKLPDQKLLPMVILQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359
Db 301 VMLKLPDQKLLPMVILQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360
QY 360 LLRGHLMABVIVVATMRCCLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLRGHLMABVIVVATMRCCLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 479
Db 421 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 480
QY 480 LHYKTDAVKDDPELOQTWCREITEIGLOQAQDRGFPVSLQARDQVCHFTVTCIGTGOH 539
Db 481 LHYKTDAVKDDPELOQTWCREITEIGLOQAQDRGFPVSLQARDQVCHFTVTCIGTGOH 540
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Db 541 ASVHLGQLDWYSWVNPACTMRLPPPTTKDLETVMATLPNFHQASLQMSITWQLGRQ 600
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QY 660 AI 661
Db 661 AI 662

RESULT 2

US-09-764-246-25
; Sequence 25, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; JISAKA, MITSUO
; BORELIN, WILLIAM E.
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESSES:
; ADDRESS: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 662 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-764-246-25
Query Match 99.7%; Score 3503.5; DB 4; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVQGHGAALGKRLWPARGKETELKVEVPYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNQVQLWLVQGHGAALGKRLWPARGKETELKVEVPYLGPL 60
QY 60 LFKLRKRHLKDDAWFCNWSIQVQPGAGDEVRFPCYRWVEGNVLSLPEGTGRTVGEDP 119
Db 61 LFKLRKRHLKDDAWFCNWSIQVQPGAGDEVRFPCYRWVEGNVLSLPEGTGRTVGEDP 120
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Db 121 QGLFQKHREELERERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 180
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Db 181 GLADLAIKDSNLVLTCKWLDLDFNRFWCQGSQKLAERVRDSWKEDALFGYQFLNGANPVV 240
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Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 300
QY 300 VMLKLPDQKLLPMVILQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359
Db 301 VMLKLPDQKLLPMVILQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360
QY 360 LLRGHLMABVIVVATMRCCLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLRGHLMABVIVVATMRCCLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 479
Db 421 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 480
QY 480 LHYKTDAVKDDPELOQTWCREITEIGLOQAQDRGFPVSLQARDQVCHFTVTCIGTGOH 539
Db 481 LHYKTDAVKDDPELOQTWCREITEIGLOQAQDRGFPVSLQARDQVCHFTVTCIGTGOH 540
QY 540 ASVHLGQLDWYSWVNPACTMRLPPPTTKDLETVMATLPNFHQASLQMSITWQLGRQ 599
Db 541 ASVHLGQLDWYSWVNPACTMRLPPPTTKDLETVMATLPNFHQASLQMSITWQLGRQ 600
QY 600 PVMVAVGQHEEYFSGPEKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 659
Db 601 PVMVAVGQHEEYFSGPEKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 660
QY 660 AI 661
Db 661 AI 662


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Db 477 LWELAIRFTAEVDIYEGDQVDEEDPELQDFVNDVYVGMGRKSGGFPKSVKSRQL 536
Qy 525 CHFVTMCITCTGQHASVHLGQDWSVWPNAPCTMRLLPPTTKD-ATLETVMATLPNFH 583
Db 537 SEYLTWVIFTASQAHAANFGQYDWCWIPNAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 596
Qy 584 QASLQMSITWOLGRQPVMAVQGEHEEYFSGPEKAVLKKPREELALDKIEIRNAKL 643
Db 597 RSCWHLGAWALSQFQENELFLGMYPPEHFIEKPVKEAMARFKNLEAIVSVIAERNKKK 656
Qy 644 DMPYELRPSVSVNSVAI 661
Db 657 QLPYYLSPDRIPNSVAI 674

RESULT 6
US-09-949-016-11692
; Sequence 11692, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11692
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11692

Query Match 37.0%; Score 1298.5; DB 4; Length 689;
Best Local Similarity 39.7%; Pred. No. 4.5e-135;
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLWVQHG---EALGKRLWP--ARGETE-LKVEVPE 54
Db 16 MPTVTVTATGSQLQWFAQTDDYIYLSVGSAGCKSEKHLDDKPFYNDFERGAVDSDYTVDE 75
Qy 55 YLGPILLFVKLRKHLLKDDAWFCNWSVQGGAGDEVFPCCYRWVGEVGLSLPSTGRT 114
Db 76 ELGETQLVRIEKRKTLWLNDDWTLYKITLTKTP-HGDIYIEFPCCYRWITGDVEVVLDRGAKL 134
Qy 115 VGEDPQGLFQKHREBELEBRRLYRWGNWKDGLILNMAKAKLYDLPVDERFLEDRVDPE 174
Db 135 ARDDQIHLKHQRKELETRQYRWMEWNPFGFSLISDAKCHKOLPRDIQPFSEKGVDFV 194
Qy 175 VSLAKGLADLAIKDSINVL-TCKDLDPNRIFWCGQSKLAERVDSWKEDALFYQFQLN 233
Db 195 LNSYKAMENLFINRMHMFQSSWDFADPEKIFVKISNTISERVNHWQEDLMFYQFQLN 254
Qy 234 GANPVVLSRAHLPARLVPPQMEEL---QAQLEKEGGTLFEADFSLLDGIKAN-VI 288
Db 255 GCNPVLIRCTELPEKLPTVTTEVMSCSLERQSLSEVQQGNIFIVDFELLDGIDANKTD 314
Qy 289 LCSQQLAALPLVWLKLPQDKLLPMVQL-QLPRTGSPPPPLFLPTDPPMALLAKCVR 347
Db 315 PCTLQFLAAPICLLYKNLANKIVTAIQNLQIP---GDNFIFLPSDAKYDWLLAKIWR 371
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Db 372 SSDFHHVHTITHLRTHLVSEVFGIMYRQPAVHPFIPKLLVAHVRFITIAINTKAREQLI 431
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Db 432 CECGLFDKANATGGGGHVQVQAMKOLTYASLCFPEAKARGMESKEDIPIYFYRDDGL 491
Qy 465 RWELIIRYVGEIVSLHYKTDVAVKDDPELQWTCREITEIGLQGAQDRGPPVSLQARQV 524
Db 492 LWELAIRFTAEVDIYEGDQVDEEDPELQDFVNDVYVGMGRKSGGFPKSVKSRQL 551
Qy 525 CHFVTMCITCTGQHASVHLGQDWSVWPNAPCTMRLLPPTTKD-ATLETVMATLPNFH 583
Db 552 SEYLTWVIFTASQAHAANFGQYDWCWIPNAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 611
Qy 584 QASLQMSITWOLGRQPVMAVQGEHEEYFSGPEKAVLKKPREELALDKIEIRNAKL 643
Db 612 RSCWHLGAWALSQFQENELFLGMYPPEHFIEKPVKEAMARFKNLEAIVSVIAERNKKK 671
Qy 644 DMPYELRPSVSVNSVAI 661
Db 672 QLPYYLSPDRIPNSVAI 689

RESULT 7
US-09-949-016-8912
; Sequence 8912, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8912
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8912

Query Match 34.2%; Score 1203.5; DB 4; Length 679;
Best Local Similarity 37.8%; Pred. No. 1.7e-124;
Matches 259; Conservative 126; Mismatches 267; Indels 33; Gaps 10;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLWVQHGEEA-----LGKRLWPARGETELKVEVPE 54
Db 4 MAEFRRVSTGEAFGATGDKVSVISVITRGESPLPLDLNLGKB-FTAGASEDFQVTLPE 62
Qy 55 YLGPILLFVKLRK-----HLLKDDAWFCNWSVQGGAGDEVFPCCYRWVGEVGLSL 107
Db 63 DVGRLVLLRVHKAHPVPLPLGLPADAWFCWFWLT-PPRGHLLFPYQWLEGAGTLVL 121
Qy 108 PEGTRTVGEDPQGLFQKHREBELEBRRLYRWGNWKDGLILNMAKAKLYDLPVDERFLE 167
Db 122 QEGTAKVSWADHPVLQOQOEELQARQEMYQWYKYNPWPCHLDEKTVDELNLNIST 181
Qy 168 DKRVDFEVSILAKGLADLAIKDSINVLTCWKDLDPNRIFWCGQSKLAERVDSWKEDALF 227
Db 182 AKNAVFLYQAGSAFAEMKIKGLDRKGLWRSLSNEKRIFFNRTPAASHAFEHQWEDAFF 241
Qy 228 GYQFLNGANPVVLSRAHLPARL-----VPPPGMEELQAQLEKEGGTLFEADFS 278
Db 242 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASVLGPG-TSLQAELEK-----GSLFLVDHG 296
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COMPUTER: IBM PC/XT/AT compatible
 OPERATING SYSTEM: Windows 3.1
 SOFTWARE: WORD PERFECT 6.1 and ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/764,246
 FILING DATE: 17-Jan-2001
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: ARLES A. TAYLOR, JR.
 REGISTRATION NUMBER: 39,395
 REFERENCE/DOCKET NUMBER: 1242/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 493-8000
 TELEFAX: (919) 419-0383
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 676 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-764-246-2

Query Match 34.2%; Score 1202.5; DB 4; Length 676;
 Best Local Similarity 37.8%; Pred. No. 2.2e-124;
 Matches 260; Conservative 126; Mismatches 264; Indels 37; Gaps 11;

QY 1 MGLYRVRSTGASLYAGSNQVQLWLVGQGEAA-----LGKRLMPARGETELKVEVPE 54
 DB 1 MAEFVRVSTGEAFGAGTWDKVSIVGTRGESPLPLDNLGKE-FTAGAEEDFQVTLPE 59
 QY 55 YLGPELLFVKLRK-----HLKDDAWFCNWNISVQPGAGDEVPPCYRWVGGNGLVLSL 107
 DB 60 DVGRVLLLRVHKAPVPLLLGLPADWAFCRNFQLT-PPRGHLLPCCQWLEGAGTLVL 118
 QY 108 PEGTGRVSGDPQGLFQKHREELERKLYRWGNKOGILLNMAGAKLYDLPVDERFLE 167
 DB 119 QEGTAKVSWADHPVLVQOQOEELQAEQYQWKA YNPGWPHCLDEKTVDELNLKYST 178
 QY 168 DKRVDFEVSIAKGLADLAIKOSLNVLTCWKDLDDFNRI FWCQSKLAERVRDSWKEDALF 227
 DB 179 AKNANFYLAGSAFAEMKIKGLLDKGLWRSINEMKRIENFRRTPAAEHAFEHQWQEDAF 238
 QY 228 GYQFLNGANPVLRSSAHLPARLVFP-----PGMEELQAOLEKELEGGTLEAD 276
 DB 239 ASQFLNGINPVLRCHYLPKN--FPVTDAMVASLLGPG--TSLQAELEK---GSLFLVD 291
 QY 277 FSLLDGKANKVILCSQOHLAAPLMLKLOPD-GKLLPMVLIQLPRTGSPPLFLPTDP 335
 DB 292 HGILSGIQTNVINGKQPSAAPTLLYQSPGCGPLPLAIQLS--QTPGNSPIFLPTDD 349
 QY 336 PMAWLLAKCWRSSDFQLHQLSHLRGHMAEVIVVATWRCILPSIHPFKLIIPIHLYRT 395
 DB 350 KDWLLAKTWVRAEFSFHEALTHLHSHLLPEVFTLATRLQPHCHPLFKLIIPIHTRYT 409
 QY 396 LEINVRARTGLVSDMGIFDQIMSTGGGHVQLLKQAGAFETYSSFCPPDDDLADRLGLGVK 455
 DB 410 LHINTLARELLIVPGQVVDSTGIGTEGSELIQRNKNQNLNYSLLCLPEDIIRTRGVEDIP 469
 QY 456 SSFYAODALRLWEIIYRYVEGIVSLHYKTDVAVKDDPELQTCWREITEIGLOAQDQRP 515
 DB 470 GYYRDDCMQWGAVERFVSEIIGIYPSDESQDDRELQAWVREIFSGFLNQESSGIP 529
 QY 516 VSLQARDQVCHFTWCITCTGQHASVHLGQLDWYVFNAPCTMELPPTTKD-ATLET 574
 DB 530 SSLTREALVQYVTVNLTCSAKHAASVAGQFDSCHAMNLPMSQMLPPTSKGLATCEG 589
 QY 575 VMATLPNFAQSLQMSITWLGRRQPVVMVAVGQHEEYFSGPEKAVLKFFREEAALDK 634

Db	530	SSLETRALVQVTVTWIETCSAKHAASAGQFDSCAWPNLPSPMQLPPTTSKGLATCEG	589
Qy	575	VNATLPNFHOASLQWSITWOLGRRQPVVAVGOEHEEVFGSPPEKAVLKKFREELAALDK	634
Db	590	FATLPDPVNATCDVIALWLWSKPGDORPUGTYPDEHFTTEAPRRSIATFQSRLAQISR	649
Qy	635	EIEIRNAKLDMPYEYLRPSVVENSVAI	661
Db	650	GICERNRGLVLPYTYLDPPLIENSVSI	676
RESULT 11			
US-09-061-768A-4			
; Sequence 4, Application US/09061768A			
; Patent No. 6204037			
; GENERAL INFORMATION:			
; APPLICANT: BRASH, ALAN R.			
; APPLICANT: BOEGLIN, WILLIAM E.			
; APPLICANT: JITSUKA, MITSUO			
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS			
; NUMBER OF SEQUENCES: 36			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: ARLES A. TAYLOR, JR.			
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD			
; CITY: DURHAM			
; STATE: NORTH CAROLINA			
; COUNTRY: USA			
; ZIP: 27707			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage			
; COMPUTER: IBM PC/XT/AT compatible			
; OPERATING SYSTEM: Windows 3.1			
; SOFTWARE: WORD PERFECT 6.1 and ASCII			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/061,768A			
; FILING DATE: APRIL 16, 1998			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA: NONE			
; APPLICATION NUMBER:			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: ARLES A. TAYLOR, JR.			
; REGISTRATION NUMBER: 39,395			
; REFERENCE/DOCKET NUMBER: 1242/5			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (919) 493-8000			
; TELEFAX: (919) 419-0383			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 677 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: unknown			
US-09-061-768A-4			
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Best Local Similarity 37.7%; Pred. No. 2.6e-122;			
Matches 259; Conservative 126; Mismatches 266; Indels 36; Gaps 12			
Qy	1	MGLYRIRVSTGASLVAGSNNOYQLWLWQHGEEA-----LGRKLWPFARGETELKVEVPE	54
Db	1	MAKCRVSTGTGACAGTWDKVSIVUTHGESPLVPLDLHGKE-PSAGAEEDFEVTLQ	59
Qy	55	YLGPLLFFVKLRK-----HLLKDDAWFCNWSVQG-PGAGDEVAFPCYRWVEGNGVL	105
Db	60	DVGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFELWLPGAA--LHFP CYQWLEGAGEL	117
Qy	106	SLPEGTGRVGDPOGLFQKREBLEERKLYRWGNWKD--LILNMAKAKLYDLPVDE	163
Db	118	VLFRGAARKVSWQDHFTLQDQRQKLESQRKQYSNKTYIEGWPRCLDHPHETVKOLDLNKY	177

Query Match	32.8%	Score 1153	DB 4	Length 711
Best Local Similarity	35.5%	Pred. No. 8.1e-119		
Matches	255	Conservative 126	Mismatches 273	Indels 64
Gaps				
QY	1	MGLYRIRYSTGASLYAGSNNOVLWLVGQHEA-----ALGKRLWPARGETELKVEPVE 54		
DB	1	MAVYELCVTTGPLYRAGTLDNISVTLVGTCEGPKQELDEMGRDFAPGSVQ-KYKVRCTA 59		
QY	55	YLGPIFLFVKLRKH--LLKODANFCNWSVOGPGAGDEVFPFCYRWVGVNGVLUSLPEGTG 112		
DB	60	ELGELLRLVRKERVAFPRKDSWYCSRICVTEPD-GSVSHFPCYQWIEGYCTVELSPGTA 118		
QY	113	RTVGEDPGCLFQKUREBELERRKLYRWGNWKDGLILNAGAKLYDLVPDERLEDK---169		
DB	119	RTICQDSLPLLDHRTRELRAQCERYRWKIYAFGFCPMVDVNSFQMESDKFALTKTTT 178		
QY	170	-----RVDF-----EVSLAKGLADI--AIKQSLNVL-----194		
DB	179	CVDQDSSGNRYLPGFPWPKIDIPSLMTWENPNRYSATKISLFLNAPSLGKMLRGLD 238		
QY	195	---CWLKDLDDFNRIWFCQSKLAERVDRDSKBKDALFGYQFLANGANPVVILRRSAHLPARLV 251		
DB	239	RKGSWKLLDDMQNIFWCHTKFTTKYVTEHWCEDHFFGCGYQLNGVNPVMLHCISLSPSKL- 297		
QY	252	FPFGMEELQAO-----LEKEEGGTLFRADPSLLDGICAKNVILCSQOHLAAPLVMLKL 304		
DB	298	--PVTNDVAPLLGQDTCLQTLQTERGNIFLADWYILAEAPTHCLNGRQOQVAAPLCLLWL 355		
QY	305	QPDGKLLPMWTLQLPRTGSPPPPLFLPTDPPMAWILLAKCWVRSSDFOLHELQSHLLRGH 364		
DB	356	SPQGLALVPAIQLS--QTGPDSPFIPLTSEWDWLLAKTWVRNSFELVHENTHFLCTH 413		
QY	365	LMAEIVIVVATMRCPLSPHPIFKLIPIHLRYTLINVRARTGLVDMGIFDQIMSTGGGH 424		
DB	414	LICEAFAMATLRQLPCHPIVKLLPHTRYTTLQVNTIARATLLNPEGLVDQVTSIGROGL 473		
QY	425	VOLLKQAGAFITYSGFCPPDDLDADGLLVKVSFYAQDALRLWEIYRYVEGIVSLHYKT 484		
DB	474	IYLMSTGLAHFTYTNFLCPDLSLRARGVLAIPNHYRDLGGLIKWAAIESFSEIVIGVYYP 533		
QY	485	DVAVKDDPELQTMCREITEIGLQGAQDRGPPSVLSQARDQOVCHFTWCIFFCTCOHASVHL 544		
DB	534	DASVQDDSELQATGEIIFAQAFUGRESSGPPSLRCTTPGENVKELTALIFNCSAQHAHVS 593		
QY	545	GOLDWYSVWPNACTMLRPLPPPTTK-DATLETVMATLFPNFHQASLQMSITWQLGRQFVMV 603		
DB	594	GOHDFGAMWNPAPSSMRQPPPTQTKTTLTYLDTLPEVNI SCNNLLFLWLSQEPKQOR 653		
QY	604	AVGOHEEYFGSGPEPKAVLKKFREELAAALKBIEIRNAKLDMPYEYILRPSVENSVAI 661		
DB	654	PUGTYPDHFTTEAPRSIAAFQSRLAQISRDQIERNQGLAPTYLTPDPLIENSYSI 711		

RESULT 14
US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian

```

; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-24

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Query Match	32.8%;	Score 1153;	DB 4;	Length 867;
Best Local Similarity	35.5%;	Pred. No. 1.1e-118;		
Matches	255;	Conservative 126;	Mismatches 273;	Indels 64; Gaps 12;
Qy	1	MGLYRVSTGASIVYAGSNNOVQLMVGQGEA-----ALGKELWPARGETELKVEVPE	54	
Db	157	MAVRLCVTTGPIYLRAGTLONISVTLVGTGESPQKQLDRMGDRFAPGSVQ-KYKVRCTA	215	
Qy	55	YLGPFLLFVKLRKH--LLKDDAMFCNWSIVQGPCAGDEVFPFCYRVWVEGNGVLSLPEGTG	112	
Db	216	ELGELLLLRVHKERYAFPRKDSWYCYSRICVTEPD-GSVSHFPYCQWIEGYCTVELRPQTA	274	
Qy	113	RTVGEDPQGLFQKHREELBERRKLYRWGNWKGILLINMAGAKLYDLPVDERFLEDK---	169	
Db	275	RTICQDSLPLLLDHRTRELRAQECYRWKIYAPGFCWVDVNSFQEMESDKKFAITKTTT	334	
Qy	170	-----RVDF-----EVSIAKGLADL--AIKDSINVLT-----	194	
Db	335	CVDPQDSSGNRYLPGPPMKDIDPSLMYNEPNRYSATKISLFPNAIPASLGMKLRGLLD	394	
Qy	195	---CWKDLDDFNRIFCWGCQSKLAERVRDSWKEDALFGYQFLINGANPVVLRARSAPHLPARLV	251	
Db	395	RKGSWKKLDDMQNIFWCHKFTFYKYVTEHWCEDHFFGYQYLVNGVNPVWLHCISLSPSKL-	453	
Qy	252	FPGMEELQAO-----LSKELEGTLFPAFSPSLLDGIKANVILCSQQHLAAPLVMKL	304	
Db	454	--PVTNDMVAFLGQDTCLOTETELRGNIFLADYWIILAEAPTHCLNGRQQYVAAPLCILWL	511	
Qy	305	QPQKLLPMVLIQLOLPTGTGPPPLFPTDPPMAWIAKACWVSSDFOLHELQSHLLRGH	364	
Db	512	SPQALVPLAIQUS--QTPGQDSPIFPTDSEWDLIAKTWVRNSEFLVHNTHFICJTH	569	
Qy	365	LMAEVIVVATMRCILPSIHPFKLIIPLHRYVLEINVRARTGLVSDMGIFFQIMSTGGGGH	424	
Db	570	LLCEAFAMATLRQLPLCHPIYKULLPHRYTLQVNTIARATLNLPEGLVQVTSIGRQGL	629	
Qy	425	VQLLKQAGAFLTYSFPCPPDDLADRGLLGVKSSFYAQDALRWELIIVRYVEGIVSLHYKT	484	
Db	630	IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYRDLGLKIWAIBSFVSEIVGYIYPS	689	
Qy	485	DVAVKDDPELOTWCREITEIGLQAGQDRPPVSLQARDQVCHFVTWICIFCTGQHASVHL	544	
Db	690	DASVQDSELSQAWTGEIFAQAFLGRESSGPFSLCTGEMVKFLTAIFNCSAQHAHAVNS	749	
Qy	545	GOLDWYSWVNAICTMRLPPPTTK-DATLETVMATLNFHOASIQMSITWOLGRQPVMV	603	
Db	750	QGDHFGAMWPNASSMQRPPQTKGTTTLKYLTDLTFLVNISCNWLLFLWLVSGEPKQDR	809	
Qy	604	AVGQHEEYFSGPEPKAVLKKFBEELAALDKIEIRNAKLDMPYEYLRPSVENSVAI	661	
Db	810	PLGYTPDEHTEAPRSIAFOSRLAISRDIQERNQGLAPPTYLDPLPIENSVEI	867	

RESULT 15

RESULT IS
US-09-087-727-2

US-09-0872727-2
: Sequence 2. Application US/09087727A: sequence 2, Application
: Patent No. 6103496

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; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: Attorney Docket NO. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-727-2

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Query Match	32.0%	Score 1124;	DB 3;	Length 701;
Best Local Similarity	34.0%	Pred. No. 1.3e-115;		
Matches	243;	Conservative 140;	Mismatches 265;	Indels 66; Gaps 12
QY	1	MGLYRVSTGASISYAGSNNOVLWLVGGEAALGKRLWPARGET-----ELKVEVP	53	
DB	1	MATYKRVATGTDLGSTRDSISLITVGTGES--HKLLNHFERDPATGAVGYTTVQCP	58	
QY	54	EYLGPLLFVKLRKH--LLKDDAWFCNWIISVQGPAGDEVRFPYRVVVEGNGVLSPGEGT	111	
DB	59	ODLGELIIIFLHKERYAFPPKDPWCNYVQICAPN-GRIVHFPAYQWMDGVETLALREAT	117	
QY	112	GRTVGEDPQGLFOKHREELERBKULRYGNWKDGL-----	147	
DB	118	GKTTADDSLPLVEHRKEEIRAKQDFVHMRVFLPGLPSYVHIPTSRVPVRRHRNPNRPWE	177	
QY	148	-----ILNMAKAKLYDLVDPERPLEDKRVDVFEYSLAKGLADLAIKOSLVNLTCKWD	198	
DB	178	NGVIPGFPILINFKATFLNLNIRYSFL--KTASFVFRGLGPMALAFKVRGLDCKHSHWR	235	
QY	199	LDDFNRIWCGQSKLAERVDSWKEDALFGYQFINGANPVVLRSAHLPARLVFP-----	253	
DB	236	LKDRIKIFPGKKSVSVEVAHWAEDTFQGYQVINGVNGPLIRCTRIPOK--FPVTDMM	293	
QY	254	--PMEE---LQALKEKEGGTFFEADFSLLDGIIKANVILCSQHLAAPLMLKLPDPG	308	
DB	294	VAPFLGEGTCLQAELEK---GNVILADYRIMEGIPITVELSGRKQHHCAPICLLHFGPEG	349	
QY	309	KLIPMWIQLQLPRTGSPPPPLFLPTDPPMAWLLAKCHVRSDDFQLHELQSHLLRGLHMAE	368	
DB	350	KMMPIAIQLS--QTPGDGCFIFLPSSEWDLAKTWVRYABFYSHSEAIHLLTHLIAE	407	
QY	369	VIVVATWRCPLSPHTPKLIIPHLYRTLEINVRARTGLVDMGTFDQIMSTGGGHHVOLL	428	
DB	408	AFCLALLRLNPMCHPLYKLIIPHTRYTVQINSIGRAVLNNEGSLAKGMSLVGVEPAGVM	467	
QY	429	KQAGAFITYSSFCPPDDLADGLLGVKSSFYAQDALRLWEIIVRYREGIVSLHYKTDVAV	488	
DB	468	VRALSELTYDSLPLNDFVERGVQDLPGYVYRDDSLAVWNALEKXVTEIITYYVPSDAAV	527	
QY	489	KDPELQTCREITEITGLQAGDRGFPVSLQARDOVCHFVTMCITFTCTGQHSHVHLGOLD	548	
DB	528	EGDPELQSWQVEIFKECLLGRESSGFPCLRTVPDELIRYVTIVITVCSAKHAAVNTGQME	587	
QY	549	WYSWVNAPCTMLRPPTTKD-ATLETVMATLNFHQASLQMSITWOLGRQPVMVAVGQ	607	
DB	588	FTAWMNFPSAMRNPPIQTKGLTFTMTDPLDVKTCTLLVLWLTLSREPDDBRPLUGH	647	
QY	608	HEBEYFSGPBFKVLKFKFREELAAALDKIEIRNAKLDMPYEYLRPSVVENSAVI	661	
DB	648	FPDIHFVERAPRESIRAFRORIWOISHDIDRKNKCLPIPYVYLPDVLIIENSISI	701	

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Job time : 33.1353 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:53:28 ; Search time 102.756 Seconds
(without alignments)
2497.095 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLYRIRVSTGASLYAGSNN.....KLDMPYELRPSVENSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 398188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3514	100.0	661	16 US-10-688-676A-2	Sequence 2, Appli
2	3503.5	99.7	662	9 US-09-764-246-25	Sequence 25, Appl
3	3503.5	99.7	662	16 US-10-716-204-25	Sequence 25, Appl
4	3494.5	99.4	684	15 US-10-398-663-5	Sequence 5, Appli
5	2316	65.9	663	16 US-10-741-601-516	Sequence 516, App
6	2316	65.9	663	16 US-10-741-601-517	Sequence 517, App
7	2316	65.9	663	17 US-10-741-600-1499	Sequence 1499, App
8	2316	65.9	663	17 US-10-741-600-1500	Sequence 1500, App
9	2280	64.9	663	15 US-10-170-097-653	Sequence 653, App
10	2280	64.9	663	17 US-10-946-684-653	Sequence 653, App
11	1969	56.0	399	17 US-10-498-788-27	Sequence 27, Appl

12	1298.5	37.0	674	14	US-10-240-305-14	Sequence 14, Appl
13	1298.5	37.0	674	16	US-10-485-310-22	Sequence 22, Appl
14	1261.5	35.9	663	14	US-10-240-305-16	Sequence 16, Appl
15	1202.5	34.2	676	9	US-09-764-246-2	Sequence 2, Appli
16	1202.5	34.2	676	16	US-10-716-204-2	Sequence 4, Appli
17	1184	33.7	677	9	US-09-764-246-4	Sequence 4, Appli
18	1184	33.7	677	16	US-10-716-204-4	Sequence 4, Appli
19	1184	33.7	677	16	US-10-688-676A-4	Sequence 2, Appli
20	1153	32.8	711	9	US-09-862-658-2	Sequence 23, Appl
21	1153	32.8	711	14	US-10-175-696-23	Sequence 2, Appli
22	1153	32.8	711	14	US-10-422-264-2	Sequence 23, Appl
23	1153	32.8	711	16	US-10-776-871-23	Sequence 24, Appl
24	1153	32.8	867	14	US-10-422-264-24	Sequence 3, Appli
25	1148	32.7	711	15	US-10-275-998-3	Sequence 2, Appli
26	1124	32.0	701	9	US-09-853-053-2	Sequence 6, Appli
27	1124	32.0	701	15	US-10-445-484-2	Sequence 10, Appl
28	954.5	27.2	556	14	US-10-422-264-6	Sequence 28, Appl
29	946.5	26.9	615	14	US-10-422-264-10	Sequence 19529, A
30	946.5	26.9	771	14	US-10-422-264-28	Sequence 12, Appl
31	761.5	21.7	671	15	US-10-369-493-19529	Sequence 4, Appli
32	748	21.3	460	14	US-10-422-264-12	Sequence 25, Appl
33	704.5	20.0	489	14	US-10-422-264-4	Sequence 25, Appl
34	704.5	20.0	645	14	US-10-422-264-26	Sequence 14, Appl
35	686.5	19.5	389	16	US-10-485-310-3	Sequence 5694, Ap
36	593.5	16.9	491	9	US-09-862-658-4	Sequence 19963, A
37	593.5	16.9	491	14	US-10-175-696-25	Sequence 8, Appli
38	593.5	16.9	491	16	US-10-776-871-25	Sequence 19726, A
39	580.5	16.5	291	14	US-10-422-264-14	Sequence 51226, A
40	522.5	14.9	917	16	US-10-739-930-5694	Sequence 19890, A
41	518	14.7	487	15	US-10-369-493-19963	
42	506	14.4	334	14	US-10-422-264-8	
43	502.5	14.3	566	15	US-10-369-493-19726	
44	494.5	14.1	814	15	US-10-425-114-51226	
45	493.5	14.0	472	15	US-10-369-493-19890	

ALIGNMENTS

RESULT 1

US-10-688-676A-2
; Sequence 2, Application US/10688676A
; Publication No. US20040248794A1
; GENERAL INFORMATION:
; APPLICANT: Alcon, Inc.
; APPLICANT: Yanni, John M.
; APPLICANT: Ganache, Daniel A.
; APPLICANT: Miller, Steven T.
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo
; FILE OF INVENTION: Activity to Ocular Surface Cells
; FILE REFERENCE: 2394 US
; CURRENT APPLICATION NUMBER: US/10/688.676A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/435,988
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 661
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-688-676A-2

Query Match	100.0%	Score 3514;	DB 16;	Length 661;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 661;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MGLYRIRVSTGASLYAGSNNQVQLWVGQHGGAALGKRLWPARGETELKVEVPEYLGPIIL	60	
Db	1	MGLYRIRVSTGASLYAGSNNQVQLWVGQHGGAALGKRLWPARGETELKVEVPEYLGPIIL	60	
QY	61	FVLRKRHLKDDAFCNWSIQVQPGAGDEVFPCYRWVEGVNLSLEGTRTVEGPQ	120	

Db 61 FVKLRKHLLKDDAWFCNWSISVQGPAGDEVFPFCYRWVEGNGVLSLPEGTGRTVGEDPQ 120
QY 121 GLFQKHREBELEBERRKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDFEVS LAG 180
Db 121 GLFQKHREBELEBERRKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDFEVS LAG 180
QY 181 LADLAIKDSNLVLTWCWLDLDDFNRI FWCQSKLAERVRDSWKEDALFGYQFLNGANPVYL 240
Db 181 LADLAIKDSNLVLTWCWLDLDDFNRI FWCQSKLAERVRDSWKEDALFGYQFLNGANPVYL 240
QY 241 RRSAPHLPARLVFPFGMEELQAQLEKELEGGTLEADFSLLDGKANKVILCSQOHLAAPLV 300
Db 241 RRSAPHLPARLVFPFGMEELQAQLEKELEGGTLEADFSLLDGKANKVILCSQOHLAAPLV 300
QY 301 MLKLPQDGLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFOLHELQSHL 360
Db 301 MLKLPQDGLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFOLHELQSHL 360
QY 361 LRGLHMAEVI VVATMRCCLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMSTG 420
Db 361 LRGLHMAEVI VVATMRCCLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMSTG 420
QY 421 GGGHVQLLKQAGAFITYSSFCPPDDDLADRGLLGVKSSFYAODALRLWEI IYRYVEGIVSL 480
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDDLADRGLLGVKSSFYAODALRLWEI IYRYVEGIVSL 480
QY 481 HYKTDVAVKDDPELQWTCREITEIGLQAGQDRGFPVSLQARQOVCHFVTWCITCTGQHA 540
Db 481 HYKTDVAVKDDPELQWTCREITEIGLQAGQDRGFPVSLQARQOVCHFVTWCITCTGQHA 540
QY 541 SVHLGQLDWYSWVPNAPCTMRLPPTTKDLETVMATL PNFHQASLQMSITWQLGRROP 600
Db 541 SVHLGQLDWYSWVPNAPCTMRLPPTTKDLETVMATL PNFHQASLQMSITWQLGRROP 600
QY 601 VMVAVGQHEEYFSGPEKAVLKKFREELAALDKEIERNAKLDMPEYELRPSVVENSVA 660
Db 601 VMVAVGQHEEYFSGPEKAVLKKFREELAALDKEIERNAKLDMPEYELRPSVVENSVA 660
QY 661 I 661
Db 661 I 661

RESULT 2

US-09-764-246-25
; Sequence 25, Application US/09764246
; Patent No. US20010046672A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

RESULT 3

US-10-716-204-25
; Sequence 25, Application US/10716204
; Publication No. US20040137483A1

NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 662 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-764-246-25
Query Match 99.7%; Score 3503.5; DB 9; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNNVQLMWVGHGGAALGKRLWPARG-ETELKVEVPEYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNNVQLMWVGHGGAALGKRLWPARGKETELKVEVPEYLGPL 60
QY 60 LPVKLRKHLLKDDAWFCNWSISVQGPAGDEVFPFCYRWVEGNGVLSLPEGTGRTVGEDP 119
Db 61 LPVKLRKHLLKDDAWFCNWSISVQGPAGDEVFPFCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREBELEBERRKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDFEVS LAK 179
Db 121 QGLFQKHREBELEBERRKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDFEVS LAK 180
QY 180 GLADLAIKDSNLVLTWCWLDLDDFNRI FWCQSKLAERVRDSWKEDALFGYQFLNGANPVY 239
Db 181 GLADLAIKDSNLVLTWCWLDLDDFNRI FWCQSKLAERVRDSWKEDALFGYQFLNGANPVY 240
QY 240 LRSAPHLPARLVFPFGMEELQAQLEKELEGGTLEADFSLLDGKANKVILCSQOHLAAPL 299
Db 241 LRSAPHLPARLVFPFGMEELQAQLEKELEGGTLEADFSLLDGKANKVILCSQOHLAAPL 300
QY 300 VMLKLPQDGLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFOLHELQSH 359
Db 301 VMLKLPQDGLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFOLHELQSH 360
QY 360 LLRGLHMAEVI VVATMRCCLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLRGLHMAEVI VVATMRCCLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDDLADRGLLGVKSSFYAODALRLWEI IYRYVEGIVS 479
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDDLADRGLLGVKSSFYAODALRLWEI IYRYVEGIVS 480
QY 480 LHYKTDVAVKDDPELQWTCREITEIGLQAGQDRGFPVSLQARQOVCHFVTWCITCTGQOH 539
Db 481 LHYKTDVAVKDDPELQWTCREITEIGLQAGQDRGFPVSLQARQOVCHFVTWCITCTGQOH 540
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDLETVMATL PNFHQASLQMSITWQLGRQ 599
Db 541 ASVHLGQLDWYSWVPNAPCTMRLPPTTKDLETVMATL PNFHQASLQMSITWQLGRQ 600
QY 600 PMVAVGQHEEYFSGPEKAVLKKFREELAALDKEIERNAKLDMPEYELRPSVVENSVA 659
Db 601 PMVAVGQHEEYFSGPEKAVLKKFREELAALDKEIERNAKLDMPEYELRPSVVENSVA 660
QY 660 AI 661
Db 661 AI 662

GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM E.
JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA: US/10/716,204
FILING DATE: 18-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-0300
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 662 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-716-204-25
Query Match 99.7%; Score 3503.5; DB 16; Length 662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNNOVQLVQHGGAALGKRLWPARG-ETELKVEVPYLGPL 59
DB 1 MGLYRIRVSTGASLYAGSNNOVQLVQHGGAALGKRLWPARGKETELKVEVPYLGPL 60
QY 60 LFKVLRKRHLKDDAWFCNWIISVQPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119
DB 61 LFKVLRKRHLKDDAWFCNWIISVQPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKREELERKRLRWGNWKDGLILNAGAKLYDLPVDERFLEDRKRVDFEVSIAK 179
DB 121 QGLFQKREELERKRLRWGNWKDGLILNAGAKLYDLPVDERFLEDRKRVDFEVSIAK 180
QY 180 GLADIAIKDSLNLVTCWKDLDPNRFICWQSKLAERVRDSWKEDALFGYQFLNGANPVV 239
DB 181 GLADIAIKDSLNLVTCWKDLDPNRFICWQSKLAERVRDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPPGMELOAQLEKELGGTLPFADPSLLDGIKANVILCSQQHAAAPL 299
DB 241 LRRSAHLPARLVFPPGMELOAQLEKELGGTLPFADPSLLDGIKANVILCSQQHAAAPL 300
QY 300 VMLKLQPDGKLLPMVIQLQPLRTGSPPPPLFTPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
DB 301 VMLKLQPDGKLLPMVIQLQPLRTGSPPPPLFTPTDPPMAWLLAKCWVRSSDFQLHELOSH 360
QY 360 LLRGLHMAEVIIVATWRCILPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
DB 361 LLRGLHMAEVIIVATWRCILPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVOLLKQAGAFITYSSPCPPDDLADRLGLLVKGSFYAODALRLWEIIRYVVEGIVS 479
DB 421 GGGGHVOLLKQAGAFITYSSPCPPDDLADRLGLLVKGSFYAODALRLWEIIRYVVEGIVS 480
QY 480 LHYKTDVAVKDDPELQWCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCIFCTCQGH 539
DB 481 LHYKTDVAVKDDPELQWCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCIFCTCQGH 540
QY 540 ASVHLGQLDWSYWPVNPACTMRLPPPTTKADLTETVMTATLNFHQASLQMSITWOLGRRQ 599
DB 541 ASVHLGQLDWSYWPVNPACTMRLPPPTTKADLTETVMTATLNFHQASLQMSITWOLGRRQ 600
QY 600 PMVAVGQHEEYFSGPEPKAVLKKFREELAALDKEIIRNAKLDMPYEYLRPSVVENS 659
DB 601 PMVAVGQHEEYFSGPEPKAVLKKFREELAALDKEIIRNAKLDMPYEYLRPSVVENS 660
QY 660 AI 661
DB 661 AI 662
RESULT 4
US-10-398-663-5
; Sequence 5, Application US/10398663
; Publication No. US20040053281A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE, CORPORATION; HARLAND, Lee;
; APPLICANT: ARVIZU, Chandra S.; DAS, Debopriya;
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;
; APPLICANT: DING, Li; CHAWLA, Narinder K.;
; APPLICANT: YAO, Montique G.; LU, Yan;
; APPLICANT: ELLIOTT, Vicki S.; THANGAVELU, Kavitha;
; APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;
; APPLICANT: TRIBOULEY, Catherine M.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0250 USN
; CURRENT APPLICATION NUMBER: US/10/398,663
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/31302
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/238,388
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,616
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/245,719
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/247,503
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/249,503
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053281A1 7484270CD1
US-10-398-663-5
Query Match 99.4%; Score 3494.5; DB 15; Length 684;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 660; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNNOVQLVQHGGAALGKRLWPARG-ETELKVEVPYLGPL 59
DB 23 MGLYRIRVSTGASLYAGSNNOVQLVQHGGAALGKRLWPARGKETELKVEVPYLGPL 82
QY 60 LFKVLRKRHLKDDAWFCNWIISVQPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119
DB 83 LFKVLRKRHLKDDAWFCNWIISVQPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 142

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QY 120 QGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 179
Db 143 QGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 202
QY 180 GLADLAIKSLNVLTCWKDLDNFNRIFWCGOSKLAERVDSWKEDALFGYQFLNGANPVV 239
Db 203 GLADLAIKSLNVLTCWKDLDNFNRIFWCGOSKLAERVDSWKEDALFGYQFLNGANPVV 262
QY 240 LRRSAHLPARLVFPFGMELOAQLEKELEGGTLPFADFSLLDGIKANVILCSQQHAAAPL 299
Db 263 LRRSAHLPARLVFPFGMELOAQLEKELEGGTLPFADFSLLDGIKANVILCSQQHAAAPL 322
QY 300 VMLKLPQDGKLLPMVILQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 359
Db 323 VMLKLPQDGKLLPMVILQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 382
QY 360 LLRGHMAEVIVVATWRCPLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGI FQOIMST 419
Db 383 LLRGHMAEVIVVATWRCPLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGI FQOIMST 442
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWEIIVRYVEGIVS 479
Db 443 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWEIIVRYVEGIVS 502
QY 480 LHYKTDAVKDDPELQTCWCREITEIGLOGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 539
Db 503 LHYKTDAVKDDPELQTCWCREITEIGLOGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 562
QY 540 ASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGRRQ 599
Db 563 ASVHLGOLDWYSWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGRRQ 622
QY 600 PWMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKBEIRNAKLDMPYELRPSVVENS 659
Db 623 PWMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKBEIRNAKLDMPYELRPSVVENS 682
QY 660 AI 661
Db 683 AI 684
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RESULT 5

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US-10-741-601-516
; Sequence 516, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 516
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-516
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Query Match 65.9%; Score 2316; DB 16; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;
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QY 1 MGLYRIRVSTGASLYAGSNQVQLMWLGQHGAEALGKRLWPARG-ETELKVEVPEYLGPL 59
Db 1 MGRYRIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFHDHVAEDLGLL 60
QY 60 LFKVLKRHLKDDDAWFCNWIWSVOGPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119
Db 61 QFVRLKHHWLVDDAWFCDRITVQGGCAEAVAFPCYRWVQGGEDILSLPEGTARLPDGN 120
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QY 120 QGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 179
Db 121 LDMFQKHREKELKQRIYCWATWKEGLPLTIAADKDDLPENMRPFHEBKRLDFFWTLKA 180
QY 180 GLADLAIKSLNVLTCWKDLDNFNRIFWCGOSKLAERVDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEMALKRVYTLSSWNCLDFDQIFWGQKSALAEKVRQCWQDDLEFSYQFLNGANPML 240
QY 240 LRRSAHLPARLVFPFGMELOAQLEKELEGGTLPFADFSLLDGIKANVILCSQQHAAAPL 299
Db 241 LRRSTSLPSRLVLPSCMEELQAQLEKELQNGSLFEADFIILLDGI PANVIRGEKQYLAAPL 300
QY 300 VMLKLPQDGKLLPMVILQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 359
Db 301 VMLKMEPNKGLQPMVIOIQPNPSSPTTFLPSDPPLAWLLAKSWVRNSDFQLHEIQVH 360
QY 360 LLRGHMAEVIVVATWRCPLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGI FQOIMST 419
Db 361 LNLTHLVAEIVATAVMRCLPLGLHPFKLIIPHIRYMEINTRARTQLISDGGIFDKAVST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLKRAAAGLTYSCLCPPDDLADRGLLGLPGALYAHADALRLWEIIVRYVEGIVH 480
QY 480 LHYKTDAVKDDPELQTCWCREITEIGLOGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 539
Db 481 LFYQRDDIVKGPDLQAWCREITEVGLCAQDRGFPVSFQSOSQLCHFELTMCVFTCTAQH 540
QY 540 ASVHLGOLDWYSWVPNAPCTMRLPPPTTK-DATLETWATLPNFHQASLQMSITWOLGRR 598
Db 541 AAINQGLDWAWVPNAPCTMRMPPTTKEDVTMATVMSGLPDVQACLQMAISWHLSSR 600
QY 599 PWMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKBEIRNAKLDMPYELRPSVVENS 658
Db 601 QDMVPLGHHKEKESGPKPXLVNLQFRITDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663
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RESULT 6

```
US-10-741-601-517
; Sequence 517, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-517
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Query Match 65.9%; Score 2316; DB 16; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;
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```
QY 1 MGLYRIRVSTGASLYAGSNQVQLMWLGQHGAEALGKRLWPARG-ETELKVEVPEYLGPL 59
Db 1 MGRYRIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFHDHVAEDLGLL 60
QY 60 LFKVLKRHLKDDDAWFCNWIWSVOGPGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119
Db 61 QFVRLKHHWLVDDAWFCDRITVQGGCAEAVAFPCYRWVQGGEDILSLPEGTARLPDGN 120
QY 120 QGLFQKHREELERKLYRWGNWKGGLILNAGAKLYDLVPDERFLEDKRVDPEVSLAK 179
```

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Db      121  LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKDDLPNNMRFHEKRLDPENTLKA 180
Qy      180  GLADLAIKDSNLVLTCKWKDLDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db      181  GALEMALKRVTYLLSSWNCLEDFOIIFWQKSALAERKVRQWQDDLEFSYQFLNGANPWL 240
Qy      240  LRRSAHLPARLVFPFGMBELOAQLEKEGGLTLEADSLLDGIIKANVILCSQQHAAAPL 299
Db      241  LRRSTSLPSRLVLPSCMBELOAQLEKELQNGSLFEADFTLLDGIIPANVIRGEKQYLAAPL 300
Qy      300  VMLKLOPDKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
Db      301  VMLKMEPNKGLQPMWIOQPPSPPTFLFSPDPLAWLLAKSWVRNSDFQLHEIQH 360
Qy      360  LLRGHLMAEVIVVATMRCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419
Db      361  LLNTHLVAEVIATVATMRCLPGLHPIFKPLIPIHRYTMEINTRARTQLISDGGIFDKAVST 420
Qy      420  GGGHVQLLKQAGAFITYSSPCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db      421  GGGHVQLLRRAAQLTYCSLCPDDLADRGLLGLPGALYAHDAHLRLWEIIVRYVEGIVH 480
Qy      480  LHYKTDVAVKDDPELOTWCREITBILQGAODRGFPVSIQARDQVCHVFTWCIFCTGQH 539
Db      481  LFYQRDDIVKGDPELOQWCREITEVGLCOADRGFPVSFQSOSQLCHFLTMCVFTCTAQH 540
Qy      540  ASVHLGQLDWMYSWVNPACTMRLPPTTK-DATLETVMATLPHNFHQASLQMSITWQLGRR 598
Db      541  AAINQGQLDWAWVNPACTMWPPTTKEDVTMATVMSLDPDVQACLQMAISWHLSSR 600
Qy      599  QPMVAVGQHEEYFSGPEPKAVLKKFREELAAALKEIERNAKLDMPEYILRPSVENS 658
Db      601  QPMVPLGHKHEKYFSGPKAVLNQFRTDLEKLEKEITARNEQDMDWPEYILKPSCIENS 660
Qy      659  VAI 661
Db      661  VTI 663

```

RESULT 7

```

US-10-741-600-1499
; Sequence 1499, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1499
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1499

```

```

Query Match      65.9%; Score 2316; DB 17; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

```

```

Qy      1  MGLYRIRVSTGASLYAGSNNOVLVQGHGAALGKRLWPARG-ETELKVEVPYVLGFL 59
Db      1  MGRYIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFDDHDAEDLGL 60
Qy      60  LFKLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGSDP 119
Db      61  QFVLRKHHWLVDDAWFCDRITVQGPAGCAEVAFFCYRWVQGEDILSLPEGTARLPDGN 120
Qy      120  QGLFQKHREELERKRLYRWGNWKGILLNAGAKLYDLPLVDRFLDKRVDPEVSLAK 179
Db      121  LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKDDLPNNMRFHEKRLDPENTLKA 180

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Db      121  LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKDDLPNNMRFHEKRLDPENTLKA 180
Qy      180  GLADLAIKDSNLVLTCKWKDLDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db      181  GALEMALKRVTYLLSSWNCLEDFOIIFWQKSALAERKVRQWQDDLEFSYQFLNGANPWL 240
Qy      240  LRRSAHLPARLVFPFGMBELOAQLEKEGGLTLEADSLLDGIIKANVILCSQQHAAAPL 299
Db      241  LRRSTSLPSRLVLPSCMBELOAQLEKELQNGSLFEADFTLLDGIIPANVIRGEKQYLAAPL 300
Qy      300  VMLKLOPDKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
Db      301  VMLKMEPNKGLQPMWIOQPPSPPTFLFSPDPLAWLLAKSWVRNSDFQLHEIQH 360
Qy      360  LLRGHLMAEVIVVATMRCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419
Db      361  LLNTHLVAEVIATVATMRCLPGLHPIFKPLIPIHRYTMEINTRARTQLISDGGIFDKAVST 420
Qy      420  GGGHVQLLKQAGAFITYSSPCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db      421  GGGHVQLLRRAAQLTYCSLCPDDLADRGLLGLPGALYAHDAHLRLWEIIVRYVEGIVH 480
Qy      480  LHYKTDVAVKDDPELOTWCREITBILQGAODRGFPVSIQARDQVCHVFTWCIFCTGQH 539
Db      481  LFYQRDDIVKGDPELOQWCREITEVGLCOADRGFPVSFQSOSQLCHFLTMCVFTCTAQH 540
Qy      540  ASVHLGQLDWMYSWVNPACTMRLPPTTK-DATLETVMATLPHNFHQASLQMSITWQLGRR 598
Db      541  AAINQGQLDWAWVNPACTMWPPTTKEDVTMATVMSLDPDVQACLQMAISWHLSSR 600
Qy      599  QPMVAVGQHEEYFSGPEPKAVLKKFREELAAALKEIERNAKLDMPEYILRPSVENS 658
Db      601  QPMVPLGHKHEKYFSGPKAVLNQFRTDLEKLEKEITARNEQDMDWPEYILKPSCIENS 660
Qy      659  VAI 661
Db      661  VTI 663

```

RESULT 8

```

US-10-741-600-1500
; Sequence 1500, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1500
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1500

```

```

Query Match      65.9%; Score 2316; DB 17; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

```

```

Qy      1  MGLYRIRVSTGASLYAGSNNOVLVQGHGAALGKRLWPARG-ETELKVEVPYVLGFL 59
Db      1  MGRYIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFDDHDAEDLGL 60
Qy      60  LFKLRKRLHLLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGSDP 119
Db      61  QFVLRKHHWLVDDAWFCDRITVQGPAGCAEVAFFCYRWVQGEDILSLPEGTARLPDGN 120
Qy      120  QGLFQKHREELERKRLYRWGNWKGILLNAGAKLYDLPLVDRFLDKRVDPEVSLAK 179
Db      121  LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKDDLPNNMRFHEKRLDPENTLKA 180

```



```
QY 540 ASVHLGOLDWYSWVPNAPCTMELPPTTK-DATLETVMATLPNPHOASIQMSITWQLGRR 598
Db 541 AAINQGOLDWYAWVPNAPCTMRMPPTTKXBDVTXATVMGSLPDVROACLQMAISWHLGRR 600
QY 599 QPVMVAVGQHEEYFSGPEKAVLKKFREELAALDKIEIRNAKLDMPYELRPSWVENS 658
Db 601 QPDMVPLGHKKEKYFSGPKPAVLNQFRDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663

RESULT 10
US-10-926-684-653
; Sequence 653, Application US/10926684
; Publication No. US20050014190A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
; TITLE OF INVENTION: CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/926,684
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/10/170,097
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 653
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 189
; OTHER INFORMATION: Xaa=Arg or His
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 225
; OTHER INFORMATION: Xaa=Asp or His
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 243
; OTHER INFORMATION: Xaa=Arg or Cys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 261
; OTHER INFORMATION: Xaa=Gln or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 322
; OTHER INFORMATION: Xaa=Ser or Asn
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 337
; OTHER INFORMATION: Xaa=Pro or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 362
```

```
; OTHER INFORMATION: Deletion of Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 568
; OTHER INFORMATION: Xaa=Asn or Thr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 574
; OTHER INFORMATION: Xaa=Met or Lys
; US-10-926-684-653
```

Query Match 64.9%; Score 2280; DB 17; Length 663;

Best Local Similarity 64.7%; Pred. No. 1.4e-216; Indels 2; Gaps 2;

Matches 429; Conservative 92; Mismatches 140; Indels 2; Gaps 2;

```
QY 1 MGLYRIRVSTGASLYAGSNQVQLVYGQHGAEALGKRLWPARG-ETELKVEYFYLGLPL 59
Db 1 MGRYIRVATGAWLFSGSYNRVQLVLTGRGAELEQLRPARGEEEFDDHVAEDLGLL 60
QY 60 LFVKLRKRLHLKDDAWFCNWNISVQPGAGDVRFPCTRWVVEGNGVLSLPEGTGRTVGDDP 119
Db 61 QFVRLRKHHWLVDDAWFCDRITVQPGACAFAVFCYRWVQGEDILSLPEGTARLPGNA 120
QY 120 QGLFQKREERELERRKLYRWGNWKGILNMACAKLYDLVDRELFEDKRVDPPEVSLAK 179
Db 121 LDMFQKREKELKDRQYCWATWKEGLPLTIAADRKODDLPPNRFHEEKKLDFEWTLKA 180
QY 180 GLADLAIKDSLNLVLTCKWKLDDFNRIFWCGGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEWALKXVYVTLSSWNLCLEDFQIFWGQKSALAERKVCQWQXELFSYQFLNGANPML 240
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLFEADPSLLDGIKANVILCSQQHAAPL 299
Db 241 LRXSTSLPSRLVLPSPGMEELXQALEKELEQNGSLFEADPILLDGI PANVIRGEKQYLAAPL 300
QY 300 VMLKLPQDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDPQLHELQSH 359
Db 301 VMLKMEPGKLPQPMVIOIQPEXSSPTTFLPSDPLXLAWLAKSWVRNSDFQLHEIQYH 360
QY 360 LLRGLHMAEVIVVATMRCPSIHPFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LANTHLVAEVIATVATMRCPLGHLHPIFKELPHINYTWENTARTQLISDGGIFDKAVST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWEIYRYVEGIVS 479
Db 421 GGGHVQLLRRAAQLTVCSLCPDDLADRGLLGLPGALYAHDAHLRLWEIARYVEGIVH 480
QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGDRGFPVSLQARDQVCHFTWCIFCTCQH 539
Db 481 LFYQRDDIVKGDPELOAWCREITEVGLCQADRGFPVSPQSQCFLFTWCVFCTTAQH 540
QY 540 ASVHLGOLDWYSWVPNAPCTMELPPTTK-DATLETVMATLPNPHOASIQMSITWQLGRR 598
Db 541 AAINQGOLDWYAWVPNAPCTMRMPPTTKXBDVTXATVMGSLPDVROACLQMAISWHLGRR 600
QY 599 QPVMVAVGQHEEYFSGPEKAVLKKFREELAALDKIEIRNAKLDMPYELRPSWVENS 658
Db 601 QPDMVPLGHKKEKYFSGPKPAVLNQFRDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663
```

```
RESULT 11
US-10-498-788-27
; Sequence 27, Application US/10498788
; Publication No. US2005011859A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Narinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
```

APPLICANT: Lee, Ernestine A.
APPLICANT: Forsythe, Ian J.
APPLICANT: Knare, Reena
APPLICANT: Tran, Uyen K.
APPLICANT: Kable, Amy E.
APPLICANT: Richardson, Thomas W.
APPLICANT: Emerling, Brooke M.
APPLICANT: Lindquist, Brika A.
APPLICANT: Baughn, Mariah R.
APPLICANT: Hafalia, April J. A.
APPLICANT: Jin, Pei
APPLICANT: Swarnakar, Anita
APPLICANT: Li, Joana X.
APPLICANT: Marquis, Joseph P.
APPLICANT: Lee, Sally
APPLICANT: Gorvad, Ann E.
APPLICANT: Sprague, William W.
APPLICANT: Becha, Shanya D.
APPLICANT: Elliott, Vicki S.
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: PF-1312 PCT
CURRENT APPLICATION NUMBER: US/10/498,788
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/340,357
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/342,962
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/343,558
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/351,107
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PERL Program
SEQ ID NO 27
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7487231CD1
US-10-498-788-27

Query Match 56.0%; Score 1969; DB 17; Length 399;
Best Local Similarity 94.2%; Pred. No. 4.7e-186;
Matches 374; Conservative 2; Mismatches 7; Indels 14; Gaps 2;
QY 1 MGLYRIVSTGASLYAGSNNOVLWVGQHGAAALGKRLWPARG-BTELKVEVPEYLGPL 59
DB 1 MGLYRIVSTGASLYAGSNNOVLWVGQHGAAALGKRLWPARGKTELEKVEVPEYLGPL 60
QY 60 LFVKLRKRHLKDDAWFCNWSVQGFAGDEVRFPCCYRWVEGNGVLSLPEGTGRTVGEDP 119
DB 61 LFVKLRKRHLKDDAWFCNWSVQGFAGDEVRFPCCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREELBERKLYRWGNWKGILLINMAGAKLYDLPVDERFLEKRYDVFVSLAK 179
DB 121 QGLFQKHREELBERKLYRWGNWKGILLINMAGAKLYDLPVDERFLEKRYDVFVSLAK 180
QY 180 GLADLAIKOSLNVLTCKWLDLDFNRIFWCQSKLAERVRDWSKEDALFGVQFLNGANPVV 239
DB 181 GLADLAIKOSLNVLTCKWLDLDFNRIFWCQSKLAERVRDWSKEDALFGVQFLNGANPVV 240
QY 240 LRSALHLPARLVFPFGMEELQAOLEKEGGTLEADFSLLDGIKANVILCSQOHLAAPL 299
DB 241 LRSALHLPARLVFPFGMEELQAOLEKEGGTLEADFSLLDGIKANVILCSQOHLAAPL 300
QY 300 VMLKQPDGKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 359
DB 301 VMLKQPDGKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 360
QY 360 LLRGHLMAEVI-----VVATWRCLEPSIHP 383
DB 361 LLRGHLMAEVIICGHEVPAVDTSYLOAVNSPPAIHP 397

RESULT 12
US-10-240-305-14
; Sequence 14, Application US/10240305
; Publication No. US20030162193A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; APPLICANT: ANDERSON, WAYNE H.
; APPLICANT: EDWARDS, Lisa D.
; APPLICANT: EMMETT, Amanda H.
; APPLICANT: PILLAI, Sreekumar
; APPLICANT: SPRANKEL, Catherine S.
; TITLE OF INVENTION: Medicine Response Assay in Respiratory Disease
; FILE REFERENCE: P03958 & P04254
; CURRENT APPLICATION NUMBER: US/10/240,305
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-305-14

Query Match 37.0%; Score 1298.5; DB 14; Length 674;
Best Local Similarity 39.7%; Pred. No. 4e-119;
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;
QY 1 MGLYRIVSTGASLYAGSNNOVLWVGQHG---EALGKRLWP--ARGETE-LKVEVPE 54
DB 1 MPSYTVVATGSGWPFAGTDDYIYLSVGSAGSEKHLDDKPFYNDFERGAUDSYDVTYDE 60
QY 55 YLGPILLFVKLRKRHLKDDAWFCNWSVQGFAGDEVRFPCCYRWVEGNGVLSLPEGTGRT 114
DB 61 ELGEIQLVRIEKKRYWLNDDWLVKYLTKTP-HGDIIEFPCCYRWITGDVEVVLDRGAKL 119
QY 115 VGEDPQGLFQKHREELBERKLYRWGNWKGILLINMAGAKLYDLPVDERFLEKRYDVE 174
DB 120 ARDDQIHILKQHRKELETRQYRWMEWNEFPGLSIDAKCHKOLPRIDFDESEKGVDFV 179
QY 175 VSLAKGLADLAIKOSLNVLTCKWLDLDFNRIFWCQSKLAERVRDWSKEDALFGVQFLN 233
DB 180 LNSYKAMENLFINRPMFMFQSSWDFADPEKIFVKISITISERVNMHWQEDLMFGVQFLN 239
QY 234 GANPVILRRSALHLPARLVFPFGMEEL----QAQLEKEGGTLEADFSLLDGIKAN-VI 288
DB 240 GGNPVILRRCTELPEKLPVTTMVECSLERQLSLEQVQGNIFIVDFELLDGIDANKTD 299
QY 289 LCSQOHLAAPLVMLKQPDGKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWR 347
DB 300 PCTLQFLAAPICLLYKNLANKIVPIAIQLNQIP---GDENPILFSDAKYDWLLAKIWR 356
QY 348 SSDFOLHQLSHLLRGHLMAEVIIVVATWRCLEPSIHPFKLIIPHLRYTLEINVRARTGLV 407
DB 357 SSDFVHQTITHLKTHLVSEVFGTAMVRLQDPAVHPIFKLLVAHVRFITAITNKAREQLI 416
QY 408 SDMGIFDQIMTSGGGHVQLLKQAQAFITYSSFCPPDDLLADRLGLG---VKSSEFYAQDAL 464
DB 417 CECGLFDRANATGGGGHVQV 476
QY 465 RWELIYRVVEGIVSLHYKTVAVKDDPELQVTCREITEIGLQAGQODRQFPVSLQARDQV 524
DB 477 LWWEAIRFTAEBVDIYEGDQVVEEDPELQVFNVDVYVYVYVYVYVYVYVYVYVYVYV 536
QY 525 CHFTVMCIPTCTGQHASVHLGOLDWYSWVPNAPCTWRLPPPTTKD-ATLETVMATLNPFH 583
DB 537 SYLTVVIFTAQAHAANFGQYDWCWMTIPNAPPTTRAPPPTAKGVVITIEQVITLDPDRG 596
QY 584 QASLQMSITWQGRQRPVAVQGHREYFSGPEPKAVLKPFREBLAALDKKEIERNAKL 643
DB 597 RSCWHLGAVWALSQFQENELFLGMYPESHFIEKPYKEAMARFRKNLEAIVSIAERNKKK 656

QY 644 DMPYELRPSVVENSVAI 661
 Db 657 QLPYYLSPDRIPNSVAI 674

RESULT 13
 US-10-485-310-22
 ; Sequence 22, Application US/10485310
 ; Publication No. US20040234990A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Takeda Chemical Industries, Ltd.
 ; TITLE OF INVENTION: A Method For Screening A Gene Related To Alzheimer's Disease
 ; FILE REFERENCE: P01-0277PCT
 ; CURRENT APPLICATION NUMBER: US/10/485,310
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 22
 ; LENGTH: 674
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-485-310-22

Query Match 37.0%; Score 1298.5; DB 16; Length 674;
 Best Local Similarity 39.7%; Pred. No. 4e-119;
 Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;
 QY 1 MGLYRIRVSTGASLYAGSNQVQLWVGQHG---EAALGKRLWP--ARGETE-LKVEYPE 54
 Db 1 MPTVTVTWSQWFAAGTDDYIYLSVGSAGCKSKHLLDKPPYNDFERGAVDSYDVTVD 60
 QY 55 YLGPLLFLVKLRKHLLKDDAWFCNWSVQGGAGDEVFPFCYRWVEGVNLSLPGTGRT 114
 Db 61 ELGEIQLVRIEKKRYWLNDDWYLYITLKP-HGDIYIEFPFCYRWITGDVEVVLDRGAKL 119
 QY 115 VGEDPQGLFOKHREBELERKLYRWGNWKGILLNMAGAKLYDLPVDERFLEDKRVDFE 174
 Db 120 ARDDQIHLKQHRKELETRQYRWMEWNPFPPLSIDAKCHKDLPRIQDSEKGVDFV 179
 QY 175 VSLAKGLADLAIKSLNVL-TCKDLDNFRIFWCGSKLAERVRDSWKEDALFGYQFLN 233
 Db 180 LNYSKAMENLFNRRFMHMFQSSWDFADFEKIFVKISNTISERVNHNQEDLMFGYQFLN 239
 QY 234 GANPVVLRSAHLPARLVFPQMBEL-----QAQLEKELEGGLTFEADPSLLDGIKAN-VI 288
 Db 240 GCNPVLIIRCTELPEKLPVTTEWVECSLERQLSLEQVQOQGNIFIVDFELLDGIDANKTD 299
 QY 289 LCSQQLAALPVLMLKLPDQKLLPMVIOL-QLPRTGSPPPPLFLPTDPPMAWLLAKVWR 347
 Db 300 PCTQLFLAIPICLLYKLNKLVPIAIQNLQIP---GDNPIFLPSDAKYDWLLAKIWR 356
 QY 348 SSDFQLHQLSHLLRGHLMAEIVVATWRCPLSIHPIFKLIIPHLYRTLEINVRARTGLV 407
 Db 357 SSDFHVHQTITHLATHLVSEVFGIAMYRQLPAVHIPFKLLVAHVFTIAINTKAREQLI 416
 QY 408 SDMGIFDQIMSTGGGHVQLLKQAGAFITYSSFCPPDDLDLADRLGLG---VKSSFYAQQAL 464
 Db 417 CECGLFDKANATGGGHVQVQRAMKDLTYASLCFPEAIKARGMESKEDIPIYFYRDDGL 476
 QY 465 RLWELIYRVVEGIVSLHYKTVAVKDDPELOQWCREITEIGLQAGDRGFPVSLQARDV 524
 Db 477 LWWEAIRFTFAEVVDIYEGDQVVEEDPELOFVNDVYVYGMGRKSSGFPKSVKSRQL 536
 QY 525 CHFVTWCIPTCTGQHASVHLGQDWYSWVPNAPCTMRLPPPTTKD-ATLETWMTLPNPH 583
 Db 537 SEYLTWIFTASAQAANVFNQYDWCWIPNAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 596
 QY 584 QASLQWISITWQGRQPVVAVQHEEYFSGPEKPAVLKKFRELAALDKIEIRNAKL 643
 Db 597 RSCWHLGAWWALSQFQENELFGWYPEEHFIEKPVKEAMARFKKNLEIVSVIAERNKK 656
 QY 644 DMPYELRPSVVENSVAI 661
 Db 657 QLPYYLSPDRIPNSVAI 674

RESULT 14
 US-10-240-305-16
 ; Sequence 16, Application US/10240305
 ; Publication No. US20030162193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GLAXO GROUP LIMITED
 ; APPLICANT: ANDERSON, WAYNE H.
 ; APPLICANT: EDWARDS, Lisa D.
 ; APPLICANT: EMMETT, Amanda H.
 ; APPLICANT: PILLAI, Sreekumar
 ; APPLICANT: SPRANKEL, Catherine S.
 ; TITLE OF INVENTION: Medicine Response Assay in Respiratory Disease
 ; FILE REFERENCE: P03958 & P04254
 ; CURRENT APPLICATION NUMBER: US/10/240,305
 ; CURRENT FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 663
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-240-305-16

Query Match 35.9%; Score 1261.5; DB 14; Length 663;
 Best Local Similarity 39.6%; Pred. No. 1.8e-115;
 Matches 262; Conservative 136; Mismatches 242; Indels 21; Gaps 11;
 QY 18 SNNOVQLWLVGQHG---EAALGKELWP--ARGETE-LKVEYPEVILGPLLFLVKLRKHLLK 71
 Db 7 TDDYIYLSVGSAGCKSKHLLDKPPYNDFERGAVDSYDVTVDDELBGEIQLVRIEKKRWL 66
 QY 72 DDWFCNWSVQGGAGDEVFPFCYRWVEGVNLSLPGTGRTVGEDPQGLFOKHREBEL 131
 Db 67 NDDWLYKYITLKP-HGDIYIEFPFCYRWITGDVEVVLDRGAKLARDQDIHLKQHRREL 125
 QY 132 EERKLYRWGNWKGILLNMAGAKLYDLPVDERFLEDKRVDFEVS LAKGLADLAIKDSL 191
 Db 126 ETRQYRWMEWNPFPPLSIDAKCHKDLPRIQDSEKGVDFVLYNYSKAMENLFNRRFMH 185
 QY 192 VL-TCKDLDNFRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVVLRSAHLPARL 250
 Db 186 MFQSSWDFADFEKIFVKISNTISERVNHNQEDLMFGYQFLNGCNPVLIIRCTELPEKL 245
 QY 251 VFPQMBEL-----QAQLEKELEGGLTFEADPSLLDGIKAN-VILCSQQLAALPVLMLK 305
 Db 246 PVTTEWVECSLERQLSLEQVQOQGNIFIVDFELLDGIDANKTDPTQLQFLAIPICLLYKN 305
 QY 306 PDGKLLPMVIOL-QLPRTGSPPPPLFLPTDPPMAWLLAKCWWRSSDPQLHQLSHLLRGH 364
 Db 306 LANKIVPIAIQNLQIP---GDNPIFLPSDAKYDWLLAKIWRSSDFHVHQTITHLRTH 362
 QY 365 LMAEIVVATWRCPLSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMSTGGGH 424
 Db 363 LVSEVFGIAMYRQLPAVHIPFKLLVAHVFTIAINTKAREQLICECGLFDKANATGGGH 422
 QY 425 VQLLKQAGAFITYSSFCPPDDLDLADRLGLG---VKSSFYAQQALRLWELIYRVVEGIVSLH 481
 Db 423 VQVQRAMKDLTYASLCFPEAIKARGMESKEDIPIYFYRDDGLLWWEAIRFTFAEVVDIY 482
 QY 482 YKTDAVAKDDPELOQWCREITEIGLQAGDRGFPVSLQARDVCHVFTWCIPTCTGQHAS 541
 Db 483 YEGDQVVEEDPELOFVNDVYVYGMGRKSSGFPKSVKSRQLSEYLTWIFTASAQA 542
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 QY 601 VMVAVGQHEEYFSGPEKPAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENSVA 660
 Db 603 NELFLGMPPEEHFIEKPVKEAMARFKKNLEIVSVIAERNKKQLPYIYLSFDRI 662

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 11:52:27 ; Search time 6694.65 Seconds

(without alignment)
18330.926 Million cell updates/sec

Title: US-10-688-676A-3

Perfect score: 3224

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hlc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3218.4	99.8	3269	3 AK028724	AK028724 Mus muscu
2	1101	34.2	2965	3 BC033294	BC033294 Homo sapi
3	1041.2	32.3	2612	3 AK076343	AK076343 Mus muscu
4	704.4	21.8	720	9 BX972732	BX972732 Reverse s
5	641	19.9	659	5 BP766317	BP766317
6	606	18.8	655	1 AV241044	AV241044 AV241044
7	586.8	18.2	648	2 BB613007	BB613007 BB613007
8	578.4	17.9	892	4 BG743633	BG743633 602633993
9	571.8	17.7	833	4 BG675395	BG675395 602621712
10	571.6	17.7	2136	9 AY415194	AY415194 Homo sapi
11	566.2	17.6	685	2 BB612677	BB612677 BB612677
12	558.8	17.3	876	4 BG674800	BG674800 602620931
13	558.6	17.3	2136	9 AY415196	AY415196 Mus muscu
14	539	16.7	863	4 BG696031	BG696031 602658180
15	529.8	16.4	875	5 BX371550	BX371550 BX371550
16	527.8	16.4	840	4 BG740579	BG740579 602633094
17	525.6	16.3	732	6 CB518927	CB518927 UI-N-GHO-
18	525.6	16.3	832	4 BG598185	BG598185 602660087
19	524.2	16.3	916	4 BG739941	BG739941 602630892
20	520.6	16.1	865	4 BG742611	BG742611 60263205
21	520.6	16.1	881	5 BX371551	BX371551 BX371551
22	517.6	16.1	893	4 BG741964	BG741964 602633405
23	516.2	16.0	845	4 BG740763	BG740763 602632735
24	512.4	15.9	843	4 BG739709	BG739709 602630403

25	495.2	15.4	761	4 BG740246	BG740246 602630664
26	492.4	15.3	494	2 BF789593	BF789593 602103693
27	491.4	15.2	697	4 BG739860	BG739860 602630592
28	478	14.8	1057	5 BX343731	BX343731 BX343731
29	464.6	14.4	2125	9 AY415195	AY415195 Pan trogl
30	463.8	14.4	885	4 BG743327	BG743327 602634623
31	460.2	14.3	637	1 AV241224	AV241224 AV241224
32	453	14.1	464	1 AA117154	AA117154 mo60d12.r
33	436.6	13.5	605	4 BI489877	BI489877 603031627
34	421.2	13.1	580	5 BP326139	BP326139 BP326139
35	414.6	12.9	867	4 BG697910	BG697910 602661342
36	414	12.8	850	4 BG675344	BG675344 602621653
37	409.8	12.7	678	6 CA405703	CA405703 1001852 H
38	396.8	12.3	1826	3 BC040450	BC040450 Homo sapi
39	396.8	12.3	1844	3 BC034464	BC034464 Homo sapi
40	391.4	12.1	585	5 BP306241	BP306241 BP306241
41	366	11.4	377	1 AA117205	AA117205 mo61e01.r
42	362.2	11.2	862	4 BG740949	BG740949 602634555
43	357.2	11.1	583	6 CD610811	CD610811 56004502H
44	351	10.9	604	6 CD610812	CD610812 56004502J
45	349.4	10.8	601	7 CV029325	CV029325 8061 Full

ALIGNMENTS

RESULT 1	AK028724	3269 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK028724	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732445G22 product:arachidonate 15-lipoxygenase, second type, full insert sequence.			
ACCESSION	AK028724	1	GI:26324661		
VERSION	AK028724	1	GI:26324661		
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research				

QY 1145 GCTGTACACATCTGCTGATGCCCATCTGATTCCAGAAAGTCTTTGCTTGGCCACATTA 1204
DB 1141 GCTGTACACATCTGCTGATGCCCATCTGATTCCAGAAAGTCTTTGCTTGGCCACATTA 1200
QY 1205 CGTCAGCTGCCCTAGGTGTACACCTCTCTTCAAGCTATTGATTCCTTCAATTCGGGTACACA 1264
DB 1201 CGTCAGCTGCCCTAGGTGTACACCTCTCTTCAAGCTATTGATTCCTTCAATTCGGGTACACA 1260
QY 1265 CTGCACATCAACACGCTTGGCCGGGAGTGTCTGTTGGCCCTGGGAAGTGTGATAGACAAG 1324
DB 1261 CTGCACATCAACACGCTTGGCCGGGAGTGTCTGTTGGCCCTGGGAAGTGTGATAGACAAG 1320
QY 1325 TCCACAGGCTTGGCACTGGGGGATCTCTGACCTGTATAAGAGAAACATGAGCAGCTG 1384
DB 1321 TCCACAGGCTTGGCACTGGGGGATCTCTGACCTGTATAAGAGAAACATGAGCAGCTG 1380
QY 1385 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCCA 1444
DB 1381 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCCA 1440
QY 1445 GGCTACTATTACCGAGATGATGGGATGCGATCTGGGGGGCAATAAGAGCTTTGTCTCT 1504
DB 1441 GGCTACTATTACCGAGATGATGGGATGCGATCTGGGGGGCAATAAGAGCTTTGTCTCTCT 1500
QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTCACATCCGTCCAAGATGACCAAGAGCTCCAG 1564
DB 1501 GAAATAGTCAGCATCTACTATCCAAAGTCACATCCGTCCAAGATGACCAAGAGCTCCAG 1560
QY 1565 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCCGAGAAAGCTCAGGTATGCC 1624
DB 1561 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCCGAGAAAGCTCAGGTATGCC 1620
QY 1625 TCCTTTGTTGGATACCCGGGAAGCCCTGTCCAGTATATCAACATGGTGATATCACTTCG 1684
DB 1621 TCCTTTGTTGGATACCCGGGAAGCCCTGTCCAGTATATCAACATGGTGATATCACTTCG 1680
QY 1685 TCAGCAGCATGACGTGTCAGTTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCCAAT 1744
DB 1681 TCAGCAGCATGACGTGTCAGTTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCCAAT 1740
QY 1745 CTGCCACCTACCATGACGTACCAACCACTACTTCCAAAGGCCAGGCCCGCTCGAGAGT 1804
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DB 1921 GAGGATGCCCCCGGGAAGCGTGGCTGCTCTCCAGAGAAAGCTGATCCAGATCTCCAAG 1980
QY 1985 GGCAATCAGGGAGAGAACCGAGGCCCTGSCACTGCCCTACACTTGGATCTCTCCCTC 2044
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QY 2045 ATTGAGAACAGTGTCTCATCTTAACATCTTGGAGAGACAGTCTGTGTGATATAGAA 2104
DB 2041 ATTGAGAACAGTGTCTCATCTTAACATCTTGGAGAGACAGTCTGTGTGATATAGAA 2100
QY 2105 CTCTTTGACCATGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACACCAAGCCCC 2164
DB 2101 CTCTTTGACCATGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACACCAAGCCCC 2160
QY 2165 ATCTTTACACACACACACACACACACCTTAATAAATAAGAAACAGAAAAACCTTAACT 2224
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QY 2225 CCCACAGAGGCAAGATCTCTCACAGCAGAGAGGCAATCCAAATGTTTGGAGACCTGAGC 2284

RESULT 2

BC033294 2965 bp mRNA linear HTC 19-NOV-2003
LOCUS Homo sapiens arachidonate 15-lipoxygenase, second type, mRNA (cdna
DEFINITION clone IMAGE:4780620), with apparent retained intron.

DB 2221 CCCACAGAGGCAAGATCTCACACAGCAGAGAGCCATCCAAATGTTTGGAGACCTGAGC 2280
QY 2285 TTCAGCTCTGATTAAACGGCTTTGCTGTTGCTTTGCTTTCTATTCCATTAAACCATGAC 2344
DB 2281 TTCAGCTCTGATTAAACGGCTTTGCTGTTGCTTTGCTTTCTATTCCATTAAACCATGAC 2340
QY 2345 GGTAAACAGAAAGCAGACAGACCTCGTTCACTGCAAAAGCCACTGAGATCTCACCTCAC 2404
DB 2341 GGTAAACAGAAAGCAGACAGACCTCGTTCACTGCAAAAGCCACTGAGATCTCACCTCAC 2400
QY 2405 CTGACACAAAGGCGAGCTTATCATACAGGCTTATCAGGAACACAGAAATTTGTCCAAATCAA 2464
DB 2401 CTGACACAAAGGCGAGCTTATCATACAGGCTTATCAGGAACACAGAAATTTGTCCAAATCAA 2460
QY 2465 GCCTACCCACTAGTGTCCATCGTGACCTACGACCTCACTGGCATGCTTTAGCTTTGAGA 2524
DB 2461 GCCTACCCACTAGTGTCCATCGTGACCTACGACCTCACTGGCATGCTTTAGCTTTGAGA 2520
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DB 2521 AGGGAATTACTGGAGTCAGGTACGAGAGAGGAGCAGGACGAGGAGGCTCCATGTCGA 2580
QY 2585 AGAACATATCTGCTTTCCAGATGACCCAGGCTAGCTCACGCCATGTCTCAATCTCTAACTC 2644
DB 2581 AGAACATATCTGCTTTCCAGATGACCCAGGCTAGCTCACGCCATGTCTCAATCTCTAACTC 2640
QY 2645 CAGAGGCTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACAGTAGACACCA 2704
DB 2641 CAGAGGCTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACAGTAGACACCA 2700
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DB 2761 TGACGTGCTCTCCAGAGATCTGAGTTCAATTCGCCAGCAACCACTGGTGCTCACACACC 2820
QY 2825 ATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCGACAGTGTATGCA 2884
DB 2821 ATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCGACAGTGTATGCA 2880
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DB 2881 CATATATAAATAAATAAATCTTTAAATAAACAAGAGAGAGGAGCATGTACCAAT 2940
QY 2945 TCTACCTCACTTCTCTCAAGCCACCCCTAAAGTGAATTTGTGAACCCAGGTCCTCTTGC 3004
DB 2941 TCTACCTCACTTCTCTCAAGCCACCCCTAAAGTGAATTTGTGAACCCAGGTCCTCTTGC 3000
QY 3005 AGAGAGTTAGAAGATATTCTCAAACTCTAATACCTTCAATCTTCAATCTTCAATCTTCAAT 3064
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QY 3065 CCAAAATTCOAATTTTATATACATCTCCAGTTTGGTGGTGGGTTGTTTTGT 3124
DB 3061 CCAAAATTCOAATTTTATATACATCTCCAGTTTGGTGGTGGGTTGTTTTGT 3120
QY 3125 TTGGTTTGGTTGGTGGGTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 3184
DB 3121 TTGGTTTGGTTGGTGGGTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 3180
QY 3185 CTCATCGAGCGTTCAATTAATGTATAAATGAGTTCAATTC 3224
DB 3181 CTCATCGAGCGTTCAATTAATGTATAAATGAGTTCAATTC 3220

ACCESSION	BC033294	Matches 1674; Conservative 0; Mismatches 415; Indels 294; Gaps 3;
VERSION	BC033294.1 GI:23959040	
KEYWORDS	HTC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 2965)	
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, S.I., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Lequellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE	22388257	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2965)	
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIA-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov Series: IRAC Plate: 29 Row: m Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557308 This clone has the following problem: retained intron.	
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	/note="Vector: pCMV-SPORT6.1"	
ORIGIN	Query Match 34.2%; Score 1101; DB 3; Length 2965; Best Local Similarity 70.2%; Pred. No. 6.8e-279;	

QY	7	GCAGTAGAGAGCTAAACT--GGTCAGAGGAGATGGCGAAATGCAGGGTGAGAGTATCCACG	64
DB	26	GCCTAGAGAGCTGGACTTAGCTGGCAGCATGGCCGAGTTCAGGGTCAGGGTGTCACAC	85
QY	65	GGGGAAGCCTGTGGGGCTGGGCACATGGGACAAAGTGTCTGTGAGCATGTGGGAACCCAC	124
DB	86	GGAGAAGCCTTCGGGGCTGGGCACATGGGACAAAGTGTCTGTGAGCATGTGGGACCCCG	145
QY	125	GGAGAGACCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCAGCGCCGGTCTGTAA	184
DB	146	GGAGAGACCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCAGCGCCGGTCTGTAA	205
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QY	305	CGCTGTTTCGAGCTGGAGTGGTACTCTGGGCTGCACCTCCACTTCCCTGTTTATCAGTGG	364
DB	323	CGCTGTTTCGAGCTGGAGTGGTACTCTGGGCTGCACCTCCACTTCCCTGTTTATCAGTGG	382
QY	365	CTGGAAGGGGGGGGAGCTGTGTCTGAGAGAGGAGGAGCAAGAGTGTCTCTGGCAAGAC	424
DB	383	CTGGAAGGGGGGGGAGCTGTGTCTGAGAGAGGAGGAGCAAGAGTGTCTCTGGCAAGAC	442
QY	425	CATCACCTTACATCTCAGGATCAGCGCCAGAAAGAGTGTAGTCCAGGACAGAGATGTAC	484
DB	443	CACCACTTGTCTCAGCAACAGCGCCAGGAGGAGTTCAGGCGCGGAGGAGATGTAC	502
QY	485	AGCTGGAAGACTTACATTTGAAGTGGCTCGCTGCTGACCAAGAGTGTCTGGAAGAC	544
DB	503	CAGTGGAAAGGCTTACACCCAGGTTGGGCTCACTGCTGAGTGAAGAGACAGTGGAAAGAC	562
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QY	613	-----TAC	615
DB	863	GAAGGCTCTCCAGGGGCTCTCTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCC	922
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QY 976 GATGACCTGTGTACACAGAGCTCAGGTCCGAGCCCTGCTTCCCATTTGCAATCCAGCT 1035
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QY 1576 GGAGATCTCTCTGAGGCTCTCTCGGCGGAGAAAGCTCAGGTATGCCCTCTGTTGGGA 1635
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QY 1636 TACCGGGAAGCCCTGCTCCAGTATATCAACATGCTGATATTCACCTGCTCAGGCAAGCA 1695
Db 1943 GACCGGGAAGCCCTGCTGCAAGTATGTCAACATGCTGATATTCACCTGCTCGGCAAGCA 2002
QY 1696 TGCAGCTCTCAGTTCCAGGCTCAGTCTCTGTTGTTGGATGCCCAATCTGCCACCTAC 1755
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QY 1816 GCTCCACAGTAACTGCTCAAGTTATACATCATCTCTGCTGCTGCTCAAGCGAGA 1875
Db 2123 CTTCCCACTCTCAATGCCACATGTGATCTATCTCTGCTGCTGCTGCTGAGCAAGGA 2182

QY 1876 ACTGGGACCNAGGCCCTCGGCACTATCCAGATGACACATTCACAGAGGATGCCCC 1935
Db 2183 GCCTGGAGACCAAGAGGCCCTCGGCACTATCCGAGTGAACATTCACAGAGGAGGCCCC 2242
QY 1936 CCGCGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAGGCGCATCAGGA 1995
Db 2243 TCGCGGAGGATCGCCACCTTCCAGAGCCGCTGCGCCAGATCTCGAGGGGCAATCCAGGA 2302
QY 1996 GAGAACCGAGGCTGCGACCTGACCTACCTACCTGATCTCCCTCATTTGAGAACAG 2055
Db 2303 GCGGAACCGGCGCTGCTGCTGCTACCTACCTAGACCTCCCTCATTCGAGAACAG 2362
QY 2056 TGTCTTCATCTAATCATCTTGGAGAGAGCTGCTGCTGATGAT 2098
Db 2363 CGTCTCATCTAATCTCCAGGGGAACACAGGCCCATGATGAT 2405

RESULT 3
AK076343
LOCUS
DEFINITION Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:473247A14 product:arachidonate 15-lipoxygenase, second type, full insert sequence.
ACCESSION AK076343.1 GI:26096751
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861

REFERENCE
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12012122

REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,


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QY 2451 TTGTGCCATCAAGCCTACCTAGCTAGTCCATCTGACCTAGCAGCTCAGCTGGCATG 2510
Db 67 TTGTGCCATCAAGCCTACCTAGCTAGTCCATCTGACCTAGCAGCTCAGCTGGCATG 126

QY 2511 CTTTGTAGCTTTGAGAGGAGTACTGAGTCAAGTACAGTACAGGAGGAGGAGGCA 2570
Db 127 CTTTGTAGCTTTGAGAGGAGTACTGAGTCAAGTACAGTACAGGAGGAGGAGGCA 186

QY 2571 TGGCTCCATGTGGAAGAACATATCTGCTCTTCCAGATGACAGGGTAGCTCAGCCCATG 2630
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QY 2691 ACCAGTACACCAAAATATATCTTTTAAAGAGAGGAGGAGTGGCTGGAGAGATGGCTCA 2750
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QY 2871 CGACAGTGTATGCATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2930
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Db 547 GACATGCTACCATTTCTACCTCAGCTCTTCTCAAGCCACCCCTAAAGTGAATTTGTAAC 606

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RESULT 5
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LOCUS          BP766317 mouse (C57BL/6) pancreatic islet library with
DEFINITION      recombination-based method Mus musculus cDNA clone mid10051 3',
                mRNA sequence.
ACCESSION      BP766317
VERSION        BP766317.1 GI:50225015
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 659)
AUTHORS        Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
                Takeda,J., Ohara,O. and Seino,S.
```

Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray

Unpublished (2004)

Contact: Susumu Seino
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Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

Location/Qualifiers

1. 659

Source

/organism="Mus musculus"

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Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2644 CCAGAGGTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACCAGTAGACACC 2703
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QY 2764 CTGACTGCTCTTCCAGAGATCTGAGTTCATTTCCAGCAACCAATGCTGGCTCAGACAC 2823
Db 479 CTGACTGCTCTTCCAGAGATCTGAGTTCATTTCCAGCAACCAATGCTGGCTCAGACAC 420

QY 2824 CATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGGAGGAGTGTATGC 2883
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QY 2884 ACATATATAAATAAATAAATCTTTTAAATAAACAAGAGAGAGGAGGAGTGTATGCAT 2943
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QY 2944 TTCTACCTCAGTCTTCTCAAGCCACCCCTAAAGTGAATTTGTGACAGGTCCTCCCTTTG 3003
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QY 3004 CAGAGAGTTAGAAGATATTTCTCAAACTCTAATACCTTCAATCTTAAATCCATCTTCAT 3063
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QY 3064 TCCAAAATTCGAATTTTATATACATCTCCAGTTTGGTGGGAGGGGTTGTTTTTGG 3123
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RESULT 6
AV2411044
LOCUS
DEFINITION
musculus cDNA full-length enriched, 10 day neonate skin Mus
8S-lipoxygenase mRNA, mRNA sequence.
AV2411044
AV241044.2 GI:15405182
EST.
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 655)
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Nov 1, 1999 this sequence version replaced gi:6193546.
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
FEATURES
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAAAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGAGTTAATAATATTCCTCCCTCCCTCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLIC 1"
ORIGIN
Query Match 18.8%; Score 606; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.6e-148;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2619 CTCACAGCCATGTGTCAATTCCTCCAGAGGTCTCTAGTGGCCATGAAGATCCAGGCA 2678
Db 1 CTCACAGCCATGTGTCAATTCCTCCAGAGGTCTCTAGTGGCCATGAAGATCCAGGCA 60
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QY 2739 AGAGATGGCTCAGCGGTTAAAGACGACTGCTCTCCAGAGATCCTGAGTTCAATTCC 2798
Db 121 AGAGATGGCTCAGCGGTTAAAGACGACTGCTCTCCAGAGATCCTGAGTTCAATTCC 180
QY 2799 CAGCAACCAATGTFGGGTCTCAACCATCTGTAATGGAGTTCGATGCCCTCTTCTGGCGT 2858
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QY 3219 CATTCC 3224
Db 601 CATTCC 606
RESULT 7
BB613007
LOCUS
DEFINITION
BB613007 RIKEN full-length enriched, 10 day neonate skin Mus
648 bp mRNA linear EST 31-AUG-2001
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musculus cDNA clone 4732445G22 5', mRNA sequence.

ACCESSION
BB613007
VERSION
BB613007.1
KEYWORDS
GI:15395393
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 648)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kondo, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE
COMMENT

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES
source

Location/Qualifiers
1..648
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATAATTAATTCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC 1"

ORIGIN

Query Match	18.2%	Score 586.8;	DB 2;	Length 648;
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Matches 617;	Conservative 0;	Mismatches 13;	Indels 3;	Gaps 2;

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Db	61	GGGGAAGCCTCTGGGGCTGGGCACATGGCAACAAGTCTGTCCAGCATCGTGGGAACCCAC	120
QY	125	GGAGAGAGCCCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCAGGCGCCGCTGCTGAA	184
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QY	604	CTCCGCGTATACGG--AGCTGAAAGTCAAAAGGG	634
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602633993F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778998 5', mRNA sequence.
BG743633
ACCESSION
BG743633.1
VERSION
BG743633.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 892)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 852.

FEATURES
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 17.9%; Score 578.4; DB 4; Length 892;
Best Local Similarity 79.3%; Pred. No. 5.6e-141;
Matches 698; Conservative 0; Mismatches 181; Indels 1; Gaps 1;

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|||||

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DB 481 GATCTTCTCAAGGGGCTTCTTAACCCAGGAGAGCTCAGGTATACCTCTCTCACTGAGAC 540
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QY 1639 CCGGGAAGCCCTGGTCCAGTATATCACCATGGTGTATTTCACTGCTCAGCCAAAGCATGC 1698
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DB 541 CCGGGAAGCCCTGGTGCAGTATGTCAACCATGGTGTATTTCACTGCTCAGCCAAAGCATGC 600
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Db 601 GGCTGTCACTGAGGGCAGTTTGACTCTCTGTGCTTGGATGCCCAACCTGCCACCAGCAT 660
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1818 TCCACAGCAGTTAAATTCGTCAAGTTATCAATCATTTGCTCTCTGGTGTCTTAAGCGCAGAAC 1877
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ACCESSION BG675395
VERSION BG675395.1 GI:13906791
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 17.7%; Score 571.8; DB 4; Length 833;
Best Local Similarity 82.1%; Pred. No. 3e-139;
Matches 682; Conservative 0; Mismatches 147; Indels 2; Gaps 2;

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DB 1 GGCATCTCTCTGGCATCCAGACCAATGTCTATTATGGAAAGCCCTCAGTTCTTCGGGCC 60
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QY 974 CGATGACCTCTGTATACACAGAGCTCAGGCTCCGACCCCTCTTCCCATTCGCCATCCAG 1033
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DB 61 CCAATGACCTCTGTATACAGAGCCAGGCTGGGGCGCTGCTGCTCTCGCCATCCAG 120
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QY 1034 CTCAAACAGATCCCGGGCCAGAACCCCATCTTCTTCCGCCAGCATGACAGTGGGAC 1093
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Db	720	GAGACCCGGGAG-CTGGTGCAGTATGTCACATGATGATGATGATGATGATGATGATGAT	778
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LOCUS	AY415194	Homo sapiens ALOXE3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	
DEFINITION	AY415194.1	GI:39771153	
ACCESSION	AY415194	GSS.	
VERSION	AY415194.1	GI:39771153	
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ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 2136) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 2136) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		

Adams M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 1..2136 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>2136 /gene="ALOXE3" /locus_tag="HCM5476"	Query Match Best Local Similarity 58.2%; Pred. No. 4.7e-139; Matches 845; Conservative 0; Mismatches 605; Indels 3; Gaps 1;	17.7%; Score 571.6; DB 9; Length 2136; 58.2%; Pred. No. 4.7e-139; 0; Mismatches 605; Indels 3; Gaps 1;
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Db	1047	ACTGTGCTGCTGGGCTCAGCCCCCAG--GGGGCGTGGTGGCTTGGCCATCCAGCT 1103
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Qy      2056  TGTCTCCACTATA 2068
Db      2124  CGTCTCCACTATA 2136

RESULT 11
LOCUS   BB612677
DEFINITION BB612677 RIKEN full-length enriched, 10 day neonate skin Mus
ACCESSION BB612677
VERSION   BB612677.1 GI:16453554
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS  Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, K., Sakai, C., Sakai, K.,
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Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATCTCGAGTTAATAATATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC 1"

ORIGIN
Query Match 17.6%; Score 566.2; DB 2; Length 685;
Best Local Similarity 97.7%; Pred. No. 8.6e-138;
Matches 585; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL 1 (bases 1 to 863)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li W.B., Gruber C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30433898.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8973.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA1018ZA06_CS01673_1&c=8973.f
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GenCore version 5.1.6
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(without alignment)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3178	98.6	3205	10	MMU93277	U93277 Mus musculus
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6	1792.8	58.6	2244	10	AP415240	AP415240 Rattus no
7	1398.4	43.4	2673	9	BC035217	BC035217 Homo sapi
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11	1395.2	43.3	2685	6	AX770522	AX770522 Sequence
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KEYWORDS	Mus musculus (house mouse)					
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AUTHORS		cDNA cloning of a 8-lipoxygenase and a novel epidermis-type				
TITLE		lipoxygenase from phorbol ester-treated mouse skin				
JOURNAL		Biochim. Biophys. Acta 1391 (1), 7-12 (1998)				
MEDLINE		98186642				
PUBMED		9518531				
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AUTHORS		Direct Submission				
TITLE		Submitted (26-AUG-1997) P. Krieg, German Cancer Research Center,				
JOURNAL		Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg,				
REMARK		Revised by [3]				
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AUTHORS		Krieg,P.				
TITLE		Direct Submission				
JOURNAL		Submitted (29-OCT-1997) P. Krieg, German Cancer Research Center,				
REMARK		Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg,				
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VERSION ARI42986.1 GI:15104272
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3205)
AUTHORS Brash,A.R., Boeglin,W.F. and Jisaka,M.
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AUTHORS Braah,A.R., Boeglin,W.E. and Jisaka,M.
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Db	1741	ACTT CCAA AGG CCAG CCCG GCTG AGAGT TTT CATAG CCAC CGT CC CAG CAGT TAAT TCG	1800
QY	1835	TCA AGT TAT CAC ATCAT TGCT CTG GCTG CTAAG CGCAG AACT TGG GAC CAAA AGGCC	1894
Db	1801	TCA AGT TAT CAC ATCAT TGCT CTG GCTG CTAAG CGCAG AACT TGG GAC CAAA AGGCC	1860
QY	1895	CT GGG CCACT ATCC AGATG AACTTT CAC AGAGT GCCCC CGG CGAAG CGTGG CTGCC	1954
Db	1861	CT GGG CCACT ATCC AGATG AACTTT CAC AGAGT GCCCC CGG CGAAG CGTGG CTGCC	1920
QY	1955	TT CCAG AGAA GCTG ATCC AGAT CTCC AA GGG CATC AGG AGG AA CCG AGG CTGG CA	2014
Db	1921	TT CCAG AGAA GCTG ATCC AGAT CTCC AA GGG CATC AGG AGG AA CCG AGG CTGG CA	1980
QY	2015	CT GGC CTAC ACCT ACCT GATCT CCCT CTCAT TTG AGAA CAGT GTCT CCATCT TAA CATCTT	2074
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QY	2075	GG AGA AGAC AGTCT GTGT GACATATAG AACT CTT GACCAT GCTCT CCAGG CTAAGTCC	2134
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Db	2101	CC GTAT GCTT CTCT GG ACAA CCAA GCCCC CATCTT ACACACACACACACACACACAC	2160
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Db	2161	TA ATA AAAT CGAA ACAG AAAA AACTTAA ACTCC ACAGAA GGCA GATCTC ACACAGC AGA	2220
QY	2255	GAG CCAT CCAA ATGTTT GG AGAC CCCT GAGCTT CAGCTCT GATTAA CGGCTT GCTGGTTT	2314
Db	2221	GAG CCAT CCAA ATGTTT GG AGAC CCCT GAGCTT CAGCTCT GATTAA CGGCTT GCTGGTTT	2280
QY	2315	GCTT TGCTT CTTAT TCC AATTA ACCAT GACCG GTAA CAGAA AGCACA GAA CCCTG GTT CAC	2374
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QY	2375	TGC AAA AGC CACT GAGAT CTCAC CCTCA CCTG ACACAA AGCAGCTAT CATAC AGGCTT	2434
Db	2341	TGC AAA AGC CACT GAGAT CTCAC CCTCA CCTG ACACAA AGCAGCTAT CATAC AGGCTT	2400
QY	2435	ATC AGG AA CAC AGG AATTT GTC CAATCA AAGCTTACC CACTAGGTC CAATCGT GACTAGC	2494
Db	2401	ATC AGG AA CAC AGG AATTT GTC CAATCA AAGCTTACC CACTAGGTC CAATCGT GACTAGC	2460
QY	2495	ACCT CAC ACT GSCAT GCTTT TAGCTTT GAGAA GGGATTA CTTGG AGTCAG GTAC GAA GAA	2554
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QY	2555	GG AC AGG ACG AAG CATGGCT CCAT GTG GAA GAA CAATAT CTGCTT CCAGAT GACC AGG	2614
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Db	3180	AGTT CAT TCC	3189

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RESULT 4
MMU93277
LOCUS
DEFINITION Mus musculus 8S-lipoxygenase mRNA, complete cds.
ACCESSION U93277
VERSION U93277.1
KEYWORDS GI:2439986
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3205)
AUTHORS Jisaka,M., Kim,R.B., Boeglin,W.E., Nanney,L.B. and Brash,A.R.
TITLE Molecular cloning and functional expression of a phorbol
ester-inducible 8S-lipoxygenase from mouse skin
JOURNAL J. Biol. Chem. 272 (39), 24410-24416 (1997)
MEDLINE 97450967
PUBMED 9305900
2 (bases 1 to 3205)
AUTHORS Jisaka,M. and Brash,A.R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1997) Clinical Pharmacology, Vanderbilt
University, 23rd Ave. at Pierce, Nashville, TN 37232-6602, USA
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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RESULT 5

BC015253
LOCUS
DEFINITION
Mus musculus arachidonate 15-lipoxygenase, second type, mRNA (cdna clone MGC:18359 IMAGE:4221815), complete cds.

ACCESSION
BC015253

VERSION
BC015253.1

KEYWORDS
MGC.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2942)

REFERENCE

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2244)
AUTHORS	Boeglin, W.E., Schneider, C. and Brash, A.R.
TITLE	Direct Submission
JOURNAL	Submitted (31-AUG-2001) Clinical Pharmacology, Vanderbilt University, 23rd Avenue South at Pierce, Nashville, TN 37232, USA
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DEFINITION clone MGC:24958 IMAGE:4778890), complete cds.
ACCESSION BC035217
VERSION BC035217.1 GI:23270880
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2673)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2673)
Strausberg,R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

TITLE
JOURNAL
PUBMED
REFERENCES
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnarone, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 29 Row: 1 Column: 2
This clone was selected for full length sequencing because it
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ORIGIN
Query Match 43.4%; Score 1398.4; DB 9; Length 2673;
Best Local Similarity 79.9%; Pred. No. 0;
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RESULT 8

BC063647

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC063647 2686 bp mRNA linear PRI 30-JUN-2004
Homo sapiens arachidonate 15-lipoxygenase, second type, mRNA (cdna
clone MGC:75485 IMAGE:4804186), complete cds.

BC063647
BC063647.1 GI:39645887

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2686)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

TITLE	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.C., Malek, J.A., Gunaratne, P.H., Richard, S., Wilfong, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalson, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettaman, M., Madan, A., Rodriguez, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, S., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2686)	
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
	Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk	
	Email: cgabbs@mail.nih.gov	
TITLE	Tissue Procurement: James Cleaver, M.D.	
	cDNA Library Preparation: Life Technologies, Inc.	
COMMENT	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;	
FEATURES	Web site: http://www.nisc.nih.gov/	
	Contact: nisc.mgc@hghri.nih.gov	
source	Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lario, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	
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Location/Qualifiers	Series: IRAK Plate: 134 Row: n Column: 5	
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DEFINITION Sequence 1 from patent US 6204037.
ACCESSION AR142985
VERSION AR142985.1 GI:15104271
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2685)
AUTHORS Brash,A.R., Boeglin,W.E. and Jisaka,M.
TITLE Lipoxigenase proteins and nucleic acids
JOURNAL Patent: US 6204037-A 1 20-MAR-2001;
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DEFINITION Sequence 1 from patent US 6649355.
ACCESSION AR430490
VERSION AR430490.1 GI:40191287
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2685)
AUTHORS Brash,A.R., Boeglin,W.E. and Jisaka,M.
TITLE Lipoxigenase proteins and nucleic acids
JOURNAL Patent: US 6649355-A 1 18-NOV-2003;
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AX770522
LOCUS AX770522 2685 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 28 from Patent WO03031650.
ACCESSION AX770522
VERSION AX770522.1 GI:32437898
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
Munnes, M., Gehrmann, M., Wick, M. and Schmitz, G.
Genes and proteins for prevention, prediction, prognosis and
therapy of cardiovascular disease
Patent: WO 03031650-A 28 17-APR-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
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Db	42 GCGTAGAGAGCTGGACTTAGGCTGSCAGCATGGCCGAGTTCAAGGTCAGGGTGTCAC 101		1025 GCCATCCAGCTCAAAACAGACTCCCGGGCCAGACAAACCCCATCTTCTCTGCCACGCGATGAC 1084
QY	65 GGGGAAGCCTGTGGGGCTGGCACAATGGGACAAGTGTCTGTACGATCTGTGGGAACCCAC 124		1059 GCCATCCAGCTCAGCAGACAGCCCGGGCCAAACAGCCCCCATCTTCTCTGCCACTGATGAC 1118
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QY	245 AAAGCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCTGCTGTGCG 304		1239 GGTCAAGCTGCTGCTGCTTCAAGCTGTGATCCCGCACACACCCGATACACC 1298
Db	282 AAGGCGCCCCC--AGTGTGCCCCCTGTGGGGCCCCCTGGCCCCGAGTGCCTGGTTCTGC 338		1265 TTGCAATCAACACAGCTTGGCCGGAGCTGTCTGTGCTGCCCTTGGGAAAGTTGATAGACAAG 1324
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Db	579 TTGGAGCTCAATATCAATCAATCTCCACAGCAAGAAATGCCAACTTTTATCTACAGCTGGC 638		1565 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGGCCGAGAAAGCTCAGGTATGCC 1624
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QY	785 CTGATTTCGCGCTGTCAAGTCTCCAAACAACCTTCCCGGTCACTGATGAATGTGTGGCC 844		1779 CTGCCACCCAGCATGCACTGCCACCAACCACTTCCAAAGGCTTGGCAACATGCGAGGGC 1838
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QY	845 CCAGTCTGGGCCCTGGAAACCACTCTGAGGCTGAGTTGGAGNAGGCTCCCTGTCTTTG 904		1839 TTCAATAGCACCCCTCCACCTGTCAATGCAATGTGATGTCTCTCTCTCTCTCTCTCTCT 1898
Db	879 TCATTGTGGTCTGGGACCAAGCTTTCAGGCTGAGCTAGAGNAGGCTCCCTGTGTCTTG 938		1865 CTAAGCGCAGAACTCTGGGACCAAAAGGCCCTTGGGCCACTATCCAGATGAACACATTCACA 1924
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QY	965 TCTGCAGCCCCGATGACCTGTGTACACAGAGCTCAGGGTCCGGAACCCCTGTCTCCATT 1024		1959 GAGGAGGCCCTTCGGGGAGCATCGCACCTTCCAGAGCCGCTGGCCCAAGATCTCGAGG 2018
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LOCUS	HSU78294				
DEFINITION	Homo sapiens 15S-lipoxxygenase mRNA, complete cds.				
ACCESSION	U78294				
VERSION	U78294.1	GI:2224906			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2685)				
AUTHORS	Braah,A.R., Boeglin,W.E. and Chang,M.S.				
TITLE	Discovery of a second 15S-lipoxxygenase in humans				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6148-6152 (1997)				
MEDLINE	97322340				
PUBMED	917185				
REFERENCE	2 (bases 1 to 2685)				
AUTHORS	Braah,A.R., Boeglin,W.E. and Chang,M.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-NOV-1996) Clinical Pharmacology, Vanderbilt				
	University, WE1 510 23rd Ave S. at Pierce, Nashville, TN				
	37232-6602, USA				
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ORIGIN					
Query Match	43.3%;	Score 1395.2;	DB 9;	Length 2685;	
Best Local Similarity	79.8%;	Pred. No. 0;			
Matches 1671; Conservative	0;	Mismatches 418;	Indels 5;	Gaps 2;	
QY	7	GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGCGAAATGACGGGTGAGAGTATCCACG	64		
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Qy 1955 TTCAGAGAAAGCTGATCCAGATCTCCAGGGCATCAGGAGAGGAAACCGAGGCTTGGCA 2014
Db 1918 TTCAGAGAGCCCTGGCCAGATCTCGAGGGGCTATCCAGAGCGGAACCCGGGCTGGTG 1977
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LOCUS sqm75173 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.
DEFINITION BV174905
ACCESSION BV174905
VERSION BV174905.1 GI:48010350
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2527)
AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2527.

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Query Match 42.9%; Score 1381.6; DB 11; Length 2527;

Best Local Similarity 79.7%; Pred. No. 0; Matches 1669; Conservative 0; Mismatches 419; Indels 6; Gaps 3;									
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Dd	102	GGAGAAGCCTTCGGGGCTGGCAGTCAGGACAAAGTGTCTGTCAAGCATCGTGGGACCCGG	161						
QY	125	GGAGAGAGCCCTTAGTACTCTGTGACACATCTGGGCAAGAGTTCAGCGCCCGTCTGAA	184						
Dd	162	GGAGAGAGCCCCCACTGCTCCCTTGGACATCTCGGCAAGAGTTCACTGCGGGCGCTGAG	221						
QY	185	GAAGACTTCGAGGTGACGCTTCCCGAGGACGTAGGCACCTGTGATGCTGCGAGTCCAC	244						
Dd	222	GAGGACTTCCAGGTGACGCTCCCGGAGGACGTAGGCCGAGTGTCTGTCTGCGCGCTGAC	281						
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QY	305	CGCTGTTTCGAGCTGAGTGGCTACTCTGGGGCTGCACTCCACTTCCCTCTGTTATCAGTGG	364						
Dd	339	CGCTGTTCCAGCTGACACCGCGCGGGCGGCCACTCTCTTCCCTCTGTACCACTGG	398						
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Dd	639	TCCTGCTTTGCAGAGATGAATCAAGGGTGTCTGAGACCGCAAGGGCTCTGGAGGAGT	698						
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RESULT 15
AL645527/c

LOCUS	AL645527	251224 bp	DNA	linear	ROD 02-MAY-2002							
DEFINITION	Mouse DNA sequence from clone RP23-26L6 on chromosome 11, complete sequence.											
ACCESSION	AL645527											
VERSION	AL645527.20	GI:20339099										
KEYWORDS	HTG.											
SOURCE	Mus musculus (house mouse)											
ORGANISM	Mus musculus											
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.											
AUTHORS	1. (bases 1 to 261224)											
TITLE	Bird, C											
JOURNAL	Direct Submission											
COMMENT	Submitted (01-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 29, 2002 this sequence version replaced gi:20145941. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-26L6 is from the RP23-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6.											
FEATURES	<p>Location/Qualifiers</p> <p>1..261224</p> <p>/organism="Mus musculus"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:10090"</p> <p>/chromosome="11"</p> <p>/clone="RP23-26L6"</p> <p>/clone_lib="RPCI-23"</p>											
ORIGIN	<p>Query Match 41.6%; Score 1340; DB 10; Length 261224;</p> <p>Best Local Similarity 98.9%; Pred. No. 0;</p> <p>Matches 1349; Conservative 0; Mismatches 15; Indels 0; Gaps 0;</p> <p>QY 1861 GCTGCTAAGCGCAGAAACCTGGGGACCAAGGCCCTTGGGCCCACTATCCAGATGAACACTT 1920</p> <p>DB 101860 GCAGCTCAACCTTGATGATTGATCCCCCAGAGGCCCTGGGCCCATATCCAGATGAACACTT 101861</p> <p>QY 1921 CACAGAGATGCCCCCCCGCGAAGCGTGCTGCCTTCCAGAGAAAGCTGATCCAGATCTC 1980</p> <p>DB 101800 CACAGAGATGCCCCCCCGCGAAGCGTGCTGCCTTCCAGAGAAAGCTGATCCAGATCTC 101741</p> <p>QY 1981 CAAGGGCATCAGGGAGAGGAACCGAGGCGCTGCGCTTCCAGAGAAAGCTGATCCAGATCTC 2040</p> <p>DB 101740 CAAGGGCATCAGGGAGAGGAACCGAGGCGCTGCGCTTCCAGAGAAAGCTGATCCAGATCTC 101681</p> <p>QY 2041 CCTCATTTGAGAACAGTGTCTCCATCTTAAACATCTTTGGAGAAAGCAGTCTCTGTGTGACATAT 2100</p> <p>DB 101680 CCTCATTTGAGAACAGTGTCTCCATCTTAAACATCTTTGGAGAAAGCAGTCTCTGTGTGACATAT 101621</p> <p>QY 2101 AGAAGCTTTGACCATGCTCTCCAGGCTTAAGTCCCGGTATGCTTCTTCCTGGACAACCAAG 2160</p> <p>DB 101620 AGAAGCTTTGACCATGCTCTCCAGGCTTAAGTCCCGGTATGCTTCTTCCTGGACAACCAAG 101561</p>											

Search completed: July 19, 2005, 17:56:51
Job time : 9131.36 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 05:18:47 ; Search time 1096 Seconds
(without alignments)
17413.610 Million cell updates/sec

Title: US-10-688-676A-3

Perfect score: 3224

Sequence: 1 cagcttgagtagagagcta.....gtcataaaggttcattcc 3224

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3205	99.4	3232	5 AAD04502	Aad04502 Mouse 8S-
2	3205	99.4	3232	12 ADQ91764	Adq91764 Mouse 8S-
3	1395.2	43.3	2647	2 AAX23827	Aax23827 Human 15S
4	1395.2	43.3	2685	5 AAD04501	Aad04501 Human 15S
5	1395.2	43.3	2685	6 ABK92181	Abk92181 Prostate
6	1395.2	43.3	2685	6 ABK64747	Abk64747 Human ben
7	1395.2	43.3	2685	8 ACA89907	ACA89907 Gene diff
8	1395.2	43.3	2685	12 ADQ91798	Adq91798 Human lip
9	1395.2	43.3	2685	12 ADQ37895	Adq37895 DNA encod
10	734.4	22.8	3127	13 ACN42888	ACN42888 Human dia
11	659.6	20.5	3320	6 ABA05868	ABA05868 Human lip
12	659.6	20.5	3320	10 RAD60556	Rad60556 Human lip
13	659.6	20.5	3384	3 AAC61761	Aac61761 cDNA enco
14	659.6	20.4	2136	12 ADQ48420	Adq48420 Human lip
15	658.6	20.4	2236	3 AAC61749	Aac61749 cDNA enco
16	658	20.4	2701	3 AAC61747	Aac61747 cDNA enco
17	658	20.4	2307	6 ABZ11921	Abz11921 Human pol
18	657	20.4	2307	12 ADM44439	ADM44439 Novel hum
19	657	20.4	2307	12 AAC61758	Aac61758 cDNA enco
20	657	20.4	2604	3 AAC61758	Aac61758 cDNA enco

21	652.2	20.2	2136	6 ABA96003	Abag96003 Human lip
22	565.8	17.5	2469	3 AAS59659	Aas59659 DNA encod
23	565.8	17.5	2469	6 AAD34466	Aad34466 Human 12R
24	565.8	17.5	2469	12 ADG46601	Adg46601 Human 12R
25	565.8	17.5	2469	12 ADN04290	Adn04290 Antipsoi
26	466.2	14.5	1383	3 AAC61752	Aac61752 cDNA enco
27	466.2	14.5	1848	3 AAC61751	Aac61751 cDNA enco
28	466.2	14.5	2316	3 AAC61760	Aac61760 cDNA enco
29	442.6	13.7	2499	1 AAN90366	Aan90366 Synthetic
30	441.8	13.7	2500	3 AAA35130	Aaa35130 Human ade
31	441.8	13.7	2500	3 AAF21252	Aaf21252 Human low
32	441.8	13.7	2500	10 ABZ96946	Abz96946 Human nuc
33	441.8	13.7	2500	11 ABD20795	Abd20795 Human pul
34	441.8	13.7	11151	3 AAA35133	Aaa35133 Human ade
35	441.8	13.7	11181	3 AAF21255	Aaf21255 Human low
36	441.8	13.7	11181	10 ABZ96949	Abz96949 Human nuc
37	441.8	13.7	11181	11 ABD20798	Abd20798 Human pul
38	440.6	13.7	2497	3 AAA35132	Aaa35132 Human ade
39	440.6	13.7	2497	3 AAF21254	Aaf21254 Human low
40	440.6	13.7	2497	6 ABL65632	Ab165632 Lung canc
41	440.6	13.7	2497	6 ABL67646	Ab167646 Oesophagu
42	440.6	13.7	2497	6 ABL67509	Ab167509 Thyroid c
43	440.6	13.7	2497	6 ABT11115	Abt11115 Human 5-1
44	440.6	13.7	2497	6 ABK83762	Abk83762 Human cDN
45	440.6	13.7	2497	6 AAD24664	Aad24664 Human 5-1

ALIGNMENTS

RESULT 1
AAD04502
ID AAD04502 standard; cDNA; 3232 BP.
XX
AC AAD04502;
XX
DT 04-JUL-2001 (first entry)
XX
DE Mouse 8S-lipoxigenase (8-Lox) cDNA.
XX
KW Mouse; 8S-lipoxigenase; 8-Lox; non-haeme iron dioxygenase;
KW arachidonic acid; feed additive; livestock; antigen; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..27
FT CDS /*tag= a
FT /*tag= b
FT /product= "Mouse 8S-lipoxigenase (8-Lox) protein"
XX
PN US6204037-B1.
XX
PD 20-MAR-2001.
XX
PF 16-APR-1998; 98US-00061768.
PR 16-APR-1998; 98US-00061768.
XX (UVA-) UNIV VANDERBILT.
PA Brash AR, Boeglin WE, Jisaka M;
PI WPI; 2001-289517/30.
XX P-FSDB; AAE00936.
DR New 15S-lipoxigenase nucleic acids and polypeptides, useful as feed
XX additives for livestock, or as antigens for producing antibodies.
PS Example 2; Fig 5A-5C; 5lpp; English.
XX The present sequence is mouse 8S-lipoxigenase (8-Lox) cDNA. Lipoxigenases
CC

CC are a structurally related family of non-haeme iron dioxygenases that
CC function in the production of fatty acid hydroperoxides. 8-Lox acts in
CC the metabolism of arachidonic acid to 8S-hydro(pero)xyicosatetraenoic
CC acid. Lipoxigenase DNA can be used as diagnostic tools to detect normal
CC and abnormal DNA sequences derived from patient cells, for detecting and
CC isolating other members of the polypeptide family and related
CC polypeptides from a DNA library potentially containing the sequences, as
CC primers for hybridising to related sequences for amplifying those
CC sequences or for altering native lipoxigenase DNA sequences. The
CC lipoxigenase is useful as feed additives for livestock and as antigens
CC for producing antibodies. Note: The present sequence is also shown in
CC column 51-58 of the specification, but lacks 27 nucleotides at its 5' end
XX
SQ Sequence 3232 BP; 823 A; 872 C; 782 G; 755 T; 0 U; 0 Other;

Query Match 99.4%; Score 3205; DB 5; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3216; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 8 CAGTAGAGAGCTAAACTGGTTCAGGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGG 67
DB 1 CAGTAGAGAGCTAAACTGGTTCAGGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGG 60
QY 68 GAAGCCTGTGGGCTGGCAGATGGGACAAAGTGTCTGTCAAGCATGTGGGAACCCACGGA 127
DB 61 GAAGCCTGTGGGCTGGCAGATGGGACAAAGTGTCTGTCAAGCATGTGGGAACCCACGGA 120
QY 128 GAGAGCCCTTACTACTCTGGACCATCTGGGCAAGAGTTCAGGCCCGGTCTGAAGAA 187
DB 121 GAGAGCCCTTACTACTCTGGACCATCTGGGCAAGAGTTCAGGCCCGGTCTGAAGAA 180
QY 188 GACTTCGAGGTGACCGCTTCCCAGGACGTAGGCACCTGTGTGATGCTGGAGTCCACAAA 247
DB 181 GACTTCGAGGTGACCGCTTCCCAGGACGTAGGCACCTGTGTGATGCTGGAGTCCACAAA 240
QY 248 GCACCCCGGAGTGTCCCTCCCGCTTATGTCTTTCCGTTGTGATGCCCTGGTTTCGCCGC 307
DB 241 GCACCCCGGAGTGTCCCTCCCGCTTATGTCTTTCCGTTGTGATGCCCTGGTTTCGCCGC 300
QY 308 TGGTTTCGAGCTGGAGTGGCTACTCTGGGGCTGCATCTCCACTTCCCTGTTTACGTGGCTG 367
DB 301 TGGTTTCGAGCTGGAGTGGCTACTCTGGGGCTGCATCTCCACTTCCCTGTTTACGTGGCTG 360
QY 368 GAAGGGCGGGGAGCTGTGTGTGAGAGGAGGAGCAAGAGTGTCTTGAAGCAAGACCAT 427
DB 361 GAAGGGCGGGGAGCTGTGTGTGAGAGGAGGAGCAAGAGTGTCTTGAAGCAAGACCAT 420
QY 428 CACCTTACACTGCAGGATCAGGCCCAAGAGGAGCTTGTGATCCAGGCAGAGATGTACAGC 487
DB 421 CACCTTACACTGCAGGATCAGGCCCAAGAGGAGCTTGTGATCCAGGCAGAGATGTACAGC 480
QY 488 TGGAGACTTACATTAAGAGTTGGCTCGCTCGCTTGACCCAGGACTGTGAAGACTTG 547
DB 481 TGGAGACTTACATTAAGAGTTGGCTCGCTCGCTTGACCCAGGACTGTGAAGACTTG 540
QY 548 GACCTCAACATCAAGTACTCTGGATGAAGATGCGAAATCTTCTTTAAAGCCCACTCC 607
DB 541 GACCTCAACATCAAGTACTCTGGATGAAGATGCGAAATCTTCTTTAAAGCCCACTCC 600
QY 608 GCGTATACGGAGCTGAAGCTTCAAGGGCTCTTGGACCGCAGAGACTCTTGGAGGAGTCTG 667
DB 601 GCGTATACGGAGCTGAAGCTTCAAGGGCTCTTGGACCGCAGAGACTCTTGGAGGAGTCTG 660
QY 668 AGGAGATGAGAGGCTGTAACTTCCGACAGACTCCAGCAGCAGAGATGTGTTTGA 727
DB 661 AGGAGATGAGAGGCTGTAACTTCCGACAGACTCCAGCAGCAGAGATGTGTTTGA 720
QY 728 CACTGCGAGAGATGCCCTTCTTCGCTCCAGTTCCTAAATGGGCATCAACCGGTCCTG 787
DB 721 CACTGCGAGAGATGCCCTTCTTCGCTCCAGTTCCTAAATGGGCATCAACCGGTCCTG 780
QY 788 ATTTCGGCTGTACAGTCTCCCAAAACAACTTCCGGTCACTGTATGAATGTGGCCCA 847

DB 781 ATTCCCGCGTGTCA CAGTCTCCAAAACAACTTCCCGGTCACTGATGAATAATGTGGCCCA 840
QY 848 GTGCTGGGCGCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTCTTGGTG 907
DB 841 GTGCTGGGCGCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTCTTGGTG 900
QY 908 GATCATGGGCAATCTTTCTGGAGTCCACCAACATCTCTCAATGGAAGGCTCAGTTCTCT 967
DB 901 GATCATGGGCAATCTTTCTGGAGTCCACCAACATCTCTCAATGGAAGGCTCAGTTCTCT 960
QY 968 GCAGCCCCGATGACCCCTGTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAATGCC 1027
DB 961 GCAGCCCCGATGACCCCTGTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAATGCC 1020
QY 1028 ATCCAGCTCAAAACAGACTCCCGGGCGAGACAAACCCCATCTTCTCCGCCAGCATGACAG 1087
DB 1021 ATCCAGCTCAAAACAGACTCCCGGGCGAGACAAACCCCATCTTCTCCGCCAGCATGACAG 1080
QY 1088 TGGGACTGGTGTCTGGCCAAAGACCTGGGTTCGCAATCTGAGTTTTACATCATGAGGCT 1147
DB 1081 TGGGACTGGTGTCTGGCCAAAGACCTGGGTTCGCAATCTGAGTTTTACATCATGAGGCT 1140
QY 1148 GTCAACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCTTGGCCACATTAAGT 1207
DB 1141 GTCAACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCTTGGCCACATTAAGT 1200
QY 1208 CAGCTGCCCTAGTGTGTCAACCTCTCTTCAAGCTATTGATTCTCTACATTCGGGTACACATG 1267
DB 1201 CAGCTGCCCTAGTGTGTCAACCTCTCTTCAAGCTATTGATTCTCTACATTCGGGTACACATG 1260
QY 1268 CACATCAAACGCTTGGCCCGGAGCTGCTCGTTGCCCTCGGGAAGTTGATAGCAAGTCC 1327
DB 1261 CACATCAAACGCTTGGCCCGGAGCTGCTCGTTGCCCTCGGGAAGTTGATAGCAAGTCC 1320
QY 1328 ACAGSCCTTGGCAGCTGGGGGATCTCTGACCTGATAAAGAGAAACATGGAGCAGCTGAC 1387
DB 1321 ACAGSCCTTGGCAGCTGGGGGATTTCTGACCTGATAAAGAGAAACATGGAGCAGCTGAC 1380
QY 1388 TACTCTGTCTGTGTCTCCCTGAAGATATCCAGGCCCGAGGTGTGGAAGACATCCAGGC 1447
DB 1381 TACTCTGTCTGTGTCTCCCTGAAGATATCCAGGCCCGAGGTGTGGAAGACATCCAGGC 1440
QY 1448 TACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA 1507
DB 1441 TACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA 1500
QY 1508 ATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCGAAGATGACCAAGAGCTCCAGGC 1567
DB 1501 ATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCGAAGATGACCAAGAGCTCCAGGC 1560
QY 1568 TGGGTGAGGAGATCTTCTGTAGGGCTTCTCTCGGCCGAGAAAGCTCAGGTATGCCCTCC 1627
DB 1561 TGGGTGAGGAGATCTTCTGTAGGGCTTCTCTCGGCCGAGAAAGCTCAGGTATGCCCTCC 1620
QY 1628 TTGTTTGGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTGCTCA 1687
DB 1621 TTGTTTGGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTGCTCA 1680
QY 1688 GCCAAGCATGACGTGTGTGTGAGGCTGAGTTCAGTCTTGTGTTTGGATGCCCAATCTG 1747
DB 1681 GCCAAGCATGACGTGTGTGTGAGGCTGAGTTCAGTCTTGTGTTTGGATGCCCAATCTG 1740
QY 1748 CCACCTTACCATGACGTACCAACCTACTTCCAAAGCCAGGCCCGGCTCAGAGTTTC 1807
DB 1741 CCACCTTACCATGACGTACCAACCTACTTCCAAAGCCAGGCCCGGCTCAGAGTTTC 1800
QY 1808 ATAGCCAGCTCCCAAGCAGTTAAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTCTA 1867
DB 1801 ATAGCCAGCTCCCAAGCAGTTAAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTCTA 1860
QY 1868 AGCGAGAACTTGGGGACAAAGGCCCTCGGCCCATCTATCCAGATGAACATTTACAGAG 1927
DB 1861 AGCGAGAACTTGGGGACAAAGGCCCTCGGCCCATCTATCCAGATGAACATTTACAGAG 1920

XX	Sequence	3232 BP; 823 A; 872 C; 782 G; 755 T; 0 U; 0 Other;	
SQ	Query Match	99.4%; Score 3205; DB 12; Length 3232;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 3216; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
QY	8 CAGTAGAGAGCTAAACTGTGTCAAGGAGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG	67	
DB	1 CAGTAGAGAGCTAAACTGTGTCAAGGAGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG	60	
QY	68 GAAGCTGTGGGGCTGGGCATATGGGACAAAGTGTCTGTGACGATCGTGGGAACCCACCGGA	127	
DB	61 GAAGCTGTGGGGCTGGGCATATGGGACAAAGTGTCTGTGACGATCGTGGGAACCCACCGGA	120	
QY	128 GAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCCAGGCCCGGTCTCAAGAA	187	
DB	121 GAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCCAGGCCCGGTCTCAAGAA	180	
QY	188 GACTTCGAGGTGACGCTTCCCGAGGACGTGAGCACTGTGCTGATGTCGAGTCCACAAA	247	
DB	181 GACTTCGAGGTGACGCTTCCCGAGGACGTGAGCACTGTGCTGATGTCGAGTCCACAAA	240	
QY	248 GCACCCCGGAAGTGTCCCTCCGCTTATGTCTTTCCGTTCTGATGCCCTGTCTGCCGC	307	
DB	241 GCACCCCGGAAGTGTCCCTCCGCTTATGTCTTTCCGTTCTGATGCCCTGTCTGCCGC	300	
QY	308 TGGTTTCGAGCTGGAGTGGCTACTCTGGGCTGCACCTCCACTTCCCTCTGTTATCAGTGGGTG	367	
DB	301 TGGTTTCGAGCTGGAGTGGCTACTCTGGGCTGCACCTCCACTTCCCTCTGTTATCAGTGGGTG	360	
QY	368 GAAGGGCGGGGAGCTGTGTGTGAGAGAGGAGAGCAAAAGTGTCTTGGCAAGACCAT	427	
DB	361 GAAGGGCGGGGAGCTGTGTGTGAGAGAGGAGAGCAAAAGTGTCTTGGCAAGACCAT	420	
QY	428 CACCTTACCTCCAGGATCAGGCCGACAGAGGAGCTTGAATCCAGGACAGAGATGTACAGC	487	
DB	421 CACCTTACCTCCAGGATCAGGCCGACAGAGGAGCTTGAATCCAGGACAGAGATGTACAGC	480	
QY	488 TGGAGACTTACATTTGAAGTGTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG	547	
DB	481 TGGAGACTTACATTTGAAGTGTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG	540	
QY	548 GACCTCAACATCAAGTACTCTGGATGAAGAATGCAAACTCTTCTTTAAAGCCCACTCC	607	
DB	541 GACCTCAACATCAAGTACTCTGGATGAAGAATGCAAACTCTTCTTTAAAGCCCACTCC	600	
QY	608 GGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAGTCTG	667	
DB	601 GGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAGTCTG	660	
QY	668 AGGGAGATCAGAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA	727	
DB	661 AGGGAGATCAGAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA	720	
QY	728 CACTGCGAGGAAGATGCTTCTTTCGCTCCCGATTCCTAAATGGCATCAACCGGTCCTG	787	
DB	721 CACTGCGAGGAAGATGCTTCTTTCGCTCCCGATTCCTAAATGGCATCAACCGGTCCTG	780	
QY	788 ATTGCGCGCTGTACAGTCTCCCAACACTTCCCGGTCACTGATGAATGTGGCCCCA	847	
DB	781 ATTGCGCGCTGTACAGTCTCCCAACACTTCCCGGTCACTGATGAATGTGGCCCCA	840	
QY	848 GTGCTGGGCGCTTGAACAGTCTGAGGCTGAGTTGGAGAAGGGCTCCCTGTTCTGGTG	907	
DB	841 GTGCTGGGCGCTTGAACAGTCTGAGGCTGAGTTGGAGAAGGGCTCCCTGTTCTGGTG	900	
QY	908 GATCATGGCATTTCTTTCTGAGTCCACCAACATCTCAATGGAAAGCCTCAGTTCTCT	967	
DB	901 GATCATGGCATTTCTTTCTGAGTCCACCAACATCTCAATGGAAAGCCTCAGTTCTCT	960	
QY	968 GCAGCCCGATGATCCCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCATGGC	1027	

DB	961 GCAGCCCGATGACCCCTGTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCATTTGCC	1020	
QY	1028 ATCCAGCTCAAAACAGACTCCCGGGGCAGACAAACCCCATCTTCTCCGCCAGAGATGACACG	1087	
DB	1021 ATCCAGCTCAAAACAGACTCCCGGGGCAGACAAACCCCATCTTCTCCGCCAGAGATGACACG	1080	
QY	1088 TGGGACTGGTTGCTGGCCCAAGACCTGGGTTCGCAATTCGTAGTTTTTACATCATCAGGGCT	1147	
DB	1081 TGGGACTGGTTGCTGGCCCAAGACCTGGGTTCGCAATTCGTAGTTTTTACATCATCAGGGCT	1140	
QY	1148 GTCACACATCTGCTGTCATGCCCATCTGATTCACAGAACTTTTGCCCTTGGCCACATTAAGT	1207	
DB	1141 GTCACACATCTGCTGTCATGCCCATCTGATTCACAGAACTTTTGCCCTTGGCCACATTAAGT	1200	
QY	1208 CAGCTGCCCTAGGTGTCACCCCTCTCTTCAAGCTATTGATTCCTCACTTCGGGTACACATG	1267	
DB	1201 CAGCTGCCCTAGGTGTCACCCCTCTCTTCAAGCTATTGATTCCTCACTTCGGGTACACATG	1260	
QY	1268 CACATCAACAGCTTGGCCGGGAGCTGCTCGTTGCCCTGGGAACTGTGATACAGATGCC	1327	
DB	1261 CACATCAACAGCTTGGCCGGGAGCTGCTCGTTGCCCTGGGAACTGTGATACAGATGCC	1320	
QY	1328 ACAGGCCCTTGGCACTGGGGGATTTCTCTGACCTGTATAAAGAGAAACATGAGAGCAGCTGAAC	1387	
DB	1321 ACAGGCCCTTGGCACTGGGGGATTTCTCTGACCTGTATAAAGAGAAACATGAGAGCAGCTGAAC	1380	
QY	1388 TACTCTGTCTGTGTCTTCCCTGGAAGATTCGAGCCCGAGAGTGTGGAAGACATCCAGGC	1447	
DB	1381 TACTCTGTCTGTGTCTTCCCTGGAAGATTCGAGCCCGAGAGTGTGGAAGACATCCAGGC	1440	
QY	1448 TACTATTACCGAGATGAGGATGCAGATCTGGGGGGCAATAAAGAGCTTTCTCTCTGAA	1507	
DB	1441 TACTATTACCGAGATGAGGATGCAGATCTGGGGGGCAATAAAGAGCTTTCTCTCTGAA	1500	
QY	1508 ATAGTCAGCATCTACTATCCAAAGTGACACATCCGTCCTCAAGATGACCAAGAGCTCCAGGCC	1567	
DB	1501 ATAGTCAGCATCTACTATCCAAAGTGACACATCCGTCCTCAAGATGACCAAGAGCTCCAGGCC	1560	
QY	1568 TGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGCCCGAGAAAGCTCAGGTTATGCCCTCC	1627	
DB	1561 TGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGCCCGAGAAAGCTCAGGTTATGCCCTCC	1620	
QY	1628 TTGTTGGATACCCGGGAGCCCTGGTCCAGTATATACCATGTGATATTCACCTGCTCA	1687	
DB	1621 TTGTTGGATACCCGGGAGCCCTGGTCCAGTATATACCATGTGATATTCACCTGCTCA	1680	
QY	1698 GCCAAGCATGCACTGTCTGAGTTCAGGCCAGTTTCGACTCTTGTGTTTGGATGCCCAATCTG	1747	
DB	1681 GCCAAGCATGCACTGTCTGAGTTCAGGCCAGTTTCGACTCTTGTGTTTGGATGCCCAATCTG	1740	
QY	1748 CCACCTACATGCACTACCACTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC	1807	
DB	1741 CCACCTACATGCACTACCACTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC	1800	
QY	1808 ATAGCCAGCTCCAGCAGTTAAATTCGTCAGTTATCACATCATTCCTCTCGGCTGCTA	1867	
DB	1801 ATAGCCAGCTCCAGCAGTTAAATTCGTCAGTTATCACATCATTCCTCTCGGCTGCTA	1860	
QY	1868 AGCGCAGAACCTTGGGGACCAAAAGGCCCTTGGGCCACTATCCAGATGAAACACTTTCACAGAG	1927	
DB	1861 AGCGCAGAACCTTGGGGACCAAAAGGCCCTTGGGCCACTATCCAGATGAAACACTTTCACAGAG	1920	
QY	1928 GATGCCCCCGCGAAGCGTGGCTGCTTTCAGAGAAAGCTGATCCAGATCTCCCAAGGCC	1987	
DB	1921 GATGCCCCCGCGAAGCGTGGCTGCTTTCAGAGAAAGCTGATCCAGATCTCCCAAGGCC	1980	
QY	1988 ATCAGGGAGAGAAACGAGGCCCTGGCACTGCCCTACACCTACTGATCCTCCCTCAAT	2047	
DB	1981 ATCAGGGAGAGAAACGAGGCCCTGGCACTGCCCTACACCTACTGATCCTCCCTCAAT	2040	
QY	2048 GAGAAACAGTGTCTCTCAATCTTAACATCTTGGAGAAGACAGTCTCTGTGTGACATATAGAACTC	2107	
DB	2041 GAGAAACAGTGTCTCTCAATCTTAACATCTTGGAGAAGACAGTCTCTGTGTGACATATAGAACTC	2100	

QY 2108 TTGACCATGCTCTCCAGGCTAAGTCCCGTATGCTTCTCTGGAACAACCAAGCCCCATC 2167
Db 2101 TTGACCATGCTCTCCAGGCTAAGTCCCGTATGCTTCTCTGGAACAACCAAGCCCCATC 2160
QY 2168 TTACACACACACACACACACACACACACCTTAATAAATCGAAACAGAAAAACCTAAACTCCC 2227
Db 2161 TTACACACACACACACACACACACACACCTTAATAAATCGAAACAGAAAAACCTAAACTCCC 2220
QY 2228 ACAGAAGCAAGATCTCAACAGCAGAGAGCCATCCAAATGTTTGGAGACCCCTGAGCTTC 2287
Db 2221 ACAGAAGCAAGATCTCAACAGCAGAGAGCCATCCAAATGTTTGGAGACCCCTGAGCTTC 2280
QY 2288 AGCTCTGATTAACGGCTTGTGGTTTGTCTTCTTCTTCTTCAATTAACCATGACCGT 2347
Db 2281 AGCTCTGATTAACGGCTTGTGGTTTGTCTTCTTCTTCTTCAATTAACCATGACCGT 2340
QY 2348 AACAGAAAGCAGACAAACCTGTCTCACTGCAACAAAGCCACTGAGATCTCACCTCACCTG 2407
Db 2341 AACAGAAAGCAGACAAACCTGTCTCACTGCAACAAAGCCACTGAGATCTCACCTCACCTG 2400
QY 2408 ACAGAAAGCAGCTATCATACAGGCTTATCAGGAACACAGGAATTTGTCCAATCAAGCC 2467
Db 2401 ACAGAAAGCAGCTATCATACAGGCTTATCAGGAACACAGGAATTTGTCCAATCAAGCC 2460
QY 2468 TACCACTAGTTCATCTGACCTACGACCTCACACTGGCATGCTTTAGCTTTGAGAAAG 2527
Db 2461 TACCACTAGTTCATCTGACCTACGACCTCACACTGGCATGCTTTAGCTTTGAGAAAG 2520
QY 2528 GATTACTGGATTCAGGTACGAGAGAGGACGAGGAGCGATGGCTCCATGTGGAAGA 2587
Db 2521 GATTACTGGATTCAGGTACGAGAGAGGACGAGGAGCGATGGCTCCATGTGGAAGA 2580
QY 2588 ACATATCTGCTCTTCCAGATGACCAAGGCTAGCTCACAGCCATGTCTATCTCACTCCAG 2647
Db 2581 ACATATCTGCTCTTCCAGATGACCAAGGCTAGCTCACAGCCATGTCTATCTCACTCCAG 2640
QY 2648 AGTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACAGTAGACACCAAAA 2707
Db 2641 AGTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACAGTAGACACCAAAA 2700
QY 2708 TTATACTTTTAAAGAGAGGAATGGCTGGAGAGATGGCTCAGCGGTTAAGCACTGA 2767
Db 2701 TTATACTTTTAAAGAGAGAGG-ATGGCTGGAGAGATGGCTCAGCGGTTAAGCACTGA 2759
QY 2768 CTGCTCTTCCAGAGATCTGAGTTCATTTCCAGCAACACATGCTGGCTCACACCAATC 2827
Db 2760 CTGCTCTTCCAGAGATCTGAGTTCATTTCCAGCAACACATGCTGGCTCACACCAATC 2819
QY 2828 TGTAAATGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCAAGTGTATGCACAT 2887
Db 2820 TGTAAATGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCAAGTGTATGCACAT 2879
QY 2888 ATATATAAATAAATCTTTAAAAAACAACAAGAGAGAGGACATGCTACCAATTTCT 2947
Db 2880 ATATATAAATAAATCTTTAAAAAACAACAAGAGAGAGGACATGCTACCAATTTCT 2939
QY 2948 ACCTCACTTCTTCAAGCCACCCCTAAAGTGAATTTGTAACAGGTCCTCTTTGACAGA 3007
Db 2940 ACCTCACTTCTTCAAGCCACCCCTAAAGTGAATTTGTAACAGGTCCTCTTTGACAGA 2999
QY 3008 GAGTTAGAAGATATTTCTCAAAACCTCTAATACCTTCCATCTTAAATTCATCTTCAATCCA 3067
Db 3000 GAGTTAGAAGATATTTCTCAAAACCTCTAATACCTTCCATCTTAAATTCATCTTCAATCCA 3059
QY 3068 AAATTCGAATATTTATATACATCTCCAGTTTGGTGGTGGGTTGTTTTGTTG 3127
Db 3060 AAATTCGAATATTTATATACATCTCCAGTTTGGTGGTGGGTTGTTTTGTTG 3119
QY 3128 GTTTGGTTGGTGGGTTTGTGTTTTGTTTTGTTTTGTTTTGTTCTCTGGTTCAAGATC 3187
Db 3120 GTTTGGTTGGTGGGTTTGTGTTTTGTTTTGTTTTGTTTTGTTCTCTGGTTCAAGATC 3179

QY 3188 CATGACGTTTCATTAAATGTCATAAATGAGTTCATTCC 3224
Db 3180 CATGACGTTTCATTAAATGTCATAAATGAGTTCATTCC 3216

RESULT 3

AAAX23827
ID AAX23827 standard; DNA; 2647 BP.

XX AC AAX23827;

XX DT 25-JUN-1999 (first entry)

XX Human 15S lipoxigenase PS213 DNA.

XX Lipoxigenase; PS213; human; diagnosis; prostate disease; cancer;
metastases; benign prostatic hypertrophy; prostatic; immunoassay;
prostatic intraepithelial neoplasia; cytotoxic agent; drug screening;
therapy; ss.

OS Homo sapiens.

XX WO9913111-A1.

XX PD 18-MAR-1999.

XX PF 11-SEP-1998; 98WO-US018983.

XX PR 11-SEP-1997; 97US-00927978.

XX PA (ABBO) ABBOTT LAB.

XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;
Stroupe SD;

XX DR WPI; 1999-229254/19.

XX DR P-PSDB; AAW93832.

XX PT Diagnosis of prostatic disease using lipoxigenase PS213 as marker.

XX Claim 1; Page 93; 101pp; English.

CC This invention describes methods for diagnosing prostate disease using
the human 15S-lipoxigenase PS213, or its nucleic acid or specific
antibodies, as markers. Detecting the presence of PS213, a derived
amplicon, the encoded polypeptide or specific antibody, basically in
standard hybridization, amplification or immuno assays, indicates
prostatic disease. These methods are used for diagnosis, staging,
monitoring, prognosticating, in vivo imaging and determining
predisposition to prostatic cancer (and metastases), benign prostatic
hyperplasia, prostatic, and prostatic intraepithelial neoplasia. Host
cells transfected with PS213 are used to produce recombinant polypeptides
which are used to generate antibodies or as immunoassay reagents. The
antibodies, and their fragments, are also immunoassay reagents and can be
used therapeutically, either directly or as carriers for cytotoxic
agents. The recombinant polypeptides are also used for drug screening and
as targets for therapy

XX SQ Sequence 2647 BP; 591 A; 828 C; 721 G; 507 T; 0 U; 0 Other;

Query Match 43.3%; Score 1395.2; DB 2; Length 2647;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY 7 GCAGTAGAGCTAAACT--GGTCAGGAGGATGGGAATCGAGGTCAGATATCCACG 64

Db 42 GCCCTAGAGAGCTGGACTTAGGCTGGCAGCATGCCGAGTTTCAGGGTCAGGGTGTCCACC 101

QY 65 GGGGAAGCCTGTGGGGCTGGCACATGGACAAAGTGTCTGTGACATCGTGGGAACCCAC 124

Db 102 GGAGAACCTTCGGGGCTGGCACATGGACAAAGTGTCTGTGACATCGTGGGACCCGG 161

QY 125 GGAGAGAGCCCTTAGTACTCTGGACCACATCTGGGCAAGAGTTTCAGCCCGGTGCTGAA 184
Db 162 GGAGAGAGCCCCCACTGGCCCTTGGAACAATCTCGCAAGAGATTCACTGGGGCGCTGAG 221
QY 185 GAAGACTTCGAGGTGACGCTTCCCAAGGACGTAGGCACTGTGATGCTGCGAGTCCAC 244
Db 222 GAGGACTTCAGGTGACGCTTCCCGAGGACGTAGGCCGAGTGTGCTGTCGCGGTGCAC 281
QY 245 AAAGCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCCCTGGTTCTGC 304
Db 282 AAGGCCCCCC---AGTGTCTCCCTGCTGGGCCCTTGGCCCGGATGCCCTGTTCTGC 338
QY 305 CGCTGTTTCGAGTGGAGTGTACTCTGGGCTGCACTCACTTCCCTCTGTTATCAGTGG 364
Db 339 CGCTGTTTCAGTGTACACCGCCGCGGCGGCCACCTCTCTTCCCTGCTACCAAGTGG 398
QY 365 CTGGAGGGCGGGGAGCTGGTGTCTGAGAGGGAGCAGCAAGGTGTCCTGGCAGAC 424
Db 399 CTGGAGGGCGGGGAGCCCTGTGTCTGCAAGGAGGTACAGCCCAAGGTGCTTGGGCGAC 458
QY 425 CATCACCTTACACTGCAGGATCAGCCCAAGAGGAGCTTGTAGTCCAGGCGAGAGATGTAC 484
Db 459 CACCACCTCTGTCTCAGCNAAGCGCCAGGAGAGCTTCAGGCCCGGCGAGGATGTAC 518
QY 485 AGCTGAAAGACTTACATTTGAAGTTGGCTCGCTGCTTGAACAAGAGACTGTGAAAGAC 544
Db 519 CAGTGAAGAGCTTACAAACAGGTTGGCTCACTGCTGGATGAAAGACAGTGAAGAC 578
QY 545 TTGGACCTCAACATCAAGTACTCTGCGATGAGAGATGCCAACTCTTCTTAAAGCCAC 604
Db 579 TTGGAGCTCAATATCAAAATCTCAAGCCCAAGAAATGCCAACTTTTATCTAAGCTGGC 638
QY 605 TCCGCGTATACGAGCTGAAAGTCAAAGGCTCTTGGACCGCACAGCACTCTGGAGGAGT 664
Db 639 TCTGCTTTTCAGAGATGAATAATCAAGGGTGTCTGGAACGCGAGGGCTCTGGAGGAT 698
QY 665 CTGAGGGAGATGAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGATATGTTTT 724
Db 699 CTGAATGAGATGAAGAGTCTTCAACTTCGAGGAGACCCAGCAGCTGAGCAGCATTT 758
QY 725 GCACACTGGCAGAGATGCTTCTTGGCTCCAGTTCTTAATGGCATCAACCCGGTC 784
Db 759 GAGCATGGCAGAGAGATGCTTCTTGGCTCCAGTTCTGAATGGTCTCAACCCGTGC 818
QY 785 CTGATTCGCGCTGTCACTGTCTCCCAACAACTTCCCGTCACTGATGAATGGTGGCC 844
Db 819 CTGATCGCGCTGTCACTGTCTCCCAAGAACTTCCCGTCACTGATGCCATGGTGGCC 878
QY 845 CCAGTGTGGGCCCTGGAAACCAAGTCTGCAAGGCTGAGTTGGAAGGGCTCCCTGTTCTTG 904
Db 879 TCATTGTTGGGTCTGGGACCAAGTTCAGAGGCTGAGTAGAAGGGCTCCCTGTTCTTG 938
QY 905 GTGGATATGGCATTTCTTGTGAGTCCACACCAATCTCTAATGGAAAGCTCAGTTC 964
Db 939 GTGGATCAGGGCATCTCTCTGAGCATCCAGACCAATGTCAATTAATGGGAAGCGCAGTTC 998
QY 965 TCTGACGCCCCGATGACCTGTGTACACCAAGCTCAGGGTCCGAGCCCGTCTTCCCAAT 1024
Db 999 TCTGGCGCCCAATGATCCCTGTCTATACAGAGCCAGGCTGCGGGCGGTGTCCTCTC 1058
QY 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGACAAACCCCATCTTCTGCCACGCGATGAC 1084
Db 1059 GCCATCCAGCTCAGCCAGACCCCGGCCCAACAGCCCCATCTTCTGCCCCACTGATGAC 1118
QY 1085 ACGTGGAGCTGGTGTGCGCAAGACTGCGGTGCGCAATCTGAGTTTTTACATCCATGAG 1144
Db 1119 AAGTGGGAGCTGGTGTGCGCAAGACTGCGGTGCGCAATGCGGAGTTCTCTTCCATGAG 1178
QY 1145 GCTGTCAACATCTGCTGATGCCCATCTGATTCAGAAAGTCTTTCCTTGGCCACATTA 1204
Db 1179 GCCTCAGGACCTGTGCACTCAATCTGCTGCTGAGGTCTTACCTTGGTACCTGCT 1238
QY 1205 CGTCAGCTGCCTAGGTGTCAACCTCTCTTTCAAGCTATTGATTCTCTCACATTCGGTACACA 1264

RESULT 4
AAD04501
ID AAD04501 standard; cDNA; 2685 BP.
XX
AC AAD04501;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human 15S-lipoxygenase (15-Lox-2) cDNA.
XX
KW Human; 15S-lipoxygenase; 15-Lox-2; non-haeme iron dioxxygenase;
XX arachidonic acid; feed additive; livestock; antigen; ss.

Db 1239 CGTCAGCTGCCCCCACTGCCACCCCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACC 1298
QY 1265 CTGCACATCAACACACCTTGGCCGGAGTGTCTGTTGCCCTTGGGAAGTTGATAGACAAG 1324
Db 1299 CTGCACATCAACACACTGCCCGGAGTGTCTTATCTGTCGCCAGGCGAGGTGTGGACAGG 1358
QY 1325 TCACAGACCTTGGCACTGGGGGATTCTCTGACCTGATAAAGAGAAACATGAGAGCAGCTG 1384
Db 1359 TCACAGGACATCGGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
QY 1385 AACTACTCTGCTCTGTGTCTCCCTGGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCCA 1444
Db 1419 AACTATTCTCTCTGTGTCTGCTGAGGATATCCCGACCCCGAGGAGTTGAAGACATCCCA 1478
QY 1445 GGCTACTATTACCGAGATGATGGGATGTCAGATCTCTGGGGGCAATAAAGAGCTTTGTCTCT 1504
Db 1479 GGCTACTACTACCGTGTGATGGGATGTCAGATTTGGGGTGCAGTGGAAAGCTTTGTCTCT 1538
QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
Db 1539 GAAATCATCGGTATCTACTACCCAAAGTGTAGTCTGTCCAAGATGACAGAGAGCTCCAG 1598
QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGCTTCTCTGCGCCGAGAAAGCTCAGGTATGCC 1624
Db 1599 GCCTGGGTGAGGAGATCTTCTTCCAAGGGCTTCTTAAACCCAGGAGAGCTCAGGTATCCCT 1658
QY 1625 TCCTTGTGTTGGATACCCCGGAAGCCCTGTCTCAGTATATACCATGTGTATATTCACCTGTC 1684
Db 1659 TCCTCAGCTGGAGACCCCGGAAGCCCTGTGTCAGTATGTACCATGTGTATATTCACCTGTC 1718
QY 1685 TCAGCAAAGCATGTCAGCTGTCTCAGTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCAAT 1744
Db 1719 TCAGCAAAGCATGCGGCTGTCTCAGTGCAGGGCAGTTTGTACTCTGTGCTTGGATGCCAAT 1778
QY 1745 CTGCCACCTACATGTCAGCTTACCACCTACTTCTTCAAAGGCCAGCCCGGCTCAGAGT 1804
Db 1779 CTGCCACCCAGCATGTCAGCTGCCACCCACCTTCAAAGGGCTTGGCAACATTCGAGGGC 1838
QY 1805 TTTCATAGCCAGCTCCCGAGCAGTTAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTG 1864
Db 1839 TTTCATAGCCACCTCCACCTGTCAATGGCAATGTGATGTCTCTGCTCTCTGTTG 1898
QY 1865 CTAAGCGCAGAACCTGGGGCCAAAGGCCCTTGGGCCACTATCCAGATGAACACTTACA 1924
Db 1899 CTGAGCAAAGGAGCTGGAGACCAAGGGCCCTTGGGCACCTATCCGATGAGCACTTACA 1958
QY 1925 GAGGATGCCCCCGCGGAGAGGTGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984
Db 1959 GAGGAGGCCCTTGGCGGAGCATCGCCACCTTCCAGAGCCCGCTGGCCCGAGATCTCGAGG 2018
QY 1985 GGCATCAGGAGAGGAACCGAGGCTTGGCCTTACCTTACCTTACCTGATCCTCCCCCTC 2044
Db 2019 GGCATCAGGAGAGGAACCGGGGCTTGGTGTGCTGCCCTACCTTACCTAGACCTTCCCTC 2078
QY 2045 ATTGGAACAGTGTCTCCATCTAACTTGGAGAAAGCAGTCTGTGTGACAT 2098
Db 2079 ATCGAGAACAGGTCTCCATCTTAATCCAGGGGAACACAGGCCCCAGATGACAT 2132

QY 1505 GAAATAGTCAGCATCTACTATCAAGTGAACAATCCGTCAAGATGACCAAGAGCTCCAG 1564
Db |||||
QY 1539 GAAATCATCGGTACTTACTACCAAGTGAATGATCTGTCTCAAGATGACAGAGAGCTCCAG 1598
Db |||||
QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGCTTCCCTGGCGGAGMAAGCTCAGGTATGCC 1624
Db |||||
QY 1599 GCCTGGGTGAGAGATCTTCTCAAGGGCTTCCCTAAACAGGAGAGCTCAGGTATCCCT 1658
Db |||||
QY 1625 TCCTTCTTGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGTGTATATTCACCTGC 1684
Db |||||
QY 1659 TCCTCACTGGAGACCCGGGAGCCCTGGTGCAGTATGTACCATGTGTATATTCACCTGC 1718
Db |||||
QY 1685 TCAGCAAGATGACAGCTGTAGTTCAGGCCAGTTCGATCTCTGTGTTGGATGCCAAT 1744
Db |||||
QY 1719 TCAGCCAAAGCATGCGCTGTCAAGTGCAGGCGAGTTTGAATCTCTGTGATGCCAAC 1778
Db |||||
QY 1745 CTGCCACCTACCATGAGCTACCAACCACTTCTCAAGGCGAGCCCGGCTGAGAT 1804
Db |||||
QY 1779 CTGCCACCCAGCATGAGCTGCCACCACTTCCAAAGGGCTTGGCAACATGCGAGGGC 1838
Db |||||
QY 1805 TCCATAGCCACGCTCCAGCAGTTAATTCGTCAAGTTATCATCATCTTCTCTGGCTG 1864
Db |||||
QY 1839 TCCATAGCCACCTCCACCTGTCAATGCCACATGTGATCATCTTCTCTGGTGTG 1898
Db |||||
QY 1865 CTAAGCGCAGAACCTGGGACCAAAAGCCCTGGGCCACTATCCAGATGAACACTTCA 1924
Db |||||
QY 1899 CTGAGCAAGGAGGCTGGAGACCAAAAGCCCTGGGCACCTATCCGATGAGCACTTCA 1958
Db |||||
QY 1925 GAGGATGCCCCCGGCGAAGCGTGGTCTTCCAGAGAAAGTATCCAGATCTCCAG 1984
Db |||||
QY 1959 GAGGAGGCCCCCTGGCGGAGCATGCGCCACTTCCAGAGCGGCTGGCCCGAGATCTCGAGG 2018
Db |||||
QY 1985 GGCATCAGGAGAGGAGAACCGAGGCGCTGGCACTGCGCTACACCTACTCTGATCTCCCTC 2044
Db |||||
QY 2019 GGCATCAGGAGGAGAACCGGCGGCTGGTCTGCTGCTTACCTACTACCTTCCCTC 2078
Db |||||
QY 2045 ATTGAAACAGTGTCTTCCATCTAATCTTGGAGAGAGACGCTCTGTGTGACAT 2098
Db |||||
QY 2079 ATCGAAGACAGCTCTCCATCTAAATCCAGGGGAAACACAGGCCCGAGATGACAT 2132
Db |||||

RESULT 5
ID ABK92181
XX standard; DNA; 2685 BP.
AC ABK92181;
XX
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #67.
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; db.
KW Mammalia.
XX
XX WO200230268-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US032045.
XX
XX 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX

PA (BOB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI: 2002-471335/50.
DR P-PSDB; ABG61866.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 351; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;
Query Match 43.3%; Score 1395.2; DB 6; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;
QY 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGGCGAAATGCAGGGTGAGATATCCACG 64
Db 42 GCCGTAGAGAGCTGGACTTAGCTGGCAGCATGGCCGAGTTTCAGGGTCAGGGTGTCCACC 101
QY 65 GGGGAAGCCTGTGGGGCTGGACATGGGACAAAGTGTCTGTGACGATGCTGGGAACCCAC 124
Db |||||
QY 102 GGAGAAGCCTTCGGGGCTGGCACAATGGGACAAAGTGTCTGTGACGATGCTGGGGACCCGG 161
Db |||||
QY 125 GGAGAGAGCCCTTAGTACCTCTGACCATCTGGGCAAGGAGTTTCAGCGCCGCTGTAA 184
Db |||||
QY 162 GGAGAGAGCCCTTAGTACCTCTGACCAATCTCGGCAAGGAGTTTCAGCGCGCTGAG 221
Db |||||
QY 185 GAAGACTTCGAGGTGACGCTTCCCGAGGACGCTAGGCACCTGTGCTGATGCTGCGAGTCCAC 244
Db 222 GAGGACTTCAGGTGACGCTCCCGGAGGACGCTAGGCCGAGTGTCTGTGCGGTGCAC 281
QY 245 AAAGCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTCCGTTCTGTGATGCTCTGGTTCGC 304
Db 282 AAGCGCCCCC---AGTGTGCCCCCTGTGGGGCCCCCTGGCCCCGATGCTGTGCTGC 338
QY 305 CGCTGTTTCGAGCTGAGTGGCTACTGGGGCTGCACCTCCACTTCCCTGTTTATCAGTGG 364
Db 339 CGCTGTTTCGAGCTGACACCCCGGGGCGGCGCACCTTCTTCCCCCTGTACAGTGG 398
QY 365 CTGGAAGGGGGGGGAGCTGGTGTGAGAGAGGAGGAGCAAAAGGTGTCTCTGGCAAGAC 424
Db 399 CTGGAAGGGGGGGGAGCCCTGTGTGTGAGAGGGGTACAGCCAAAGTGTCTCTGGGCAGAC 458
QY 425 CATCAACCTACACTGACGATCAGGCCAGAGAGGCTTGTAGTCCAGGCAGAGATGTAC 484
Db 459 CACCACCTGTGCTCCAGCAACAGCGCCAGGAGGAGTTCAGGCCCGGCGAGAGATGTAC 518
QY 485 AGCTGGAAGACTTACATTTGAAGTTGGCTCGCTCCCTTGACACGAGACTGTGAAAGAC 544
Db 519 CAGTGAAGGGCTTACACCCAGGTTGGGCTCTACTCCCTGGATGAAAGACAGTGAAGAC 578

Qy	545	TTGGACCTCAACATCAAGTACTCTGCGGATGAAGAAATGCCAAACTCTTCTTTTAAAGCCCAAC	604
Db	579	TTGGAGCTCAATATACAAATATCTCCACAGCAAGAATGCCAACTTTTATCTACAAGCTGGC	638
Qy	605	TCCGCGTATACGGAGCTGAAGTCAAAAGGGCTCTGGACCGCACAGGACTCTCGAGGAGT	664
Db	639	TCTGCTTTTGAGAGATGAATAATCAAGGGGTGCTGGACCCGAAGGGCTCTCGAGGAGT	698
Qy	665	CTGAGGGAGATGAGAAGCTGTTTAACTTCCGCGAAGACTCCAGCAGCAGAGTATGTGTGTTT	724
Db	699	CTGAATGAGATGAAGAAGTCTTCAACTTCCGGAGGACCCAGCAGCTGAGCAGCATTT	758
Qy	725	GCACACTGGCAGAGATGCTCTTTCGCTCCAGTCTCTTAATGCGATCAACCCGGTCT	784
Db	759	GAGCACTGGCAGGAGATGCTCTTTCGCTCCAGTCTCTGAAATGGTCTCAACCCCTGTC	818
Qy	785	CTGATTCCGCGCTGFCACAGTCTCCCAAAACAATCCCGGTCACTGATGAATGGTGGCC	844
Db	819	CTGATCCGCGCTGTCACTCTCCAAAGAACTTCCCGGTCACTGATGCCATGGTGGCC	878
Qy	845	CCAGTGTGGGCCCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAAGGGCTCCCTGTTCTTG	904
Db	879	TCAITGTTGGTCTCGGACCAGCTTGACGCTGAGCTAGNAGAAGGGCTCCCTGTTCTTG	938
Qy	905	GTGATCATGCGATCTTTCTGAGTCCACACCAACATCTCAATGAAGAAAGCTCAGTTC	964
Db	939	GTGGATCAGCGCATCTCTTGGCATCCAGACCAATGTCTAATTAATGGAAGCCGAGTTC	998
Qy	965	TCTCGAGCCCGATGACCTGTTACACGAGGCTCAGGTCGGGACCCCTGCTTCCCATT	1024
Db	999	TCTCGGCCCCAATGACCCCTGCTATACGAGACCCAGGCTCGGGCGGCTGCTGCCCTCTC	1058
Qy	1025	GCCATCCAGCTCAAAACAGACTCCCGGGCCAGACAAACCCCATCTTCTCGCCCAGCGATGAC	1084
Db	1059	GCATCCAGCTCAGCCAGACCCCGGCCCAAGACGCCCATCTTCTTGCCTGCCACTGATGAC	1118
Qy	1085	ACGTGGGACTGGTCTGTGGCCAGACCTGGGTTCGCAATTTCTGAGTTTTACATCCATGAG	1144
Db	1119	AAGTGGGACTGGTGTCTGGCCAGACACTGGGTGGCAATCCGAGTCTCTCCTTCCATGAG	1178
Qy	1145	GCTGTCAACATCTGTGTCATGCCCATCTGATTTCCAGAGTCTTTGCTTGGCTTGGCCACATTA	1204
Db	1179	GCCCTCAGCACCTGCTGCATCTCATCTGCTGCTGAGTCTTCAACCTGGCTTACCCTG	1238
Qy	1205	CGTCAGCTGCCCTAGGTGTCAACCTCTCTTCAAGCTATTGATTCTCTCACTTCCGTACACA	1264
Db	1239	CGTCAGCTGCCCTAGGTGTCAACCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACCC	1298
Qy	1265	CTGCACATCAACAGCTTTGCCCGGGAGCTGCTGCTGCCCTGGGAAGTTGATAGACAAG	1324
Db	1299	CTGCACATCAACACACTCGCCCGGGAGCTGCTTATCGTGGCCAGGGAGGTGGACAGG	1358
Qy	1325	TCCACAGGCTTTGGCATGGGGGATTTCTTGACCTGATTAAGAGAAACATGAGGACGCTG	1384
Db	1359	TCCACAGGCATCGGCATTGAAGGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG	1418
Qy	1385	AACACTCTGTCTGTGCTCCCTGAAGATATCCGAGCCGAGGTGTGGGAAGACATCCCCA	1444
Db	1419	AACATTTCTCTCTGTGCTGCGCTGAGGATATCCGGACCCGAGGAGTTGAAGACATCCCA	1478
Qy	1445	GGCTACTATTACCGAGATGATGGGATGCGAGTCTGGGGGGCAATAAAGAGCTTTGTCTCT	1504
Db	1479	GGCTACTACTACCGTATGATGGGATGCGAGATTTGGGGTGCAGTGGAAACGCTTTGTCTCT	1538
Qy	1505	GAATATGTCAGCATCTACTATCCAGTGAACACATCCGTCGAGATGACCAAGAGCTCCAG	1564
Db	1539	GAATATCATCGGTATCTACTATCCCAAGTGAAGTCTGTCTCCAAAGATGACAGAGAGCTCCAG	1598
Qy	1565	GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGCGCGAGAAAGCTCAGGTATGCCCT	1624
Db	1599	GCCTGGGTGAGAGATCTTCTTCCAAAGGGCTTCTTAAACAGGAGAGCTCAGGTATCCCT	1658
Qy	1625	TCCTTTGTTGGATACCCGGGAAGCCCTGGTCCAGTATATCAACATGGTGAATATCACTGTC	1684

Db	1659	TCCTCACTGGAGACCCGGGAAGCCCTGGTGCAGATATGTTCACCATGGTGATATTCACCTGC	1718
Qy	1685	TCAGCCAAAGCATGCAGCTGTTCAGTTCAAGGCCAGTTGCAGTCTTGTGTTCGATGCCCCAAT	1744
Db	1719	TCAGCCAAAGCATGGCGTGTTCAGTGCAGGCCAGTTTGAATCTCTGTGCTTGGATGCCCAAC	1778
Qy	1745	CTGCCACCTACCATGCACTACCAACCACTTCTTCCAAAGGCCAGGCCCGCCTGAGAGT	1804
Db	1779	CTGCCACCCAGCATGCAGCTGCCACCACTCCAAAGGCCCTGGCAACATCGAGGGC	1838
Qy	1805	TTCAATAGCCAGCTCCAGCAGTTAATTCGTCAAGTTATCATCATCTTGTCTCTGGCTG	1864
Db	1839	TTCAATAGCCACCTCCCACTGTCAATGCCCACATGTGATGTCTATCTCTCTGTGTTG	1898
Qy	1865	CTAAGCCGAGAACTGGGGACCAAGGCCCTGGCCACTATCCAGATGAACACTTCACA	1924
Db	1899	CTGAGCAAGAGAGCTTGAGACCAAGGCCCTGGGCACCTATCCGATGAGCACTTCACA	1958
Qy	1925	GAGGATCCCCCGGGAAGCGTGGCTTCCAGAGAAAGTGTATCCAGATCTCCAAAG	1984
Db	1959	GAGGAGGCCCTCGGCGGAGCATGCCACCTTCCAGAGCGCCTGGCCAGATCTCGAGG	2018
Qy	1985	GGCATCAGGAGAGAGAACCGAGCGCTGGCACTGCCCTACACTTACCTGATCTCTCCCTC	2044
Db	2019	GGCATCCAGGAGGGGAACCGGGCGCTGGTCTGCTGCTTACACTTACCTAGACCTCCCTC	2078
Qy	2045	ATTGAGAACAGTGTCTCATCTAACATCTTGGAGAGACAGTCTCTGTGCACAT	2098
Db	2079	ATCAGAACAGCGTCTCCATCTTAATCCAGGGGAACACAGGCCAGATGACAT	2132
RESULT 6			
ABK64747			
ID	ABK64747 standard; DNA; 2685 BP.		
AC	ABK64747;		
XX	18-JUN-2002 (first entry)		
DT	Human benign prostatic hyperplasia gene #642.		
DE	Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.		
XX	Homo sapiens.		
XX	WO200212440-A2.		
PN	14-FEB-2002.		
XX	07-AUG-2001; 2001WO-US024708.		
PF	07-AUG-2000; 2000US-0223323P.		
XX	05-JUN-2001; 2001US-00873319.		
PR	(GENE-) GENE LOGIC INC.		
XX	(NLSB) JAPAN TOBACCO INC.		
PA	Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;		
XX	WPI; 2002-257476/30.		
DR	Identifying drugs for and diagnosing benign prostatic hyperplasia, by		
XX	detecting expression levels of one or more genes in prostate cells from		
PT	patient that are differentially regulated compared to normal prostate		
PT	cells.		
XX	Disclosure; Page 351; 44pp; English.		
PS	The invention relates to a method of diagnosing (I) the onset or		
XX	progression of benign prostatic hyperplasia (BPH), or screening (II) for		
CC	or identifying an agent that modulates the onset or progression of BPH.		
CC	The method is based on changes in gene expression in BPH tissue isolated		

Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate cells.

Disclosure; Page 351; 444pp; English.

The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolated

CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles. (I)
CC is useful for diagnosing the onset or progression of BPH. (II) is useful
CC for identifying an agent that modulates the onset or progression of BPH.
CC The methods are useful to present information identifying the expression
CC level in a tissue or cells, by comparing the expression level of genes
CC given in the specification in the tissue or cells to the level of
CC expression of gene in the database, and displaying the expression levels
CC of at least one gene in the tissue or cell sample compared to the
CC expression level in BPH. Agents using (II) are useful for treating BPH or
CC prostate cancer. ABK64106-ABK64860 represent human benign prostatic
CC hyperplasia gene sequences of the invention
XX
SQ Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;

Query Match 43.3%; Score 1395.2; DB 6; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY 7 GCAGTAGAGAGCTAACT--GGTCAGGAGGATGGCGAATGACAGGGTGAGAGATCCACG 64
DB 42 GCCGTAGAGAGCTGGACTTAGCTGSCAGCATGGCCGAGTTTCAGGGTCAGGGTCTCCACC 101
QY 65 GGGGAAGCCTGTGGGGCTGGACATGGGACAAGATGTCTGTGAGCATGTGGGAACCCAC 124
DB 102 GGAGAAGCCTTCGGGGCTGGGCATGGGACAAGATGTCTGTGAGCATGTGGGGACCCGG 161
QY 125 GGAGAGAGCCCTTAGTACTCTCGACCATCTGGCAAGAGTTTCAGGCCCGCTGTGA 184
DB 162 GGAGAGAGCCCCCACTGCCCTTGGACAATCTGGCAAGAGTTTCACTGGGGCGCTGAG 221
QY 185 GAAGACTTCGAGGTGACGCTTCCCAGGACGTAGGCACCTGTGCTGATGTCGGAGTCCAC 244
DB 222 GAGGACTTCAGGTGACGCTCCCGGAGGACGTAGGCCGAGTGTCTGCTGCGCTGCAC 281
QY 245 AAGCAACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCCCTGGTTCTGC 304
DB 282 AAGGCCCCCCC---AGTGTGCCCTCTGCTGGGGCCCTCGGCCCGGATGCCCTGGTTCTGC 338
QY 305 CGCTGGTTCGAGCTGAGTGGCTTACCTGGGGCTGCATCCACTTCCCTGTTTACAGTGG 364
DB 339 CGCTGGTTCCAGCTGACACCGCCGCGGGGGCGGCACCTCTCTTCCCTGCTACAGTGG 398
QY 365 CTGGGAAGGGCGGGGAGCTGTGCTGAGAGAGGAGCAGCAAGAGTGTCTTGGCAAGAC 424
DB 399 CTGGAGGGGGCGGGACCCCTGTGCTGCAGGAGGGTACAGCCAAGTGTCTTGGGCAGAC 458
QY 425 CATCACCTTACCTGAGGATCAGCCCAAGAGGAGCTTGTAGTCCAGGAGAGATGTAC 484
DB 459 CACCACCTGTGTCTCAGCAACAGCCCGCAGGAGGAGCTTCAGGCCCGGCGAGAGATGTAC 518
QY 485 AGCTGGAAGACTTACATTGAAGTGGCTCGCTGCTTGGACACAGAGACTGTGAAGAC 544
DB 519 CAGTGAAGGCTTACAAACAGGTTGGCTCTACCTGCTGGATGAAGAAGACATGTGAAGAC 578
QY 545 TTGGAGCTCAACATCAAGTACTCTGCGATGAAGAATGCCAAACTCTTCTTTTAAAGCCCA 604
DB 579 TTGGAGCTCAATATCAATTAATCTCCAGCAAGAGTCCCACTTTTATCTACAAGCTGGC 638
QY 605 TCCGCGTATACGAGCTGAAGTCAAGGGCTCTGGACCGGACAGGACTCTGGAGAGT 664
DB 639 TCTGCTTTTGCAGAGATGAATAACAAGGGTGTCTGGACCGCAAGGGGCTCTGGAGGAGT 698
QY 665 CTGAGGGAGATGAGAGGCTGTTTAACTTCCGACAGACTCCAGGACGAGATGTGTTT 724
DB 699 CTGAATGAGATGAAGAGGATCTTCAACTTCCGAGGAGCCCGAGCAGCTGAGCACGCAATTT 758

QY 725 GCACACTGGCAGGAAGATGCCTTCTTGCCTCCAGTTCTTAATGGCATCAACCCGGTC 784
DB 759 GAGCACTGGCAGGAGATGCCTTCTTGCCTCCAGTTCTTGAATGGTCTCAACCTGTCTC 818
QY 785 CTGATTCCGCCCTGTCTCAGCTCTCCAAACAACACTTCCCGGTCACTGATGAATGTGGCC 844
DB 819 CTGATCCGCCCTGTCTCTCTCCAAAGAATCTTCCCGTCACTGATGCCATGTGGTGGCC 878
QY 845 CCAGTGTCTGGGCCCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAAGGGCTCCCTGTCTTG 904
DB 879 TCATTTGTTGGGTCTCTGGACAGCTTGCAGGCTGAGCTAGAGAAGGGCTCCCTGTCTTG 938
QY 905 GTGATCATGAGATCTTTCTTGTGAGTCCACCAACATCTCTCAATGGAAGAGCTCAGTTC 964
DB 939 GTGGATCAACGGCATCTCTCTGGCATCCAGACCAATGTCAATTAATGGGAAGCGCAGTTC 998
QY 965 TCTGCAGCCCGATGACCTGTATACACAGAGCTCAGGTCGGGACCCCTGCTTCCCATTT 1024
DB 999 TCTGCGGCCCAATGACCTGTATACAGAGCCAGGCTGCGGGCCCGCTGCTGCTCTC 1058
QY 1025 GCCATCCAGCTCAAAACAGACTCCCGGGCCAGACAACCCCATCTTCTGCCCCAGCGATGAC 1084
DB 1059 GCCATCCAGCTCAGCCAGACCCCGGCCCAACAGCCCCCATCTTCTGCCCCACTGATGAC 1118
QY 1085 ACGTGGGACTGGTGTCTGGCCAGACCTGGGTTCGCAATTTCTGAGTTTTTACATCATGAG 1144
DB 1119 AAGTGGGACTGGTGTCTGGCCAAAGACCTGGGTGGGCAATGCGGAGTTCTCTCTTCCATGAG 1178
QY 1145 GCTGTACACATCTGCTGATGCCCATCTGATTCACAGAAGTCTTTGCTTGGCCACATTA 1204
DB 1179 GCCCTTACGCACTGCTGCACTCATCTGCTGCTGAGGCTTCCACCTGGCTTACCCTG 1238
QY 1205 CGTCAGCTGCTAGGTGTCACTCTCTTCAAGCTTATGATTTCTTCAATTTGGGTACACA 1264
DB 1239 CGTCAGCTGCCCACTGCACTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACC 1298
QY 1265 CTGCACATCAACACGCTTTGGCGGAGCTGCTGTTGGTCCCTCGGAAAGTTGATGACAAAG 1324
DB 1299 CTGCACATCAACACACTCGCCGGGAGCTGCTTATCGTGCAGGGCAGGTGGTGACAGG 1358
QY 1325 TCCACAGGCTTGGCACTGGGGGATCTCTGACCTGATAAAGAGAAACATGAGAGAGCTG 1384
DB 1359 TCCACAGGATCGGCAATGAAGGCTTCTCTGAGTTGATACAGAGGAAATGAAGCAGCTG 1418
QY 1385 AACTACTCTGCTGTCTCTTCAAGATATCCGAGCCCGAGGTGTGGAGACATCCCA 1444
DB 1419 AACTATTTCTCTCTGTCTGCTGAGATATCCGGACCCCGAGGATTTGAAGACATCCA 1478
QY 1445 GGCTACTATTACCGAGATGATGGGATGAGATCTTGGGGGGCAATAAAGAGCTTTGTCTCT 1504
DB 1479 GGCTACTACTACCGTATGATGGGATGAGATTTTGGGGTGCAGTGGAAACGCTTTGTCTCT 1538
QY 1505 GAATAGTCAGCATCTACTATCCAAAGTACACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
DB 1539 GAATCATCGGTATCTACTACCCAAAGTATGAGTCTGTCTCAAGATGACAGAGCTCCAG 1598
QY 1565 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTGGCCCGAGAAAGCTTCAGGTATGCC 1624
DB 1599 GCCTGGGTGAGAGATCTTCTTCAAGGGCTTCTTCAAGGGCTTCCTAAACAGGAGCTCAGTATCCCT 1658
QY 1625 TCCTTTGTTGGATPACCCGGGAAGCCCTGTGTCAGTATATCAACATGGTATATTCACCTGC 1684
DB 1659 TCCTCACTGGAGACCCGGGAAGCCCTGTGTGAGTATGTCAACATGGTATATTCACCTGC 1718
QY 1685 TCAGCCAGCATGACAGCTGCTGAGTTCAGGCCAGTTCTGACTCTTGTGTTGGATGCCAAT 1744
DB 1719 TCAGCAAGCATGCGGCTGTGAGTGCAGGGCAGTTTGTACTCTCTGTGCTTGGATGCCAAT 1778
QY 1745 CTGCCACCTTACCATGCAGTACCACTACTTCCAAAGGCGAGGCCCGGCTCTGAGAGT 1804
DB 1779 CTGCCACCCAGCATGACAGTGCACCACTCCAAAGGCTCCAAAGCAACATGCCAGGGC 1838
QY 1805 TTCATAGCAAGCTCCCGAGAGTTAAATTCGTCAAGTTATACATCATTTGCTCTCTGGGCTG 1864

Db	1839	TTATAGCCACCCCTCCCACTGTCAATGCCACATGTATGTCACTTGTCTCTGTGTTG	1898
Qy	1865	CTAAGCCGAGAACTGGGGGACCAAGGCCCTGGGCCCACTATCCAGATGAACACTTCCACA	1924
Db	1999	CTGAGCAAGAGAGCTGGAGACCAAGGCCCTGGGCACTATCCGATGAGCACTTCCACA	1958
Qy	1925	GAGATGCCCCCCCGGAGAGCGTGGCTGCTTCAGAGAAAGCTGATCCAGATCTCCAAG	1984
Db	1959	GAGGAGGCCCTCGCGGAGCATGCCACCTTCCAGAGCGGCTGGGCCAGATCTCGAGG	2018
Qy	1985	GGCATCAGGAGAGAACCGAGGCCCTGGCACTGCCCTACACCTACCTGGATCTCCGCCCTC	2044
Db	2019	GGCATCAGGAGCGGAACCGGGGCTGGTGTGCCCTTACACCTACCTAGACCTCCGCCCTC	2078
Qy	2045	ATTGAGAACAGTGTCTCCATCTAATCATCTTGGAGAGACAGTCTCTGTGTGCATAT	2098
Db	2079	ATCAGAACAGCGTCTCCATCTAATCCAGGGGACACAGGCCAGATGACAT	2132
RESULT 7			
ACA89907			
ID	ACA89907 standard; cDNA; 2685 BP.		
AC	ACA89907;		
DT	10-JUL-2003 (first entry)		
XX	Gene differentially regulated in cardiovascular disease #28.		
DE	Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;		
KW	myocardial infarction; caridant; antiarteriosclerotic; antianginal;		
KW	gene therapy; differential gene expression; gene; ss.		
OS	Homo sapiens.		
XX	WO2003031650-A2.		
FN	17-APR-2003.		
XX	02-OCT-2002; 2002WO-EP011034.		
PF	08-OCT-2001; 2001GB-00024145.		
XX	(FARB) BAYER AG.		
PR	Munnes M, Gehrman M, Wick M, Schmitz G;		
XX	WPI; 2003-403108/38.		
DR	P-PSDB; ABU89734.		
PT	Predicting, diagnosing or prognosing a cardiovascular disease, e.g.		
PT	angina, ischemia, myocardial infarction or arteriosclerosis by detection		
PT	of a polynucleotide in a biological sample comprises detecting a		
PT	hybridization complex.		
XX	Claim 1; Page 176-178; 454pp; English.		
PS	The invention describes a method of predicting, diagnosing or prognosing		
XX	a cardiovascular disease by detection of a polynucleotide in a biological		
CC	sample comprises hybridising at least one of the polynucleotide to a		
CC	nucleic acid material of a biological sample, thus forming a		
CC	hybridisation complex, and detecting the hybridisation complex. The		
CC	polynucleotides, polypeptides, antisense molecule, antibody and reagent		
CC	are useful for preparing compositions for preventing, predicting or		
CC	diagnosing, or a medicament for treating a cardiovascular disease, e.g.		
CC	arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.		
CC	This sequence represents a gene identified in the invention, a being		
CC	differentially regulated in individuals with cardiovascular disease		
XX	Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;		
SQ	Query Match 43.3%; Score 1395.2; DB 8; Length 2685;		

Query Match

[illegible]

Db 1059 GCCATCCAGCTCAGCCAGACCCCGCCCAAAACAGCCCCCATCTTCTGTCGCCACTGATGAC 1118
QY 1085 ACCTGGGACTGTGTGTCGCCAAGACCTGGGTTCGCAATCTTGAGTTTACATCATGAG 1144
Db 1119 AAGTGGGACTGTGTGTCGCCAAGACCTGGGTTCGCAATCTTGAGTTTACATCATGAG 1178
QY 1145 GCTGTACACATCTGTGTGATGCCATCTGATTTCCAGAAAGTCTTTGCTTGGCCCAATPA 1204
Db 1179 GCCTCAGCACCTGTGTGACTCACATCTGTGCTGAGTCTTCACTCCCTGCTACCCCTG 1238
QY 1205 CGTCAGCTGCTAGGTGATCAGCTCTCTTCAAGCTATTGATTCCTCACATTCGGTACACA 1264
Db 1239 CGTCAGCTGCCACCTGCCACCCCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACAC 1298
QY 1265 CTGCACATCAACACGCTTGCCTGGGAGCTGCTGTTGCCCTGGGAAGTTGATAGACAAG 1324
Db 1299 CTGCACATCAACACCTGCTGGGAGCTGCTTATCGTCCAGGGCAGGTGTGNCAGG 1358
QY 1325 TCCACAGGCTTGGCACTGGGGGATTTCTCTGACCTGATAAAGAGAAACATGAGCAGCTG 1384
Db 1359 TCCACAGGCTTGGCACTGGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
QY 1385 AACTACTCTGTCTGTCTCTCTGAGATATCCGAGCCCGAGGTGTGAAGACATCCCA 1444
Db 1419 AACTATTCTCTCTGTCTCTGCTGAGGATATCCGAGCCCGAGGTGTGAAGACATCCCA 1478
QY 1445 GGCTACTATTACCGAGATGATGGGATGTCAGATCTGGGGGCAATAAAGAGCTTTGTCTCT 1504
Db 1479 GGCTACTACTACCGTATGATGGGATGTCAGATTTGGGGTGCAGTGAACGCTTTGTCTCT 1538
QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTGACACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
Db 1539 GAAATCATCGGTATCTACTACCCCAAGTGATGAGTCTGTCCAAAGTGACAGAGAGCTCCAG 1598
QY 1565 GCCTGGGTAGGAGATCTTCTCTGAGGGTCTCTCGCGCGGAGAAAGCTCAGTATGCC 1624
Db 1599 GCCTGGGTAGGAGATCTTCTCTCAAGGGCTTCTCTAAACCGAGGAGCTCAGGTATCCCT 1658
QY 1625 TCCTTGTGTGATACCCGGGAAGCCCTGCTCCAGTATATCACCATGTGTATATTCACCTCG 1684
Db 1659 TCCTCACTGGAGACCCGGAGAGCCCTGTGTGAGTATGTCCACATGTGTATATTCACCTGC 1718
QY 1685 TCAGCCAAGATGACGTGTGAGTTCAGGCCAGTTCGACTCTGTGTGTTTGGATGCCAAT 1744
Db 1719 TCAGCCAAGATGACGTGTGAGTTCAGGCCAGTTCGACTCTGTGTGTTTGGATGCCAAT 1778
QY 1745 CTGCCACCTACCATGACGTACACACCTACTTCCAAAGGCGAGCCCGGCTGAGAT 1804
Db 1779 CTGCCACCTACCATGACGTACACACCTACTTCCAAAGGCGAGCCCGGCTGAGAT 1838
QY 1805 TCCATAGCCACGCTCCCGAGCAATTAATCGTCAAGTTATCAGATCATTTGCTCTCTGGCTG 1864
Db 1839 TCCATAGCCACCTCCCGAGCAATTAATCGTCAAGTTATCAGATCATTTGCTCTCTGGCTG 1898
QY 1865 CTAAGCCGCAAACTCTGGGACCAAAAGCCCTGGGCCACTATCCAGATGAACACTTCACA 1924
Db 1899 CTGAGCAAGAGGCTCTGGAGACCAAAAGCCCTGGGCCACTATCCAGATGAACACTTCACA 1958
QY 1925 GAGGATGCCCCCGGCGAAGCGTGGCTGCTCCAGAGAAAGTATCCAGATCTCCAG 1984
Db 1959 GAGGATGCCCCCGGCGAAGCGTGGCTGCTCCAGAGAAAGTATCCAGATCTCCAG 2018
QY 1985 GGCATCAGGAGAGGAACCGAGGCTGGCACTGSCCTACACCTTACCTGGATCTCTCCCTC 2044
Db 2019 GGCATCAGGAGAGGAACCGAGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2078
QY 2045 ATTGAGAACAGTGTCTCCATCTTAACATCTTGGGAAGACAGCTCTGTGTGACAT 2098
Db 2079 ATCGAGAACAGCTGTCTCCATCTTAATCCCAAGGGGAACACAGGCCCGAGATGACAT 2132

RESULT 8
ADQ91798

ID ADQ91798 standard; cDNA; 2685 BP.
AC ADQ91798;
DT 07-OCT-2004 (first entry)
XX Human lipoxxygenase 15-Lox-2 cDNA.
DE lipoxxygenase; iron ligand; arachidonic acid metabolism; human;
KW lipoxxygenase 15-Lox-2; ss; gene.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 72..2102
FT /tag= a
FT /product= "Human lipoxxygenase 15-Lox-2"
XX
PN US2004137483-A1.
XX
PD 15-JUL-2004.
XX
PF 18-NOV-2003; 2003US-00716204.
XX
PR 16-APR-1998; 98US-00061768.
PR 17-JAN-2001; 2001US-00764246.
XX (BRAS/) BRASH A R.
PA (BOEG/) BOEGLIN W E.
PA (JISA/) JISAKA M.
XX
PI Brash AR, Boeglin WE, Jisaka M;
XX
DR WPI: 2004-533356/51.
DR P-PSDB; ADQ91763.
XX
PT New lipoxxygenase nucleic acid segment comprises an isolated gene encoding
PT a lipoxxygenase containing an iron ligand comprising a serine, useful for
PT arachidonic acid metabolism.
XX
PS Claim 10; SEQ ID NO 1; 39pp; English.
XX
CC The invention describes a nucleic acid segment (I) comprising an isolated
CC gene encoding a lipoxxygenase containing an iron ligand comprising a
CC serine, or comprises at least a 10 nucleotides long contiguous stretch of
CC the nucleic acid sequence not given in the specification (SEQ ID NO. 1)
CC or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a
CC nucleic acid segment comprising at least 10 nucleotides long contiguous
CC stretch of the nucleic acid sequence not given in the specification (SEQ
CC ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is
CC a polypeptide having the amino acid sequence Trp-Leu-Ala-Lys (SEQ ID
CC NO. 5) and Gly-Gln-Tyr-Asp-Tip (SEQ ID NO. 35). The lipoxxygenase nucleic
CC acids and proteins are useful in arachidonic acid metabolism. This
CC sequence encodes human lipoxxygenase 15-Lox-2.
SQ Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;

Query Match 43.3%; Score 1395.2; DB 12; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY 7 GCAGTAGAGAGCTAACT--GGTCAGGAGGATGGCGAAATGACGGGTGAGATATCCACG 64
Db 42 GCCGTAGAGAGCTGACTAGGCTGGCAGCATGGCCGAGTTCCAGGTTCAGGTGTCACC 101
QY 65 GGGGAAGCCTGTGGGCTGGCAGCATGGGACAAAGTGTCTGTTCAGCATGTGGGAACCCAC 124
Db 102 GGAGAAAGCCTTTCGGGCTGGCAGCATGGGACAAAGTGTCTGTTCAGCATGTGGGACCCG 161
QY 125 GGAGAGAGCCCTTAGTACCTCTGCACCATCTGGGCAAGGAGTTCCAGGCGCGGTCTGAA 184
Db 162 GGAGAGAGAGCCCTTAGTACCTCTGCACCATCTGGGCAAGGAGTTCTCTGGGCGCTGAG 221

185 GAAGACTTCGAGGTGACGCTTCCCGAGGAGCTAGGCACTGTGCTGATGTCGGATCCAC 244
Db |||||
222 GAGGACTTCCAGGTGACGCTCCCGAGGAGCTAGGCGGAGTCTGCTGCGCTGAC 281
Qy |||||
245 AAAGCACCCCCGGAAGTGTCCCTCCCGCTTATGTCTTCCGTTCTGTGATGCTCTGCTGCG 304
Db |||||
282 AAGGCGCCCC--AGTGTGCTGCTGCTGGGCGCCCTGGCCCGGATGCTTGGTTCTGCG 338
Qy |||||
305 CGCTGGTTCGAGCTGAGTGGTACTCTGGGGCTGCACTCCACTTCCCTCTGTTATCAGTGG 364
Db |||||
339 CGCTGGTTCGAGCTGACACCGCGCGGGCGGCCACCTCTCTCCCTGCTACCACTGG 398
Qy |||||
365 CTGGAAGGGCGGGGAGTGTGCTGAGAGGGAGCAGCAAGGTGTCTTGGCAAGC 424
Db |||||
399 CTGGAAGGGCGGGGACCCCTGTGTGTCAGGAGGGTACAGCAAGGTGTCTTGGGACAG 458
Qy |||||
425 CATCACTTACACTGCAAGATCAGGCGCCAGAGGAGCTTGAAGTCCAGGCGAGAAAGTGTAC 484
Db |||||
459 CACCACTGTCTCCAGCAACAGCGCCAGGAGAGCTTCAGGCCCGGCGAGAGATGTAC 518
Qy |||||
485 AGCTGGAAGACTTACATTAAGGTTGGCTCGCTGCTGACCAAGAGTGTGAAAGAC 544
Db |||||
519 CAGTGGAGGCTTACAAACCGAGTTGGCTCACTGCTGGATGAAAGAGACAGTGGAGAC 578
Qy |||||
545 TTGGACCTCAACATCAAGTACTCTGGATGAAGATGCCAACTCTCTTTAAAGCCAC 604
Db |||||
579 TTGGAGCTCAATATCAATATCTCCAGCAGCAAGAAATGCCAACTTTTATCTCAAGCTGCG 638
Qy |||||
605 TCCGGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCAGCAGGACTCTGGAAGAGT 664
Db |||||
639 TCTGCTTTTGCAGAGATGAANAATCAAGGGTTGCTTGGACCGCAGGGGCTCTGGAAGAGT 698
Qy |||||
665 CTGAGGAGATGAGAAGGCTGTTTAACTTCCCAAGACTCCAGCAGCAGAGTATGTGTT 724
Db |||||
699 CTGAATGAGATGAAGAAGATCTTCAACTTCCGAGGAGCCCGCAGCAGCTGAGCAACATTT 758
Qy |||||
725 GCACTGCGAGGAAGATGCTTCTTGGCTCCAGATTCCTTAATGGGATCAACCGGCTG 784
Db |||||
759 GAGCATGGCAGGAGGATGCTTCTTGGCTCCAGTTCTGAAATGGTCTCAACCTGTG 818
Qy |||||
785 CTGATTCCCGCTGTACAGTCTCCCAACAACTTCCCGGTCACTGATGAATGTGGCC 844
Db |||||
819 CTGATCCCGCTGTCTACTCTCCCAAGAACTTCCCGGTCACTGATGCCATGTGGCC 878
Qy |||||
845 CCAGTGTGCGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAAGGGCTCCCTGTTCTTG 904
Db |||||
879 TCATTGTTGGTCTTGGGACAGCTTGCAGGCTGAGCTAGAGAAGGGCTCCCTGTTCTTG 938
Qy |||||
905 GTGGATCATGGCATTTCTTCTGGAGTCCACCAACATCCTCAATGGAAAGCTCAGTTTC 964
Db |||||
939 GTGGATCACGGCATCTCTCTGGCATCCAGACCAATGTCTTAATGGGAAGCCGAGTTTC 998
Qy |||||
965 TCTGAGCCCGCATGACCTGTGTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAT 1024
Db |||||
999 TCTGGGCCCCAATGACCTGTCTATACAGAGCCAGGGCTGGGGCCGTGCTGCTCTC 1058
Qy |||||
1025 GCCATCCAGCTCAAAACAGACTCCCGGGCGAGCAACCCCATCTTCTGCGCCAGCGATGAC 1084
Db |||||
1059 GCCATCCAGCTCAGCCAGACCCCGGGCCCAACAGCCCCCATCTTCTGCGCCACTGATGAC 1118
Qy |||||
1085 ACGTGGAGCTGTTGCTGGCCGAAGACCTGGGTTGCGAATCTGAGTGTTTTACATCATGAG 1144
Db |||||
1119 AAGTGGAGCTGTTGCTGGCCGAAGACCTGGGTGCGCAATGTCTCTTCCATGAG 1178
Qy |||||
1145 GCTGTACACATCTGCTGCATGCCATCTGATTCCAGAGTCTTGGCTTGGCCACATTA 1204
Db |||||
1179 GCGCTTACGCACTCTGCTGCACTCACTGTGCTGCTGAGGTCTTCACTGCTGCTACCCCTG 1238
Qy |||||
1205 GGTGAGTGCCTTAGGTGTCAACCTCTCTTCAAGCTATTGATTCCTCACATTCGGTACACA 1264
Db |||||
1239 GGTGAGTGCCTTAGGTGTCAACCTCTCTTCAAGCTATTGATTCCTCACATTCGGTACACA 1298
Qy |||||
1265 CTGCACTCAACACGCTTGGCCGGAGTGTGCTGTTGCCCTGGGAAGTTGATAGACAAG 1324

1299 CTGCACATCAACACACTCGCCCGGAGCTGCTTATCTGTGCCAGGCGAGTGTGTGACAGG 1358
Qy |||||
1325 TCCACAGGCTTGGCACTGGGGGATTTCTCTGACCTGTATAAGAGAAACATGGAGCAGCTG 1384
Db |||||
1359 TCCACAGGCACTCGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
Qy |||||
1385 AACTACTCTGTCTGTGTCTCTCTGAGATATCCAGGCCCGAGGTGTGGAAGACATCCCA 1444
Db |||||
1419 AACTATTCTCTCTGTGTCTCTCTGAGGATATCCGGACCCGAGGAGTTGAAGACATCCCA 1478
Qy |||||
1445 GGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTCTCTCT 1504
Db |||||
1479 GGCTACTACTACCGTGTGATGGGATGCGATTTGGGGTGAGTGGGAACGCTTTGTCTCT 1538
Qy |||||
1505 GAAATAGTTCAGCATCTACTATCCAAAGTGCACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
Db |||||
1539 GAAATCATCGTATCTACTATCCCAAGTGTAGTGTCTGTCCAAGATGACAGAGAGCTCCAG 1598
Qy |||||
1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTTCGGCCGAGAAAGCTCAGGTATGCC 1624
Db |||||
1599 GCCTGGGTGAGGAGATCTTCTTCCAAGGGCTTCTTAAACAGGAGAGCTCAGGTATCCCT 1658
Qy |||||
1625 TCCTTGTGTGATACCCGGAGAGCCCTGTCTCCAGTATATCACCATGTGATATTCACCTGC 1684
Db |||||
1659 TCCTACTTGGAGACCCGGGAAGCCCTGTGTGAGTATGTACCATGTGATATTCACCTGC 1718
Qy |||||
1685 TCAGCAAGCATGCACTGTCTCAGTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCCAAT 1744
Db |||||
1719 TCAGCAAGCATGCGGCTGTCTCAGTTCAGGCGAGTTTGACTCTCTGTGCTTGGATGCCCAAC 1778
Qy |||||
1745 CTGCACCTTACCATGCACTACCACTTCTTCCAAAGGCGAGGCCCGGCTCAGAGT 1804
Db |||||
1779 CTGCACCTTACCATGCACTACCACTTCTTCCAAAGGCGAGGCCCGGCTCAGAGT 1838
Qy |||||
1805 TTCTATGCGCAGCTCCCGAGGATTAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTG 1864
Db |||||
1839 TTCTATGCGCAGCTCCCGAGGATTAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTG 1898
Qy |||||
1865 CTAAAGCGAGAACCTTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACACTTTCACA 1924
Db |||||
1899 CTGAGCAAGGAGCTTGGAGACCAAGGCCCTTGGGCCACTATCCGATGAGCACTTTCACA 1958
Qy |||||
1925 GAGGATGCCCCCGGCGAAGCGTGGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984
Db |||||
1959 GAGGAGGCCCTCGCGGAGCATCGCACCTTCCAGAGCCGCTGGGCCAGATCTCGAGG 2018
Qy |||||
1985 GGCATCAGGAGAGAACCGAGGCTTGGCACTGCGCTTACACTTACCTGATCTCCCTCCCTC 2044
Db |||||
2019 GGCATCAGGAGAGAACCGGGGCTTGGTGTGCGCTTACACTTACCTAGACCTCCCTC 2078
Qy |||||
2045 ATTGAGAACAGTGTCTCCATCTAACTCTTGGAGAAGACAGTCTCTGTGTGACAT 2098
Db |||||
2079 ATCGAGAACAGCTCTCCATCTAACTCTTGGAGAAGACAGTCTCTGTGTGACAT 2132

RESULT 9

ADQ37895

ID ADQ37895 standard; DNA; 2685 BP.

XX ADQ37895;

XX ADQ37895;

XX 07-OCT-2004 (first entry)

XX DNA encoding the human 15-lipoxygenase 2 protein.

XX Dry eye; 15-lipoxygenase; 15-LO; ophthalmological; gene therapy;

XX postmenopausal; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 72.2102

FT CDS

```
FT      /*tag= a
XX      /product= "Human 15-lipoxygenase 2 protein"
PN      WO2004060274-A2.
XX
XX      22-JUL-2004.
XX
XX      17-OCT-2003; 2003WO-US033139.
XX
XX      20-DEC-2002; 2002US-0435988P.
XX
XX      (ALCO-) ALCON INC.
XX
XX      Yanni JM, Gamache DA, Miller ST;
XX      WPI: 2004-543776/52.
XX      P-PSDB; ADQ37896.
XX
XX      Treating dry eyes in postmenopausal women comprises administering a
XX      composition comprising the 15-lipoxygenase (15-LO)-1 or 15-LO-2 gene to
XX      the ocular surface cells of the post-menopausal women with dry eyes.
XX
XX      Claim 1; SEQ ID NO 3; 20pp; English.
XX
XX      The invention relates to a novel method for treating dry eyes. The method
XX      comprises obtaining a composition containing the nucleotide sequence of
XX      15-lipoxygenase (15-LO)-1 or 15-LO-2, and administering the composition
XX      to a patient suffering from dry eye under conditions such that the
XX      nucleotide sequence of 15-LO-1 or 15-LO-2 is expressed. The invention
XX      further comprises a composition for the treatment of dry eye, comprising
XX      a vector having the above nucleotide sequence and an excipient. The 15-LO
XX      compositions have ophthalmological activity and may be used in gene
XX      therapy to treat disorders. The method is useful for treating dry eyes in
XX      postmenopausal women. This polynucleotide sequence represents the DNA
XX      encoding the 15-lipoxygenase 2 protein of the invention.
XX
XX      Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;
XX
XX      Query Match      43.3%; Score 1395.2; DB 12; Length 2685;
XX      Best Local Similarity 79.8%; Pred. No. 0;
XX      Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;
XX
XX      7 GCAGTAGAGCTTAACT--GGTCAGGAGGATGGCGAAATGCAGGGTGAGATATCCACG 64
XX      42 GCGGTAGAGCTGGACTTAGGCTGGCAGATGGCCGAGTTCAGGGTCAGGGTGCTCCACC 101
XX
XX      65 GGGGAAGCCTTGGGGCTGGCAGATGGGACAAAGTGTCTGTCAGCATCGTGGGAACCCAC 124
XX
XX      102 GGAGAAGCCTTCGGGGCTGGCAGATGGGACAAAGTGTCTGTCAGCATCGTGGGACCCGG 161
XX
XX      125 GGAGAGAGCCCTTAGTACTCTGGACCATCTGGGCAAGGAGTTCAGCGCCGGTGTCTGAA 184
XX      162 GGAGAGAGCCCCCACTGCCCTCTGGACAAATCTCGGCAAGGAGTTCAGTGGGGCGCTGAG 221
XX
XX      185 GAAGACTTCGAGGTGACGCTTCCCAAGGACGTAGGCACATGTGCTGATGCTGGAGTCCAC 244
XX      222 GAGGACTTCCAGGTGACGCTCCCGAGGACGTAGGCCGAGTGTGCTGCTGCGCGTGCAC 281
XX
XX      245 AAAGCAACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCTGTTCTGCG 304
XX      282 AAGGGCCGCC---AGTGTGCCCTCTGCTGGGGCCCTTGGGCCCGGATGCTGGTCTGCG 338
XX
XX      305 CGCTGGTTCGAGTGGAGTGGGTACCTGGGGCTGCATCCACTTCCCTCGTTATCAGTGG 364
XX      339 CGCTGGTTCGAGTGCACCGCGCGGGGGGGCGGCACCTCTCTTCCCTGCTACAGTGG 398
XX
XX      365 CTGGAAAGGGGCGGGGAGCTGTGTCTGAGAGGGGAGCAAGAGTGTCTCTGGCAAGAC 424
XX      399 CTGGAGGGGGCGGGGACCCCTGTGTGCTGAGGAGGGTACAGCCAAAGTGTCTCTGGGCAG 458
XX
XX      425 CATCACCTTACACTGAGGATCAGCCGACAGAGGAGCTTGAGTCCAGGACAGAGATGTAC 484
XX      459 CACCACCCCTGTGTCTCAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGGCGAGAGATGTAC 518
```

```
QY      485 AGCTGGAAAGACTTACATTGAAGGTTGGCTCGCTGCTTGAGCCAGAGACTGTGAAAGAC 544
XX      |||||
XX      519 CAGTGGAAAGGCTTACAACCCAGGTTGGCTCACTGCTGGATGAAAGACAGAGAC 578
XX
XX      545 TTGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 604
XX      |||||
XX      579 TTGGAGCTCAATATCAAAATACTCCACAGCAAGATGCCAACTTTTATCTACAAGCTGC 638
XX
XX      605 TCCGGTATACGGAGCTGAAAGTCAAGGGCTCCTGGACCGCACAGGACTCTGGAGGAGT 664
XX      |||||
XX      639 TCTGCTTTTGAGAGATGAAATCAAGGGGTGCTGGACCGCAAGGGGCTCTGGAGGAGT 698
XX
XX      665 CTGAGGGAGATGAGAAAGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTT 724
XX      |||||
XX      699 CTGAATGAGATGAAAGGATCTTCAACTTCCGAGGACCCAGCAGAGCTGAGCACGATTT 758
XX
XX      725 GCACATGCGAGGAGATGCTTCTTCGCTCCAGTTCTTAAATGGGATCAACCGGTC 784
XX      |||||
XX      759 GAGCACTGCGCAGGAGATGCTTCTTCGCTCCCAAGTTCTGAAATGGTCTCAACCTGTC 818
XX
XX      785 CTGATTCCGCCGCTGCACAGTCTCCCAAAACAACATTCGCCGTCACATGATGAATGTGGC 844
XX      |||||
XX      819 CTGATCCGCCGCTGTCATCTCTCCAAAGAACTTCCCGCTCACTGATGCCATGTGGCC 878
XX
XX      845 CCAGTGTCTGGGCCCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTTGG 904
XX      |||||
XX      879 TCATTGTTGGTCTCTGGACAGCTTGCAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938
XX
XX      905 GTGATCATGGATCTTCTTCTGGAGTCCACACCAACATCTCTCAATGGAAAGCTCAGTTC 964
XX      |||||
XX      939 GTGGATCAAGGATCTCTCTGGCATCCAGACCAATGTCAATTAATGGGAAGCGCAGTTC 998
XX
XX      965 TCTGAGCCCGCAGTACACCTGTGTACACAGAGCTCAGGCTCGGACCCCTGCTCCCAT 1024
XX      |||||
XX      999 TCTGGGCCCAATGACCTCTATACAGAGCCAGGCTGCGGGCCGCTGCTGCTCTC 1058
XX
XX      1025 GCCATCCAGCTCAAAACAGACTCCCGGGCCAGACAAACCCCATCTTCTGCCACGCGATGAC 1084
XX      |||||
XX      1059 GCCATCCAGCTCAGCAGACAGCCCGGCCCAAGAGCCCATCTTCTCTGCCCATGATGAC 1118
XX
XX      1085 AGTGGGAGCTGGTCTGGCCAGAGCTGGGTTCGCAATCTGAGTTTACATCATGAG 1144
XX      |||||
XX      1119 AAGTGGGAGCTGTTGCTGGCCAAAGCTGGGTGCGCAATCCGAGTTCTCTCTTCCATGAG 1178
XX
XX      1145 GCTGTACACATCTGCTCATGCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204
XX      |||||
XX      1179 GGCCTCAGCACCTCTGCTGACATCACTGCTGCTGAGGTTTCACTGCTGCTACCTG 1238
XX
XX      1205 CGTCAGCTGCTTAGGTGTCACTCTCTTCAAGCTATTGATTCCTCACAATTCGGTACACA 1264
XX      |||||
XX      1239 CGTCAGCTGCCCATCTGCCACCTCTCTTCAAGCTGTGATCCCGCACACCCGATACACC 1298
XX
XX      1265 CTGCAATCAACACAGCTTGGCCGGAGCTGCTGTTGGTCCCTCGGAAAGTTGATAGACAAG 1324
XX      |||||
XX      1299 CTGCACATCAACACACTCGCCGGAGCTGCTTATCGTGCAGGCGCAGGTGGTGACAGG 1358
XX
XX      1325 TCCACAGGCTTGGCACTGGGGGATTTCTGACCTGATAAGAGAAACATGAGGAGCTG 1384
XX      |||||
XX      1359 TCCACAGGATCGGCATTTGAAGGCTTCTGTGATTTGATACAGGAAACATGAAGCAGCTG 1418
XX
XX      1385 AACTACTCTGCTGCTGCTCTCCCTGAAGATATCCAGAGCCGAGGTTGTGGAAGACATCCCA 1444
XX      |||||
XX      1419 AACTATTCTCTCTGCTGCTGCTGAGGATATCCCGACCCGAGGAGTTGAAGACATCCCA 1478
XX
XX      1445 GGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTGTCTCT 1504
XX      |||||
XX      1479 GGCTACTACTACCGTATGATGGGATGAGATTTGGGGTGCAGTGGAAAGCTTTGTCTCT 1538
XX
XX      1505 GAAATAGTCAGCATCTACTATCCAAAGTCACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
XX      |||||
XX      1539 GAAATCATCGGTATCTACTTACCCAAAGTATGAGTCTGTCTCCAAAGATGACAGAGCTCCAG 1598
```

QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGCGCGAGAAAGCTCAGGTATGCC 1624
Db |||||
QY 1599 GCCTGGGTGAGGAGATCTTCTTCAAGGGCTTCTTAAACAGGAGAGCTCAGGTATCCCT 1658
Db |||||
QY 1625 TCCTTGTGTGGATACCCGGGAAGCCCTGTGTCAGTATATCACCATGGTATATTCACCTGCG 1684
Db |||||
QY 1659 TCCTCACTGGAGACCCGGGAGCCCTGTGTCAGTATATCACCATGGTATATTCACCTGCG 1718
Db |||||
QY 1685 TCAGCAAGCATGACAGCTGTCTAGTTCAGCCAGTTCGACTCTTGTGTTGGATGCCCAAT 1744
Db |||||
QY 1719 TCAGCAAGCATGACAGCTGTCTAGTTCAGCCAGGAGTTCGACTCTTGTGTTGGATGCCCAAT 1778
Db |||||
QY 1745 CTGCACTTACCATCAGCTACCACTTCTTCCAAAGGCCAGCCGCGCTGAGAGT 1804
Db |||||
QY 1779 CTGCACTTACCATCAGCTACCACTTCTTCCAAAGGCCAGCCGCGCTGAGAGT 1838
Db |||||
QY 1805 TTCAATAGCCACCTCCAGCAGTAAATTCGTCAAGTTCATCATATTCATCTCTGCGTG 1864
Db |||||
QY 1839 TTCAATAGCCACCTCCAGCAGTAAATTCGTCAAGTTCATCATATTCATCTCTGCGTG 1898
Db |||||
QY 1865 TTAAGCGCAGAACTTGGGAGCAAAAGGCCCTTGGGCCACTATCCAGATGAACACTTCACA 1924
Db |||||
QY 1899 CTGAGCAAGGAGCTGGAGACCAAAAGGCCCTTGGGCCACTATCCGATGAGCACTTCACA 1958
Db |||||
QY 1925 GAGGATGCCCCCGCGGAGCGTGTGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984
Db |||||
QY 1959 GAGGAGGCCCTTCGCGGAGCATCGCCACTTCCAGAGCGCGCTGCGCCAGATCTCGAGG 2018
Db |||||
QY 1985 GGCATCAGGAGGAGAAACCGAGGCGCTGGCAGCTGCCTACACCTACCTGATCTCCCTC 2044
Db |||||
QY 2019 GGCATCAGGAGGAGAAACCGGCGCTGGTGTGCTGCTTACCTTACCTTACCTTACCTT 2078
Db |||||
QY 2045 ATTGAGAACAGTGTCTTCCATCTTAACATCTTGGAGAGAGAGCTGCTGTGTGACAT 2098
Db |||||
QY 2079 ATCGAGACAGCGTCTCCATCTTAATCCAGGAGGAGACAGCGGCCAGATGACAT 2132
Db |||||
RESULT 10
ACN42888
ID ACN42888 standard; cDNA; 3127 BP.
AC ACN42888;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1763.
XX
KW es; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez C;
XX WPI; 2004-329368/30.
DR

P-PSDB; ABM84236.
New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
Claim 1; Page; 190pp; English.
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorders, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
SQ Sequence 3127 BP; 667 A; 1014 C; 821 G; 625 T; 0 U; 0 Other;
Query Match 22.8%; Score 734.4; DB 13; Length 3127;
Best Local Similarity 61.2%; Pred. No. 8.9e-182;
Matches 1248; Conservative 0; Mismatches 766; Indels 24; Gaps 3;
QY 35 ATGCGGAAATGACGGGTGAGAGTATCCACGGGGAGAGCCTGTGGGGCTGGGACATGGGAC 94
Db |||||
QY 537 ATGCGAGGTATCCGCTGTGTGTCACCATGTGCTTACCTAGAGGGCGGCACACTGGAC 596
Db |||||
QY 95 AAAGTGTCTGTCAGCATCTGTGGGAAACCCACGAGAGAGCCCTTAGTACTCTGACCAT 154
Db |||||
QY 597 AACATCTCTGTCACTGGTGGGACGCTGTGTGAAAGCCCAAGCAGCGGTAGATCGA 656
Db |||||
QY 155 CTGGGCAAGGAGTTCAGCGCGGTGCTGAAGAAAGACTTCGAGGTGACGCTTCCCCAGGAC 214
Db |||||
QY 657 ATGGCAGGAGCTTGGCCCTGGATCGGTACAGAGTACAGGTGCGTGTGCACAGCGGAG 716
Db |||||
QY 215 GTAGGCACTGTGTGATGCTCGAGTCCAAAGACACCCCGGAGAGTTCCTCCCGCTT 274
Db |||||
QY 717 CTGGGTGAGCTTGTGCTGCTGCTGTCACAAAGGAGCGCTACG----- 759
QY 275 ATGCTTTTCCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334
Db |||||
QY 760 -CTTTCTTCCGCAAGGAGCTTGGTACTGTAGCCGCACTCTGTGTACCCGACCGGATGGT 818
Db |||||
QY 335 GTCGCACTCCACTTCCCTGTTATCAGTGGCTGGAAGGGCGGGGAGCTGGTGTCTGAGA 394
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QY 819 AGTGATCCCACTTCCCTGCTATCAGTGGATGAGGCTACTGCACTGAGGTGAGGCTGAGG 878
Db |||||
QY 395 GAGGAGCAGCAAAAGGTGCTCTGGCAGAGCAGCATCCCTACACTGACAGATCAGCGCCAG 454
Db |||||
QY 879 CCAGGACAGCAAGAACTATTTGTGAGGACTCTCTTCCCTCTCTCTGATCAGGCA 938
Db |||||
QY 455 AAGGAGCTTGTAGTCCAGGAGAGAGATGTA----CAGCTGGAAGACTTACATTTGAAGTTGG 511
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QY 939 CGGAGCTCCGGGCGCGCAAGAAATGCTACGCGAGTGGGAAATCGGTACTCTGCGCGCTTC 998
Db |||||
QY 512 CCTCGCTGCTTGGACAGGAGCTGTGAAGACTTGGACCTCAACATCAAGTACTCTGCG 571
Db |||||
QY 999 CCCATGAAATGACATCCCATCCCTGATGTACATGAGGCCCAATGTTTCGATCTCAGCC 1058
Db |||||
QY 572 ATGAAGATGCAAACTCTTCTTTAAAGCCCACTCCCGGTATACGAGCTGAAGAGTCAAA 631
Db |||||
QY 1059 ACCAAGAGCATCTCGCTGCTCTTCAATGTCATCCCTGCTCTCTGGGAATGAAGCTTGA 1118
Db |||||
QY 632 GGGCTCTTGGACCGCAGAGGAGCTCTGGAGGAGTCTGAGGGAGATGAGAGGCTGTTTAA 691

Db	1119	GGGCTGTTGGATCGCAAGGGCTCTCTGGAAGAAGCTGGATGACATGCAGAAACATCTTCTCTGG	1178
Qy	692	TTCCGCAAGACTCCAGCAGCAGAGTAGTGTGTTTGACACTGCGCAGGAAGATGCTTCTTCTC	751
Db	1179	TGCCATNAGACTTTCACGACAAAGTAGTGTACAGAGCAGCTGGTGTGAAGATCACTTCTTT	1238
Qy	752	GCCTCCAGTTCTTAATGGCATCAACCCGGTCTGTATTCGCGCTGTGCACAGTCTCCCA	811
Db	1239	GGGTACCAGTACCTGAATGGTGCATCCCGTCACTGCATCTCTAGCTTGCC	1298
Qy	812	AACAACTTCCGGTCACTGATGAAAAATGGTGGCCCCAGTGTCTGGGCCCTTGAAACAGACTGTG	871
Db	1299	AGCAAGCTGCTGTGCACAAATGACATGGTGGCCCCCTTGTCTGGGACAGGACACATGCTG	1358
Qy	872	CAGCTCAGTTTGAGAAGGGCTCCCTGTTCTTGGTGGATCATGGCATTTCTTCTGGAGTC	931
Db	1359	CAGACAGCTTAGAGAGGGGAAACATCTTCTAGCGGACTATGEGATCTCTGGCGAGGCC	1418
Qy	932	CACACCAACATCTCTCAATGGAAGCCCTCAGTTCTCTGCAGCCCCGATGACCCCTGTTACAC	991
Db	1419	CCCACCCACTGCCCTAAACGGCCGCCAGCAGTACGTGSCCGCCCCACTGTGCCTGCTGTGG	1478
Qy	992	CAGAGCTCAGGCTCCGAGCCCCCTGTCTCCATATGGCCATTCAGTCAAAAGACTCCCGGG	1051
Db	1479	CTCAGCCCCCAG--GGGGGGCTGGTGCCTTGGCCATCCAGCTCAGCCAGACCCCGGG	1535
Qy	1052	CCAGACAACCCCATCTTCTCTGCCAGCGATGACAGCTGGGACACTGGTTCGTCGGCCAGAGCC	1111
Db	1536	CTTGACAGCCCCATCTTCTCTGCCCACTGACTTCGGAATGGGACTGTGCTGTGGCCAGAGC	1595
Qy	1112	TGGGTTCCGCAATCTCGAGTTTTCATCCATGAGGCTGTCCACATCTGCTGTCATGCCCAT	1171
Db	1596	TGGGTGGCAACTCTGAGTTCTTGTTGTCACGAAAAACAACGACACTTCTCTGTCACGCAT	1655
Qy	1172	CTGATTCGAAAGTCTTGTGGCCACATATAGTCAGTGCTGAGTGTCACTCTTC	1231
Db	1656	TTGCTGTGCAGGCTTCGCGCATGGCCACGCTGCGCCAGCTGCGCTCTGCCACCCCATC	1715
Qy	1232	TTCAAGCTATGATCTCTCATTTCCGTCACACTGCACATCAACAGCTTTCGCCGGAG	1291
Db	1716	TACAAGTCTCTACTCTCCCCACACTCGATACACGCTGCAGGTGAACCACTCGCGAGGCC	1775
Qy	1292	CTGCTCTTGCCCCCTGGGAAAGTTGATAGACAAAGTCCAAGGCCCTTGGCACTGGGGGATTC	1351
Db	1776	ACGCTGCTCAACCCGAGGGCCTCGTGCACAGGTCAAGTCCATCGGGAGGCAAGGCCTC	1835
Qy	1352	TCTGACCTGATAAAGAGAAACATGGAGCAGCTGAACTACTCTGTCTGTCTCTCCCTGAA	1411
Db	1836	ATCTACCTCATGAGCAGGGCTGGCCCACTTCACTTACACCAATTTCTGCCTTCGGAC	1895
Qy	1412	GATATCCGAGCCCGAGGTGTGGAAGACATCCAGGCTACTATTACCCAGATGATGGGATG	1471
Db	1896	AGGCTGGGGCCCGCGGCTCTGGCTATCCCCAACTACCACTACCCAGACGAGCGGCTG	1955
Qy	1472	CAGATCTGGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTTCAGCATCTACTATCCAAGT	1531
Db	1956	AAGATCTGGGGGGCATTTGAGAGCTTTGTCTCAGAAATCGTGGGCTACTATTATCCAGT	2015
Qy	1532	GACACATCCGTCGAAGATGACCAAGAGCTCCAGGCTGGGTGAGGGAGATCTTCTCTGAG	1591
Db	2016	GAGCATCTGTGCAGCAGGATTCGGAGCTGCAGGCTCGGAGTACCACTACCCAGACGAGCGCTG	2075
Qy	1592	GGCTTCCTCGGCGAGAAAGCTCAGGTATGCCCTCTTGTGGATACCCGGGAGCCCTG	1651
Db	2076	CGCTTCTGGGCGGGAAAGCTCAGGTTTCCCAAGCCGGCTGTGCACTCCAGGAGAGATG	2135
Qy	1652	GTCAGTATATCACCATGGTGATATTCACTGCTCAGCCCAAGCATGAGCTGTCTGAGTCA	1711
Db	2136	GTGAAGTTCCTCACTGCAATCATCTTCAATTGCTCTGCCAGCAGCTGTGTCTCAACAGT	2195
Qy	1712	GGCCAGTTCCGACTCTTGTGTTTGGATGCCCAATCTGCCACTTACCTACGAGCTACCACTCA	1771

D	b	2196	G G G C A G A T G A C T T T G G G G C C T G G A T G C C A A T G C T C C A T C A T C C A T G A G G C A G C C C C C A	2255
Q	y	1772	C C T A C T T C C A A A G G C C A G G C C C G G C C T G A G A G T T T C A T A G C C A C G T C C C A G C A G T T A A T	1831
D	b	2256	C C C A G A C C A A G G G G A C C A C C C C T G A A G A C T T A C C T A G A C A C C C T C C C T G A A G T G A A C	2315
Q	y	1832	T C G T C A A G T T A T C A C A T C A T T G C T C T C T G G C T G C T A A G C C A G A A C C T G G G A C C A A A G G	1891
D	b	2316	A T C A G C T G T A A C A A C C T C C T C C T T C T G T G T T A G C C A A G A A C C C A A G G A C C A G A G G	2375
Q	y	1892	C C C T G G G C A C T A T C C A G A T G A C A C T T C A C A G A G G A T G C C C C C G G C A A G C G T G G C T	1951
D	b	2376	C C C C T G G G C A C C T A C C C A G A T A G A C T T C A C A G A G G A G G C C C C G G C C G A G A T C G C C	2435
Q	y	1952	G C C T T C C A G A G A A G C T G A T C C A G A T C T C C A A G G G C A T C A G G A G A G A A C C G A G G C C T G	2011
D	b	2436	G C C T T C C A G A G C C G C C T G G C C C A G A T C T C A A G G A C A T C C A G G A G C G A A C C A G G G T C T G	2495
Q	y	2012	G C A C T G C C T A C A C C T A C C T G G A T T C C T C C C C T C A T T G A G A A C A G T G T C T C C A T C T A A C	2069
D	b	2496	G C A C T G C C T A C A C C T A C C T G G A C C C T C C C C C T C A T T G A G A A C A G C G T C T C C A C T C T A A C	2553
 RESULT 11 ABA05868 ID ABA05868 standard; cDNA; 3320 BP. XX AC ABA05868; XX DT 21-MAR-2002 (first entry) XX DE Human lipoxxygenase 46638 coding sequence. XX KW Human; lipoxxygenase; 46638; cytostatic; antiarrhythmic; hypotensive; KW antiatherosclerotic; cardiant; vasotropic; hypertensive; KW antiinflammatory; neuroprotective; nootropic; antiparkinsonian; KW anticonvulsant; hepatotropic; dermatological; antipsoriatic; fungicide; KW antidiartheaic; antidiabetic; antitumor; antiasthmatic; antiarthritic; KW antirheumatic; osteopathic; antithyroid; antiallergic; gene therapy; KW ophthalmological; antianaemic; analgesic; virucide; anorectic; vulnerary; KW immunomodulator; ss. XX OS Homo sapiens. XX FH Key Location/Qualifiers FT CDS 459..2594 FT FT /*tag= a FT FT /product= "lipoxxygenase 46638" FT FT /note= "this region is specifically claimed" XX PN WO200190323-A2. XX PD 29-NOV-2001. XX PF 21-MAY-2001; 2001WO-US016380. XX PR 19-MAY-2000; 2000US-0205675P. XX PA (MTLL-) MILLENNIUM PHARM INC. XX PI Meyers RA; XX DR WPI; 2002-083104/11. DR P-PADB; ABB04578. XX PT Novel human lipoxxygenase family member polypeptide and polynucleotide for PT diagnosing, treating immune, blood vessel, cardiovascular, inflammatory, PT ovarian, lung, colon, skin disorders and disorders involving placenta. XX PS Claim 1; Page 100-102; 118pp; English. XX CC The present invention provides the protein and coding sequences of a CC human protein, which is a member of lipoxxygenase family, and is referred				

CC to as 46638. The sequences can be used in the treatment of immune, blood
CC vessels, cardiovascular, inflammatory, cell differentiation,
CC neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,
CC disorders associated with bone metabolism, pain or metabolic disorders,
CC disorders involving the placenta and vital diseases. The present sequence
CC is the coding sequence of the invention
XX
SQ

Sequence 3320 BP; 706 A; 1074 C; 852 G; 683 T; 0 U; 5 Other;

Query Match 20.5%; Score 659.6; DB 6; Length 3320;
Best Local Similarity 63.9%; Pred. No. 4.1e-162;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;
Qy 484 CAGCTGGAAGACTTACATTGAGGTTGGCCCTCGCTGCTGACACAGAGACTGTGAAGA 543
Db 1013 CAGTGGGAATCGGTACCTGCGCCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGA 1072
Qy 544 CTGAGCTCAACATCAAGTACTCTGGATGAGAAATGCCAAATCTTCTTTAAAGCCCA 603
Db 1073 CATGGAGCCCAATGTTGATGACTCAGCCACCAAGACGATCTCGCTCTTTCAATGCCAT 1132
Qy 604 CTCGCGGTATACGAGCTGAAAGTCAAGGGCTCTCTGGACCGCACAGGACTCTGGAGGAG 663
Db 1133 CCCTGGCTTGGGAATGAGCTTCGAGGGCTGTGGATCGCAAGGGCTCTCTGAAGAA 1192
Qy 664 TCTGAGGAGATGAGAGGCTGTTTAACTTCGGAAGACTCCAGCAGAGAGATGTGTT 723
Db 1193 GCTGGATGACATGCAGAACATCTTCTGGTGCATGAAGACCTTCACGACAAAGTATGTCC 1252
Qy 724 TGCACACTGGCAGGAGATGCTTCTTCCCTCCAGTTCCTTAATGCGCATCAACCCGCT 783
Db 1253 AGAGCAGTGGTGAAGATCACTTCTTGGGTACGAGTACCTGAATGGTGTCAATCCCGT 1312
Qy 784 CCTGATTCGCGCTGTACAGCTTCCCAAACTTCCCGGTCACTGATGAATGGTGGC 843
Db 1313 CATGCTCACTGATCTCTAGCTTCCCGCAGCAGCTGCTTCCCAATGACATGGTGGC 1372
Qy 844 CCCAGTGTGGGCGCTGGAACAGTCTGACGGCTGAGTTGAGAGGGCTCCCTGTTCTT 903
Db 1373 CCCCTTGTGGGACAGGACACATGCTGTCAGACAGAGCTAGAGAGGGGGAACATCTTCT 1432
Qy 904 GGTGGATCATGGCATCTTCTGAGTCCACACCAATCTCAATGGAAGGCTCAGTT 963
Db 1433 AGCGGACTACTGGATCTCTGGCGGAGGGCCCCACCCACTGCTTAAACGGCGCCAGCAGTA 1492
Qy 964 CTCTGACGCCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAT 1023
Db 1493 CGTGGCGCCCACTGTGCTGCTGTGGCTCAGCCCCAG---GGGGGCTGTGGTCCCTT 1549
Qy 1024 TGCCATCCAGCTCAACAGACTCCCGGCCACAGAACCCCACTTCTTCCGCCCCAGCGATGA 1083
Db 1550 GGCCATCCAGCTCAGCCAGACCCCGGGGCTTGACAGCCCCATCTTCTGCCCCACTGACTC 1609
Qy 1084 CAGCTGGAGCTGGTGTGGGCAAGACCTGGGTTGCGAATCTGAGTTTACATCCATGA 1143
Db 1610 CGAATGGGACTTGGCTGTGGGCAAGACGTTGGGTGCGCAACTCTGAGTTTCTGGTGCAGGA 1669
Qy 1144 GGCTGTACACATCTGCTGTCATGCCATCTGATTCACAGAGCTTGTGCTTGGCCACATT 1203
Db 1670 AAACAACGCACTTCTGTGCAAGCATTTCTGTGAGAGGCTTTCGCCATGGCAACGCT 1729
Qy 1204 ACGTCAGCTGCTAGGTGTACCCCTCTCTCAAGCTATTTGATTTCTCAATTCGGTACAC 1263
Db 1730 GCGCCAGCTGCGCTCTGCCACCCCATCTCAAGCTCTCTACTCCGCCACACTCGATACAC 1789
Qy 1264 ACTGCACATCAACAGCTTGGCGGAGCTGCTGTTGCCCTCTGGGAAGTTGATAGACAA 1323
Db 1790 GCTCGAGGTGAACACCATTCGGGAGGGGCCACGCTGCTCAACCCGAGGGCCCTCGTGGACCA 1849
Qy 1324 GTCCACAGGCGCTTGGCACTGGGGGATTTCTGACCTGATGAAGAGAACATGGAGCAGCT 1383
Db 1850 GGTCACTGCCATCGGGAGGCAAGGCGCTCATCTACTCATGACGAGGCGCTTGGGCCACTT 1909

Qy 1384 GAACCTACTGTCTGTCTCTCCTCTGAAGATATCCGAGCCCGAGGTGTGGAGACATCCC 1443
Db 1910 CACCTACACAAATTTCTGCTTCCGAGACGCTGCGGGCGCGCGCTCTGGGTATCCC 1969
Qy 1444 AGGCTACTATTACCGAGATGATGGATGTCAGATCTGGGGGCAATAAAGAGCTTTGTCTC 1503
Db 1970 CAATACACTACCGAGACGAGGCTTGAAGATCTGGGCGCCATTTGAGAGCTTTGTCTC 2029
Qy 1504 TGAATAGTCAGCATCTTACTATCAAGTGACACATCCGTCAAGATGACCAAGAGCTCCA 1563
Db 2030 AGAATCGTGGGCTACTATTATCCAGTGACGACTGTGTGAGCAGGATTCGGAGCTGCA 2089
Qy 1564 GGCTGGTGGAGGAGATCTCTCTGAGGGCTTCTCGGGGCTTCTCGGGGCAAGAGCTCAGTATGCC 1623
Db 2090 GGCTGGAGCTGGGAGATTTTGTCTCAGGGCTTCTCGGGGCGGAAAGCTCAGGTTTCCC 2149
Qy 1624 CTCCTGTTGGATACCCGGGAAGCCCTGGTCCAGTATATACCATGGTATATTACACCTG 1683
Db 2150 AAGCGGCTGTGACCCCGAGGAGATGGTGAAGTTCTCACTGCAATCATCTTCAATTG 2209
Qy 1684 CTCAGCCAAAGCATGACGCTGTCTGAGTTCAGGCAAGTTCGACTCTTGTGTTGGATGCCAA 1743
Db 2210 CTCTGCCAGCAGCTGCTGTCAACAGTGGGAGCATGACTTTGGGGCTTGGATGCCAA 2269
Qy 1744 TCTGCCACCTACCATGACGCTACCAACCACTACTTCCAAAGGCCAGGCCCGCTGAGAC 1803
Db 2270 TGTCTCATCTATCCATGAGGAGCGCCCCACCCAGACCAAGGGGACCACCCCTGGAAGAC 2329
Qy 1804 TTTTCATAGCAGCGCTCCAGCAGTTAATTCGTCAAGTTATCACATCATTTGCTCTGCTGCT 1863
Db 2330 TTACTTAGACACCTCTCCTGAAGTGAACATCAGCTGTAAACACCTCTCTCTCTGCTT 2389
Qy 1864 GCTAAGCGCAGAACTCTGGGACCAAGGCCCTTGGGGCACTTATCCAGATGAACACTTCCAC 1923
Db 2390 GGTTAGCAAGAACCCCAAGGACAGAGGCCCTTGGGCACTTACCCAGATGAGCACTTCCAC 2449
Qy 1924 AGAGATGCCCCCGGCAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
Db 2450 AGAGGAGGCCCGGAGCGGAGCATCGCGCTTTCAGAGCGGCTTGGCCAGATCTCAAG 2509
Qy 1984 GGGCATCAGGAGGAGAAACGAGGCTGGCACTGCGCTTACACCTACCTGATCTCCCT 2043
Db 2510 GGCATCCAGAGCGGAACCAAGGCTTGGCACTGCGCTTACCTTACCTTGGACCTTCCCT 2569
Qy 2044 CATTGAGAACAGTGTCTTCCATCTAAC 2069
Db 2570 CATTGAGAACAGTGTCTTCCATCTAAC 2595

RESULT 12

AAD60556

ID AAD60556 standard; cdna; 3320 BP.

XX AAD60556;

XX 18-DEC-2003 (first entry)

XX Human lipoxigenase, 46638 cdna.

XX Human; cytochrome p450; dehydrogenase/reductase; osteomalacia; psoriasis;

XX lipoxigenase; hydratase; proliferative disorder; haematopoietic disorder;

XX differentiative disorder; carcinoma; sarcoma; leukaemia; immune disorder;

XX anorexia nervosa; neural degeneration; muscular disorder; lipid disorder;

XX multiple sclerosis; encephalomyelitis; metabolic disorder; osteoporosis;

XX myasthenia gravis; bone metabolism; immunomodulator; obesity; anorectic;

XX eating disorder; osteodys trophy; arthritis; diabetes; anabolic; rickets;

XX milk fever; diabetes mellitus; gene; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FH CDS 458..2594

FT /*tag= a

CC cardiovascular disorders, blood vessel disorders, neutrophil disorders
CC (neutropenia, lupus), testicular disorder (mumps) and platelet disorders.
CC The present sequence is a coding sequence for a lipoxigenase of the
CC invention.

SQ Sequence 2136 BP; 459 A; 683 C; 569 G; 425 T; 0 U; 0 Other;

Query Match 20.4%; Score 658.6; DB 12; Length 2136;

Best Local Similarity 63.9%; Pred. No. 6e-162; Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAAGACTTACATTGAAGGTTGGCCTCGCTGCCCTTGACCACGAGACTGTGAAAGA 543

Db
555 CAGTGGGAATCGGTACCTGCCCGGCTTCCCCATGAAATTGACATCCCATCCCTGATGTA 614

QY. 544 CTTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCCAACTCTTCTTTAAAGCCCA 603

Db 615 CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT 674

QY 604 CTCGCGTATACGGAGCTGAAAGTCAAGGGCTCCTGGACCGCACAGGACTCTGGAGGAG 663

D_b 675 CCCTGCGTCCTTGGGAATGAAGCTTCGAGGGCTGTGGATCGCAAGGGCTCCTGGAA 734

QY 664 TCTGAGGAGATGAGAAGGCTGTTTAACTCCGCAAGACTCCAGCAGCAGATATGTGTT 723

Db 735 GCTGGATGACATGCAGAACATCTTCTGGTGCCATAAGACCTTCACGACAAAGTATGTCAC 794

QY 724 TGCACACTGGCAGGAAGATGCCCTTCTTCGCCCTCCCAGTTCCTAAATGGCATCAACCCGGT 783

Db 795 AGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCAAGTACCTGAATGGTGTCAATCCCCGT 854

784 CCTGATTGCGCGTGTCACAGTCTCCCAACAACCTCCCGGTCACTGATGAAATGGTGGC 843
QY
QY

Db 855 CATGCTCCACTGCATCTCTAGCTTGCCCAAGCTGCCTGTACCAATGACATGGTGGC 914

844 CCCAGTGCTGGGCCCCTGGAACCAAGTCTGCAGGCTGAGTTGGAGAAAGGCTCCCTGTTCTT 903

DB 915 CCCCCTGCTGGGACAGGACACATGCCCTGCAGACAGAGCTAGAGAGGGGAACATCTTCTT 974

904 GGTTGGATCATGGCAATCTTTCTGGAGTCCACACCAACATCTCAATGGAAAGCCTCAGTT 963
QY
QY

DB 9/5 AGCGGACTACTGGATCCCTGGCGGAGGGCCCCACCCCACTGGCTAAACGGGCCGAGCAGTA 103

QY C C T G C A G C C C C G A T G A C C C T G T T A C A C C A G A G C C C A G G G C C C G G A C C C C T G C T T C C C A T T O Z

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A vertical ruler with markings from 1 to 10 cm. The markings are in millimeters, with major ticks every centimeter and minor ticks every millimeter. The ruler is oriented vertically with the 0 mark at the top and the 10 cm mark at the bottom.

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A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with major ticks every centimeter. The ruler is oriented vertically, with the 0 mark at the top and the 10 cm mark at the bottom.

1452	Db	CACCTACACAAATTTCTGCCTTCGGACAGCCTGCGGGCCCGGCGTCTCTGCCTATCCC	1511
1444	Qy	AGGCTACTATTACCGAGATGATGGATGACAGATCTCTGGGGGGCAATAAAGAGCTTTTGTCTC	1503
1512	Db	CAACTACCACTACCGAGACGACGGCTGAAATCTCTGGCGGGCCATTGAGAGCTTTTGTCTC	1571
1504	Qy	TGAAATAGTTCAGCATCTACTATCCAAAGTGCACATCCGTCCAAAGATGACCAAGAGCTCCA	1563
1572	Db	AGAAATCGTGGGTACTATTATCCCAAGTACGCATCTGTGCACGAGATTCGCGAGCTGCA	1631
1564	Qy	GGCTCTGGTGAGGGAGATCTTCTCTCAGGGCTTCTCTGGCCGAGAAAGCTCAGGTATGCC	1623
1632	Db	GGCTGAGCTGGCGAGATTTTGTCTCAGGCGTTTCTCTGGCCGGGAAAGCTCAGGTTCCTCC	1691
1624	Qy	CTCTGTTGTGGATACCCGGGAAGCCCTGGTCCAGTATATACACCATGGTGTATTCACCTTG	1683
1692	Db	AAGCCGGCTGTGCACCCCCCAGGAGAGATGGTGAAGTTCTCTCACTGCAATCATCTTCAATTG	1751
1684	Qy	CTCAGCCAAAGCATGACGCTCTCAGTTTCAGGCCAGTTTCGACTCTTGTGTGTTGGATGCCAA	1743
1752	Db	CTCTGCCACGACGCTGCTGTCAACAGTGGCAGCATGACTTTTGGGCGCTGGATGCCAA	1811
1744	Qy	TCGTGCCACCTACCATGAGCTACAACAACCTATTTCCAAAGCCAGCGCCCGGCTCTGAGAG	1803
1812	Db	TGCTTCATCATCTCATGAGCGAGCCGCCACCCACAGACCAAGGGGACCAACCCTCTGAAGAC	1871
1804	Qy	TTTTCATAGCACCGCTCCACGAGTTAATTCGTCAAGTTATCATCATCTCTCTCTGGCT	1863
1872	Db	TTACTTAGACACCCCTCCCTGAAGTGAACATCAGCTGTAAACAACCTCTCTCTTCTGTGTT	1931
1864	Qy	GCTAAGCGCAGAACCTGGGACCAAAAGGCCCTCTGGCCACTATCCAGATGAACACTTCAC	1923
1932	Db	GGTTAGCCAAAGAACCCAAAGGACCAGAGGCCCTCTGGCACCTACCCAGATGAGCACTTCAC	1991
1924	Qy	AGAGGATGCCCCCGGGGAAGCTGGCTGSCCTTCAGAGAAAGCTGATCCAGATCTCCAA	1983
1992	Db	AGAGGAGGCCCCCGAGCGGAGCATCGCCGCTTTCCAGAGCGCGCTGGCCAGATCTCAAG	2051
1984	Qy	GGGCATCAGGGGAGGAACCGAGCGCTGGCACTGGCCCTACACCTACTCTGGATCTCTCCCT	2043
2052	Db	GGACATCCAGAGGGGNAACAGGGTCTGGACATCTGCCCTACACCTACTCTGACCCCTCTT	2111
2044	Qy	CATTGAAACAGTGTCTTCCATCTAA	2069
2112	Db	CATTGAAACAGTGTCTTCCATCTAA	2136

Search completed: July 19, 2005, 13:18:45
Job time : 1104 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:45:07 ; Search time 1284.13 Seconds
(without alignments)
15928.199 Million cell updates/sec

Title: US-10-688-676A-3

Perfect score: 3224

Sequence: 1 cagcttcgagtagagagta.....gtcataaagtggtcattcc 3224

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3224	100.0	3224	20	US-10-688-676A-3
2	3178	98.6	3205	9	Sequence 3, Appli
3	3178	98.6	3205	19	Sequence 3, Appli
4	1395.2	43.3	2685	9	Sequence 1, Appli
5	1395.2	43.3	2685	9	Sequence 985, App
6	1395.2	43.3	2685	10	Sequence 642, App
7	1395.2	43.3	2685	19	Sequence 1, Appli

8	659.6	20.5	3320	9	US-09-862-658-1	Sequence 1, Appli
9	659.6	20.5	3320	14	US-10-175-696-22	Sequence 22, Appli
10	659.6	20.5	3320	19	US-10-776-871-22	Sequence 22, Appli
11	658.6	20.4	3384	16	US-10-422-264-29	Sequence 29, Appli
12	658.6	20.4	2136	9	US-09-862-658-3	Sequence 3, Appli
13	658.6	20.4	2136	14	US-10-175-696-24	Sequence 24, Appli
14	658.6	20.4	2136	19	US-10-776-871-24	Sequence 24, Appli
15	658	20.4	2236	16	US-10-422-264-5	Sequence 5, Appli
16	658	20.4	2301	16	US-10-422-264-1	Sequence 1, Appli
17	657	20.4	2307	18	US-10-302-172-803	Sequence 803, App
18	657	20.4	2604	16	US-10-422-264-23	Sequence 23, Appli
19	652.2	20.2	2136	17	US-10-275-998-8	Sequence 8, Appli
20	565.8	17.5	2469	9	US-09-853-053-1	Sequence 6, Appli
21	565.8	17.5	2469	17	US-10-445-484-1	Sequence 1, Appli
22	466.2	14.5	1383	16	US-10-422-264-11	Sequence 11, Appli
23	466.2	14.5	1848	16	US-10-422-264-9	Sequence 9, Appli
24	466.2	14.5	2316	16	US-10-422-264-27	Sequence 27, Appli
25	440.6	13.7	2497	9	US-09-964-824A-543	Sequence 543, App
26	440.6	13.7	2497	9	US-09-962-832-97	Sequence 97, Appli
27	440.6	13.7	2497	9	US-09-954-456-942	Sequence 942, Appli
28	440.6	13.7	2497	16	US-10-240-305-13	Sequence 13, Appli
29	440.6	13.7	2497	18	US-10-641-643-1155	Sequence 1155, Ap
30	440.6	13.7	2497	19	US-10-071-411-3	Sequence 3, Appli
31	440.6	13.7	2497	20	US-10-741-292-1	Sequence 1, Appli
32	440.6	13.7	2497	21	US-10-514-799-3	Sequence 3, Appli
33	440.6	13.7	2497	21	US-10-843-641A-3969	Sequence 3969, Ap
34	440.6	13.7	2497	21	US-10-843-641A-5846	Sequence 5846, Ap
35	440.6	13.7	2497	21	US-10-843-641A-5983	Sequence 5983, Ap
36	440.2	13.7	2484	17	US-10-191-997-91	Sequence 91, Appli
37	440.2	13.7	2484	19	US-10-283-975A-296	Sequence 296, App
38	439.8	13.6	2076	20	US-10-485-310-21	Sequence 21, Appli
39	439.6	13.6	2420	16	US-10-240-305-15	Sequence 15, Appli
40	427.8	13.3	2107	20	US-10-741-292-18	Sequence 18, Appli
41	423	13.1	2107	20	US-10-741-292-17	Sequence 17, Appli
42	407.2	12.6	1441	16	US-10-422-264-13	Sequence 13, Appli
43	336.4	10.4	2368	19	US-10-741-601-232	Sequence 232, App
44	336.4	10.4	2368	21	US-10-741-600-671	Sequence 671, App
45	336.4	10.4	2867	19	US-10-741-601-233	Sequence 233, App

ALIGNMENTS

RESULT 1

US-10-688-676A-3
; Sequence 3, Application US/10688676A
; Publication No. US20040248794A1
; GENERAL INFORMATION:
; APPLICANT: Alcon, Inc.
; APPLICANT: Yanni, John M.
; APPLICANT: Gamache, Daniel A.
; APPLICANT: Miller, Steven T.
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo-
; TITLE OF INVENTION: Activity to Ocular Surface Cells
; FILE REFERENCE: 2394 US
; CURRENT APPLICATION NUMBER: US/10/688.676A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/435,958
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 3224
; TYPE: DNA
; ORGANISM: homo sapiens
; ORGANISM: 676A-3

Query Match 100.0%; Score 3224; DB 20; Length 3224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTTCGAGTAGAGCTAACTGGTCAGAGATGCCAAATGCGAGGTGAGAGTATC 60

Db 1 CAGCTTGCAGTAGAGAGCTAAACTGGTCCAGGAGGATGGCGAAATGACAGGGTGAGAGTATC 60
QY 61 CACGGGGGAAGCCTGTGGGGCTGGGACATGGGACAAAGTGTCTGTCTCAGCATCGTGGGAAAC 120
Db 61 CACGGGGGAAGCCTGTGGGGCTGGGACATGGGACAAAGTGTCTGTCTCAGCATCGTGGGAAAC 120
QY 121 CACCGGAGAGAGCCCTTATAGTACCTCTGTGACCATCTGGGCAAGAGGAGTTCAGCGCCGGTGC 180
Db 121 CACCGGAGAGAGCCCTTATAGTACCTCTGTGACCATCTGGGCAAGAGGAGTTCAGCGCCGGTGC 180
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Db 181 TGAAGAGACTTCGAGGTGACGCTTCCCGAGGAGCTGAGGACATGTGCTGATGCTGGAGT 240
QY 241 CCACAAAGCACCCTGGGAAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGTAGTCCCTGGTT 300
Db 241 CCACAAAGCACCCTGGGAAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGTAGTCCCTGGTT 300
QY 301 CTGCCGCTGGTTTCGAGCTGGAGTGGCTACCTGGGGCTGCACCTCCACTTCCCTCTGTATCA 360
Db 301 CTGCCGCTGGTTTCGAGCTGGAGTGGCTACCTGGGGCTGCACCTCCACTTCCCTCTGTATCA 360
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Db 361 GTGGCTGGAAGGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAAAGTGTCTGGCA 420
QY 421 AGACCATCACCTTACACTGCAGATCAGCGCCAGAGGAGCTTGTAGTCCAGGACAGAGAT 480
Db 421 AGACCATCACCTTACACTGCAGATCAGCGCCAGAGGAGCTTGTAGTCCAGGACAGAGAT 480
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QY 541 AGACTTGGACCTCAACATCAAGTACTCTCGGATGAAGATGCAAACTCTTCTTTAAAGC 600
Db 541 AGACTTGGACCTCAACATCAAGTACTCTCGGATGAAGATGCAAACTCTTCTTTAAAGC 600
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Db 661 GAGTCTGAGGGAGATGAGAAGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGAGATGT 720
QY 721 GTTTGCACACTGGCAGGAGATGCTTCTTCCGCTCCAGTTCTTAAATGGGCATCAACC 780
Db 721 GTTTGCACACTGGCAGGAGATGCTTCTTCCGCTCCAGTTCTTAAATGGGCATCAACC 780
QY 781 GGTCTCTGATTTCGCGCTGTACAGTCTCCAAACACTTCCCGGTCACTGTATGAATGGT 840
Db 781 GGTCTCTGATTTCGCGCTGTACAGTCTCCAAACACTTCCCGGTCACTGTATGAATGGT 840
QY 841 GGGCCCGAGTGTGGGCGCTGGAACCAAGTCTGCAAGGCTGAGTTGGAGAAAGGCTCCCTGTT 900
Db 841 GGGCCCGAGTGTGGGCGCTGGAACCAAGTCTGCAAGGCTGAGTTGGAGAAAGGCTCCCTGTT 900
QY 901 CTTGTGGATCATGGCATTTCTTCTGGAGTCCACCAACATCCTCAATGGAAAGCCTCA 960
Db 901 CTTGTGGATCATGGCATTTCTTCTGGAGTCCACCAACATCCTCAATGGAAAGCCTCA 960
QY 961 GTTCTCTGAGCCCGATGACCTGTTTACACAGAGCTCAGGGTCGGGACCCCTGCTCC 1020
Db 961 GTTCTCTGAGCCCGATGACCTGTTTACACAGAGCTCAGGGTCGGGACCCCTGCTCC 1020
QY 1021 CATTTGCCATCCAGCTCAACAGACTCCCGGGCCAGACAAACCCCATCTTCTGCCCCAGCGA 1080
Db 1021 CATTTGCCATCCAGCTCAACAGACTCCCGGGCCAGACAAACCCCATCTTCTGCCCCAGCGA 1080
QY 1081 TGACAGTGGGACTGTGTGCTGCCAAGACCTGGGTTCCGAATCTGTAGTTTATACCA 1140
Db 1081 TGACAGTGGGACTGTGTGCTGCCAAGACCTGGGTTCCGAATCTGTAGTTTATACCA 1140

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QY 1261 CACACTGCACATCAACAGCTTGGCCGGGAGCTGCTCGTTCGCCCTGGGAAAGTTCATAGA 1320
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Db 1321 CAAGTCCAAGGCTTGGCACTGGGGGATTCCTGACCTGATAAAGAGAAAATCGAGCA 1380
QY 1381 GCTGAACTACTCTGTCTGTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACAT 1440
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QY 1681 CTGCTCAGCCAAAGCATGCACTGTTCAGGCGAGTTCGACTCTTGTGTGGATGCC 1740
Db 1681 CTGCTCAGCCAAAGCATGCACTGTTCAGGCGAGTTCGACTCTTGTGTGGATGCC 1740
QY 1741 CAACTGCGCACTACCATGCACTACCACTTCTTCCAAGGCGAGGCGCCGCTGA 1800
Db 1741 CAACTGCGCACTACCATGCACTACCACTTCTTCCAAGGCGAGGCGCCGCTGA 1800
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Db 1801 GAGTTTCATAGCCACGCTCCCGAGAGTAAATTCGTCAGAGTTATCACATCATTTGCTCTG 1860
QY 1861 GCTGCTAAGCGCAGAACCTGGGGACCAAAGGCCCTGGGCCACTATCCAGATGAACACTT 1920
Db 1861 GCTGCTAAGCGCAGAACCTGGGGACCAAAGGCCCTGGGCCACTATCCAGATGAACACTT 1920
QY 1921 CACAGAGATGCCCCCGCGGAGGCTGCTGCTTCCAGAGAAAGCTGATCCAGTCTC 1980
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QY 1981 CAAAGGCTCAGGAGAGGACCCGAGGCTGGCACTGCCCTACACTACTCTGGATCCTCC 2040
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QY 2041 CCTCATTTGAGAACAGTGTCTCCATCTAAACATCTTGGAGAAAGACAGTCTCTGTGACATAT 2100
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Db 2101 AGAACTCTTGACCATGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGGACCAACCAAG 2160
QY 2161 CCCCCTTTTACCTTA 2220
Db 2161 CCCCCTTTTACCTTA 2220

Qy	2221	A	CTCC	CAC	AGG	CGA	AGT	CTC	CAC	ACG	AGG	AGC	CA	TCAA	TGTT	TGG	AG	CCCT	2280
Db	2221	A	CTT	CCC	CAC	AGG	CGA	AGT	CTC	CAC	ACG	AGG	AGC	CA	TCAA	TGTT	TGG	AG	CCCT
Qy	2281	G	AGT	TC	CAG	CTC	TG	ATTA	ACG	CGT	TTG	CTG	CTT	GC	TTT	GC	TTT	GC	TTT
Db	2281	G	AGT	TC	CAG	CTC	TG	ATTA	ACG	CGT	TTG	CTG	CTT	GC	TTT	GC	TTT	GC	TTT
Qy	2341	G	AG	CGT	TAA	CAC	AG	AAG	CAC	AG	AC	CC	TG	TTT	CA	CTG	CAC	AA	CGC
Db	2341	G	AG	CGT	TAA	CAC	AG	AAG	CAC	AG	AC	CC	TG	TTT	CA	CTG	CAC	AA	CGC
Qy	2401	T	CAC	TC	GAC	CAA	AGG	CAG	CTA	TAT	CAC	AGC	TTT	TAT	CAG	GA	CA	TG	CA
Db	2401	T	CAC	TC	GAC	CAA	AGG	CAG	CTA	TAT	CAC	AGC	TTT	TAT	CAG	GA	CA	TG	CA
Qy	2461	C	AA	AGC	CT	A	CC	CAC	TAG	GT	CC	AT	C	GT	G	AC	CT	C	A
Db	2461	C	AA	AGC	CT	A	CC	CAC	TAG	GT	CC	AT	C	GT	G	AC	CT	C	A
Qy	2521	G	AG	AGG	GT	TAC	TG	AG	TAC	GAG	AGG	AT	G	GG	CT	G	AG	AGG	AT
Db	2521	G	AG	AGG	GT	TAC	TG	AG	TAC	GAG	AGG	AT	G	GG	CT	G	AG	AGG	AT
Qy	2581	T	G	GA	AG	A	A	C	A	T	A	T	C	T	T	C	A	G	A
Db	2581	T	G	GA	AG	A	A	C	A	T	A	T	C	T	T	C	A	G	A
Qy	2641	A	CT	C	A	G	A	G	T	C	T	C	T	A	G	A	G	A	G
Db	2641	A	CT	C	A	G	A	G	T	C	T	C	T	A	G	A	G	A	G
Qy	2701	A	C	C	A	A	A	T	T	A	C	T	T	T	T	A	G	A	G
Db	2701	A	C	C	A	A	A	T	T	A	C	T	T	T	T	A	G	A	G
Qy	2761	G	C	A	T	G	A	T	C	C	T	C	A	G	A	T	C	C	A
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Qy	2821	A	A	C	A	T	C	T	G	A	T	C	T	G	G	G	T	G	A
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Qy	2881	T	G	C	A	T	A	T	A	A	A	T	C	T	T	A	A	A	A
Db	2881	T	G	C	A	T	A	T	A	A	A	T	C	T	T	A	A	A	A
Qy	2941	C	A	T	T	C	A	C	T	C	T	C	T	C	A	A	A	A	A
Db	2941	C	A	T	T	C	A	C	T	C	T	C	T	C	A	A	A	A	A
Qy	3001	T	T	G	A	G	A	G	A	T	A	T	C	T	A	A	A	A	A
Db	3001	T	T	G	A	G	A	G	A	T	A	T	C	T	A	A	A	A	A
Qy	3061	C	A	T	T	C	C	A	A	A	T	T	A	T	A	T	A	T	A
Db	3061	C	A	T	T	C	C	A	A	A	T	T	A	T	A	T	A	T	A
Qy	3121	T	T	G	T	T	G	T	T	G	T	T	G	T	T	T	T	T	T
Db	3121	T	T	G	T	T	G	T	T	G	T	T	G	T	T	T	T	T	T
Qy	3181	C	A	G	A	C	T	G	A	G	T	T	C	A	T	A	A	A	A
Db	3181	C	A	G	A	C	T	G	A	G	T	T	C	A	T	A	A	A	A

GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM E.
JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,246
FILING DATE: 17-Jan-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3205 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-246-3

Query Match	98.6%;	Score 3178;	DB 9;	Length 3205;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 3189;	Conservative	0;	Mismatches	0; Indels 1; Gaps 1;
Qy	35	ATGCGCAATGCGAGGTGAGAGTATCCACGGGGGAAGCCTGTGGGGCTGGCACATGGGAC	94	
Db	1	ATGCGGNAATGCGAGGTGAGAGTATCCACGGGGGAAGCCTGTGGGGCTGGCACATGGGAC	60	
Qy	95	AAAGTGTCTCTGAGCAATCGTGGGAACCCACGGAGAGAGCCCTTTAGTACCTCTGACCAAT	154	
Db	61	AAAGTGTCTCTGAGCAATCGTGGGAACCCACGGAGAGAGCCCTTTAGTACCTCTGACCAAT	120	
Qy	155	CTGGGCAAGAGTTACGCGCGGTGCTGAGAGACACTTCGAGGTGACGCTTCTCCCCAGGAC	214	
Db	121	CTGGGCAAGAGTTACGCGCGGTGCTGAGAGACACTTCGAGGTGACGCTTCTCCCCAGGAC	180	
Qy	215	GTAGGCACCTGTGCTGATGCTGCGAGTCCACAAAGCACCCCGGAAGTGTCTCCTCCCGTT	274	
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Qy	275	ATGTCCTTCCGTTCTGATGCTGGTTCGCGGCTGGTTCGAGCTGGAGTGGCTACCTGGG	334	
Db	241	ATGTCCTTCCGTTCTGATGCTGGTTCGCGGCTGGTTCGAGCTGGAGTGGCTACCTGGG	300	
Qy	335	GCTGCACTCCACATTCCCTCTGTTATCAGTGGCTGGAAGGGGGGGGAGCTGGTCTGAGA	394	
Db	301	GCTGCACTCCACATTCCCTCTGTTATCAGTGGCTGGAAGGGGGGGGAGCTGGTCTGAGA	360	
Qy	395	GAGGGAGCAGCAAGGTGTCTCTGGCAAGACCATCACCTCTACATCTGACGGATCAGCGCCAG	454	
Db	361	GAGGGAGCAGCAAGGTGTCTCTGGCAAGACCATCACCTCTACATCTGACGGATCAGCGCCAG	420	

QY 455 AAGGAGCTTTGAGTCCAGGAGAGAGTGTACAGCTGGAGACTTACATTTGAAGGTTGGCCT 514
DB 421 AAGGAGCTTTGAGTCCAGGAGAGAGTGTACAGCTGGAGACTTACATTTGAAGGTTGGCCT 480
QY 515 CGCTGCTTTGACACGAGACTGTGAAAGACTTGGACCTCAACATCAAGTACTCTCGGATG 574
DB 481 CGCTGCTTTGACACGAGACTGTGAAAGACTTGGACCTCAACATCAAGTACTCTCGGATG 540
QY 575 AAGATGCCAAACTCTTTCTTAAAGCCCACTCCGCGTATACGGAGCTGAAGCTCAAGGG 634
DB 541 AAGATGCCAAACTCTTTCTTAAAGCCCACTCCGCGTATACGGAGCTGAAGCTCAAGGG 600
QY 635 CTCCTCGACCGCACAGGACTCTGGAGGAGTCTGAGGAGATGAGAAGGCTGTTTAACTTC 694
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QY 695 CGCAAGACTCCAGCAGCAGAGTATGTTTGGACACTGGCAGGAGATGCCCTTCTTCGCG 754
DB 661 CGCAAGACTCCAGCAGCAGAGTATGTTTGGACACTGGCAGGAGATGCCCTTCTTCGCG 720
QY 755 TCCAGCTTCTTAAATGGCATCAACCCGGTCCCTGATTCGCGGCTGTACACAGTCTCCCAAC 814
DB 721 TCCAGCTTCTTAAATGGCATCAACCCGGTCCCTGATTCGCGGCTGTACACAGTCTCCCAAC 780
QY 815 AACTTCCCCTGCTCACTGATGAATGGTGGCCGCCAGTCTGGGCCCTGGAAACCAAGTCTGCGAG 874
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QY 875 GCTGAGTTGGAGAAAGGCTCCCTGTTTCTGGTGGATCATGGCATCTTCTTCTGGAGTCCAC 934
DB 841 GCTGAGTTGGAGAAAGGCTCCCTGTTTCTGGTGGATCATGGCATCTTCTTCTGGAGTCCAC 900
QY 935 ACCAATCTCTCAATGGAAAGCTCAGTTCTCTGACAGCCCGATGACCTGTACACAG 994
DB 901 ACCAATCTCTCAATGGAAAGCTCAGTTCTCTGACAGCCCGATGACCTGTACACAG 960
QY 995 AGCTCAGGGTCCGAGCCCTGCTTCCCATTTGCCATTCAGCTCAAAACAGACTCCCGGGCCA 1054
DB 961 AGCTCAGGGTCCGAGCCCTGCTTCCCATTTGCCATTCAGCTCAAAACAGACTCCCGGGCCA 1020
QY 1055 GACAAACCCATCTTCTGCTGCCAGCGATGACAGTGGGACTGGTGTGCTGCCAAGACTG 1114
DB 1021 GACAAACCCATCTTCTGCTGCCAGCGATGACAGTGGGACTGGTGTGCTGCCAAGACTG 1080
QY 1115 GTTCGCAATCTGAGTTTACATCCATGAGGCTGTACACATCTGCTGATGCCCATCTG 1174
DB 1081 GTTCGCAATCTGAGTTTACATCCATGAGGCTGTACACATCTGCTGATGCCCATCTG 1140
QY 1175 ATTCCAGAAAGTCTTTGCTTGGCCACATTAAGCTCAGCTGCTAGGTGTCAACCTCTCTTC 1234
DB 1141 ATTCCAGAAAGTCTTTGCTTGGCCACATTAAGCTCAGCTGCTAGGTGTCAACCTCTCTTC 1200
QY 1235 AAGCTATTGATTCCTCACTTGGTGTACACTGCAATCAACAGCTTGGCCGGAGCTG 1294
DB 1201 AAGCTATTGATTCCTCACTTGGTGTACACTGCAATCAACAGCTTGGCCGGAGCTG 1260
QY 1295 CTCGTTGCCCTGGGAGTTGTAGACAGTCCACAGGCTTGGCACTGGGGATTCCTCT 1354
DB 1261 CTCGTTGCCCTGGGAGTTGTAGACAGTCCACAGGCTTGGCACTGGGGATTCCTCT 1320
QY 1355 GACCTGATAAAGAAACATGGAGCAGCTGAATCTCTGCTGTGTCTCCCTGAAGAT 1414
DB 1321 GACCTGATAAAGAAACATGGAGCAGCTGAATCTCTGCTGTGTCTCCCTGAAGAT 1380
QY 1415 ATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTAACGAGATGATGGGATGCGAG 1474
DB 1381 ATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTAACGAGATGATGGGATGCGAG 1440
QY 1475 ATCTGGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAGTGCAC 1534
DB 1441 ATCTGGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAGTGCAC 1500

QY 1535 ACATCCGTCCAAAGATGACCAAGAGCTCCAGGCTCGGTGAGGGAGATCTTCTCTGAGGGC 1594
DB 1501 ACATCCGTCCAAAGATGACCAAGAGCTCCAGGCTCGGTGAGGGAGATCTTCTCTGAGGGC 1560
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DB 1561 TTCTCTGGCCGAGAAAGCTCAGGTATGCCCTCTGTTGGATACCCGGGAAGCCCTTGGTC 1620
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QY 1775 ACTTCCAAAGGCCAGGCCCGGCTGAGAGTTTCATAGCAACGCTCCAGCAGTGAATTCG 1834
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DB 1801 TCAAGTTATCACTCATTTGCTCTCTGGCTGTCTTAAGCGCAGAACCTTGGGGACCCAAAGGCC 1860
QY 1895 CTGGGCCACTATCCAGATGAACACTTTCACAGAGGATGCCCGCGGAGAGCTGTGGCTGCC 1954
DB 1861 CTGGGCCACTATCCAGATGAACACTTTCACAGAGGATGCCCGCGGAGAGCTGTGGCTGCC 1920
QY 1955 TTCCAGAGAAAGCTGATCCAGATCTCCAAAGGCAATCAGGAGAGGAAACCGAGGCTTGCA 2014
DB 1921 TTCCAGAGAAAGCTGATCCAGATCTCCAAAGGCAATCAGGAGAGGAAACCGAGGCTTGCA 1980
QY 2015 CTGCCCTACACTACTCTGGATCTCCCTCTCATTTGAGAAACAGTGTCTCCATCTAAACATCTT 2074
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QY 2075 GGAGAAAGCAGTCTCTGTGTGATATAGAACTCTTTGACATGCTCTCTCAGGCTAAGTCC 2134
DB 2041 GGAGAAAGCAGTCTCTGTGTGATATAGAACTCTTTGACATGCTCTCTCAGGCTAAGTCC 2100
QY 2135 CGGTATGCTTCTCTGAGAACCAACGAGCCCACTTTTACACACACACACACACACACAC 2194
DB 2101 CGGTATGCTTCTCTGAGAACCAACGAGCCCACTTTTACACACACACACACACACACAC 2160
QY 2195 TAAATAAATTCGAAAACAGAAAACCTTAAACTCCCAACAGAGGCAAGATCTCACACAGCAGA 2254
DB 2161 TAAATAAATTCGAAAACAGAAAACCTTAAACTCCCAACAGAGGCAAGATCTCACACAGCAGA 2220
QY 2255 GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTCTGATTAACGGCTTTTGTGGTTT 2314
DB 2221 GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTCTGATTAACGGCTTTTGTGGTTT 2280
QY 2315 GCTTTGCTTCTTATTTCCATTAACCATGAGCCGTACAGAAAGCAGACAGACCCCTGTTTAC 2374
DB 2281 GCTTTGCTTCTTATTTCCATTAACCATGAGCCGTACAGAAAGCAGACCCCTGTTTAC 2340
QY 2375 TGCACAAAAGCCACTGAGATCTCACCTCACTGACACAAAAGGCGAGTATCATACAGGCTT 2434
DB 2341 TGCACAAAAGCCACTGAGATCTCACCTCACTGACACAAAAGGCGAGTATCATACAGGCTT 2400
QY 2435 ATCAGGAAACAGAGGAATTTGTCCCAATCAAGCCTTACCACTAGGTCCTATCGTGACCTAG 2494
DB 2401 ATCAGGAAACAGAGGAATTTGTCCCAATCAAGCCTTACCACTAGGTCCTATCGTGACCTAG 2460
QY 2495 ACCTCACACTGGCATGCTTTAGCTTTGAGAGGGATTAATGGAGTCAGTACGAGAGAA 2554
DB 2461 ACCTCACACTGGCATGCTTTAGCTTTGAGAGGGATTAATGGAGTCAGTACGAGAGAA 2520
QY 2555 GGACAGGACGAGGAGCATGGCTCCATGTGGAAGAAACATATCTCTCTTCCAGATGACAGG 2614
DB 2521 GGACAGGACGAGGAGCATGGCTCCATGTGGAAGAAACATATCTCTCTTCCAGATGACAGG 2580
QY 2615 GTAGCTCACAGCCATGTGTCTATTCTTAACTTCACAGAGGTCTCTAGTGCCCATGAACTCCA 2674


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Db 2581 GTAGCTCAGCCATGTGTCTTCACTTCACTCCAGAGTCTCTAGTGGCCATGAAGACTCCA 2640
Qy 2675 GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATATCTTTTAAAGAGAGAGGAATGGG 2734
Db 2641 GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATATCTTTTAAAGAGAGAGG-ATGGG 2699
Qy 2735 CTGGAGAGATGGCTCAGCGGTTAAGAGACACAGCTGCTCTTCCAGAGATCTCTGAGTTCAA 2794
Db 2700 CTGGAGAGATGGCTCAGCGGTTAAGAGACACAGCTGCTCTTCCAGAGATCTCTGAGTTCAA 2759
Qy 2795 TTCCAGCAACACATGGTGGCTCAACACCATCTCTAATGGGATTCGATGCCCTTTCTG 2854
Db 2760 TTCCAGCAACACATGGTGGCTCAACACCATCTCTAATGGGATTCGATGCCCTTTCTG 2819
Qy 2855 GGGTGTCTGGAAGACAGCAGCTGTATGCACATATATAAAATAAAATAAATCTTTAAAAA 2914
Db 2820 GGGTGTCTGGAAGACAGCAGCTGTATGCACATATATAAAATAAATAAATCTTTAAAAA 2879
Qy 2915 CAAAACAGAGAGAGGACATGCTACCATTTCTACCTCACTTCTTCAAAGCCACCCCT 2974
Db 2880 CAAAACAGAGAGAGGACATGCTACCATTTCTACCTCACTTCTTCAAAGCCACCCCT 2939
Qy 2975 AAAGTGAATTGTGAACACAGTCCCTTTTCAGAGAGTTAGAGATATTTCTAAACCTCTA 3034
Db 2940 AAAGTGAATTGTGAACACAGTCCCTTTTCAGAGAGTTAGAGATATTTCTAAACCTCTA 2999
Qy 3035 ATACCTTCACATCTAAATTCATTTCAATTCCAAATTCCAAATTTTATATACACTCTC 3094
Db 3000 ATACCTTCACATCTAAATTCATTTCAATTCCAAATTCCAAATTTTATATACACTCTC 3059
Qy 3095 CAGTTTGGTGGTGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3154
Db 3060 CAGTTTGGTGGTGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3119
Qy 3155 GTTTTGTATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3214
Db 3120 GTTTTGTATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3179
Qy 3215 AGTTCATTCC 3224
Db 3180 AGTTCATTCC 3189

RESULT 3
US-10-716-204-3
; Sequence 3, Application US/10716204
; Publication No. US20040137483A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF INVENTIONS: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10716,204
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-716-204-3

Query Match 98.6%; Score 3178; DB 19; Length 3205;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 35 ATGCGCAAAATCAGGGTGAGAGTATCCACGGGGGGAAGCCTGTGGGGCTTGGCACATGGGAC 94
Db 1 ATGCGCAAAATCAGGGTGAGAGTATCCACGGGGGGAAGCCTGTGGGGCTTGGCACATGGGAC 60
Qy 95 AAAGTGTCTGTACGATCTGTGGGAAACCCACGAGAGAGCCCTTTAGTACCTCTTGACCAT 154
Db 61 AAAGTGTCTGTACGATCTGTGGGAAACCCACGAGAGAGCCCTTTAGTACCTCTTGACCAT 120
Qy 155 CTGGCAAGAGATTCAGGGCCGGTGTGGAAGAAGACTTCGAGGTGACGCTTCCCCAGGAC 214
Db 121 CTGGCAAGAGATTCAGGGCCGGTGTGGAAGAAGACTTCGAGGTGACGCTTCCCCAGGAC 180
Qy 215 GTAGCACTGTGCTGATGCTCGAGTCCACAAAGCACCCCGGAAGTGTCCCTCCCGCTT 274
Db 181 GTAGCACTGTGCTGATGCTCGAGTCCACAAAGCACCCCGGAAGTGTCCCTCCCGCTT 240
Qy 275 ATGCTTTTCGTTCTGATGCTGTGTTCTGCGCTGTGTTGAGCTGGAGTGGCTACCTGG 334
Db 241 ATGCTTTTCGTTCTGATGCTGTGTTCTGCGCTGTGTTGAGCTGGAGTGGCTACCTGG 300
Qy 335 GCTGCACTCCACTTCCCTGTATCAGTGGTGGAGGGGGGGGAGCTGGTGTGAGA 394
Db 301 GCTGCACTCCACTTCCCTGTATCAGTGGTGGAGGGGGGGGAGCTGGTGTGAGA 360
Qy 395 GAGGAGCAGCAAAAGGTGTCTCGCAAGACCATCACCTACACTGCAGGATCAGGCCAG 454
Db 361 GAGGAGCAGCAAAAGGTGTCTCGCAAGACCATCACCTACACTGCAGGATCAGGCCAG 420
Qy 455 AAGGAGCTTGAGTCCAGGCAAGATGTACAGCTGGAGAATTACATTTGAAGGTTGGCT 514
Db 421 AAGGAGCTTGAGTCCAGGCAAGATGTACAGCTGGAGAATTACATTTGAAGGTTGGCT 480
Qy 515 CGTGCCTTGAACAGAGACTGTGAAGACTTGGACCTCAACATCAAGTACTCTCGGATG 574
Db 481 CGTGCCTTGAACAGAGACTGTGAAGACTTGGACCTCAACATCAAGTACTCTCGGATG 540
Qy 575 AAGATGCCAAACTCTCTTTAAAGCCCACTCCCGTATACGAGCTCAAGAGTCAAAAGG 634
Db 541 AAGATGCCAAACTCTCTTTAAAGCCCACTCCCGTATACGAGCTCAAGAGTCAAAAGG 600
Qy 635 CTCCTGGACCGCACAGGACTCTGGAGGAGTCTGGAGGAGATGAGAGGCTGTTTAACTTC 694
Db 601 CTCCTGGACCGCACAGGACTCTGGAGGAGTCTGGAGGAGATGAGAGGCTGTTTAACTTC 660
Qy 695 CGCAAGACTCCAGCAGAGATGTGTTCACACTCGGAGGAGATGCCTTCTTCGCC 754
Db 661 CGCAAGACTCCAGCAGAGATGTGTTCACACTCGGAGGAGATGCCTTCTTCGCC 720
Qy 755 TCCAGTTCCTAAATGGCATCAACCCGCTCTGATTCGCCCTGTACAGTCTCCCAAC 814
Db 721 TCCAGTTCCTAAATGGCATCAACCCGCTCTGATTCGCCCTGTACAGTCTCCCAAC 780
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QY	815	AACTTCCCGTCACTGATGAATGATGAGGCGCCCAAGTGTCTGGGCGCTGGAAACCAAGTCTGGAG	874
Db	781	AACTTCCCGTCACTGATGAATGATGAGGCGCCCAAGTGTCTGGGCGCTGGAAACCAAGTCTGGAG	840
QY	875	GCTGAGTTCGAGAGGCGTCCCTGTTCTTGTGGATCATGGCATCTTCTCGAGTCCAC	934
Db	841	GCTGAGTTCGAGAGGCGTCCCTGTTCTTGTGGATCATGGCATCTTCTCGAGTCCAC	900
QY	935	ACCAACATCCTCAATGGAAAGCCTCAGTTCTCTGACGCGCCGATGACCCCTGTTACACCAAG	994
Db	901	ACCAACATCCTCAATGGAAAGCCTCAGTTCTCTGACGCGCCGATGACCCCTGTTACACCAAG	960
QY	995	AGCTCAGGTCGGACCCCTGCTTCCCATTCGCATCCAGCTCAACAGACTCCCGGGCA	1054
Db	961	AGCTCAGGTCGGACCCCTGCTTCCCATTCGCATCCAGCTCAACAGACTCCCGGGCA	1020
QY	1055	GACAAACCCATCTTCTGCGCCAGCATGACAGTGGGACTGGTGTGCTGCGCAGACCTGG	1114
Db	1021	GACAAACCCATCTTCTGCGCCAGCATGACAGTGGGACTGGTGTGCTGCGCAGACCTGG	1080
QY	1115	GTTTCGCAATTCAGATTTTACATCCATGAGGCTGTCAACATCTGCTGCATGCCCCTCTG	1174
Db	1081	GTTTCGCAATTCAGATTTTACATCCATGAGGCTGTCAACATCTGCTGCATGCCCCTCTG	1140
QY	1175	ATTCCAGAACTCTTTCCTTGGCCACATTAAGTCAAGTCCCTAGTGTCAACCTCTCTTC	1234
Db	1141	ATTCCAGAACTCTTTCCTTGGCCACATTAAGTCAAGTCCCTAGTGTCAACCTCTCTTC	1200
QY	1235	AACTATTGATTCCTCACATTCGGTACACATTCGACATCAACCGTTGCCCGGAGCTG	1294
Db	1201	AACTATTGATTCCTCACATTCGGTACACATTCGACATCAACCGTTGCCCGGAGCTG	1260
QY	1295	CTCGTTGCCCTTGGGAAGTTGATAGAACAGTCCACAGGCTTGGCACTGGGGGATTCCT	1354
Db	1261	CTCGTTGCCCTTGGGAAGTTGATAGAACAGTCCACAGGCTTGGCACTGGGGGATTCCT	1320
QY	1355	GACCTGATAAAGAAACATGAGCAGCTGAATCTCTGTCTGTGTCTCCCTGAAGAT	1414
Db	1321	GACCTGATAAAGAAACATGAGCAGCTGAATCTCTGTCTGTGTCTCCCTGAAGAT	1380
QY	1415	ATCCGAGCCGAGGTGTGGAAGCATCCAGGCTACTATTACCGAGATCATGGATGCAG	1474
Db	1381	ATCCGAGCCGAGGTGTGGAAGCATCCAGGCTACTATTACCGAGATCATGGATGCAG	1440
QY	1475	ATCTGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAAAGTGAC	1534
Db	1441	ATCTGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAAAGTGAC	1500
QY	1535	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTTGAGGGC	1594
Db	1501	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTTGAGGGC	1560
QY	1595	TTCTCTCGGCGGAGAAAGCTCAGGTATGCCCTCTTGTGGATACCGGGAAGCCCTGGTC	1654
Db	1561	TTCTCTCGGCGGAGAAAGCTCAGGTATGCCCTCTTGTGGATACCGGGAAGCCCTGGTC	1620
QY	1655	CAGTATATCACCATGTGTATTTACCTGCTCAGCCAAGCATGCTCAGTTTCAGGCTCAGGC	1714
Db	1621	CAGTATATCACCATGTGTATTTACCTGCTCAGCCAAGCATGCTCAGTTTCAGGCTCAGGC	1680
QY	1715	CAGTTCGACTCTTGTGTTGGATGCCCAATCTGCCACCTACCATGCAGTACCAACACT	1774
Db	1681	CAGTTCGACTCTTGTGTTGGATGCCCAATCTGCCACCTACCATGCAGTACCAACACT	1740
QY	1775	ACTTCCAAAGGCGGCGGCTGAGTTTCATAGCCACCGTCCAGCAGTTAATTCG	1834
Db	1741	ACTTCCAAAGGCGGCGGCTGAGTTTCATAGCCACCGTCCAGCAGTTAATTCG	1800
QY	1835	TCAAGTTATCACATCTCTCTGGCTGTAAAGCGAGAACCTGGGACCAAGGCGCC	1894
Db	1801	TCAAGTTATCACATCTCTCTGGCTGTAAAGCGAGAACCTGGGACCAAGGCGCC	1860
QY	1895	CTGGGCCACTATCCAGATGAACACTTTCACAGGATGCCCGCGGCGAAGCGTGGCTGCC	1954

Db	1861	CTGGGCCACTATCCAGATGAAACACTTTCACAGAGGATCCCCCGCGAAGCGTGGCTGCC	1920
QY	1955	TTCCAGAGAAAAGCTGATCCAGATCTTCCAAAGGCGATCAGGAGAGAGAAACCGAGGCCCTGGCA	2014
Db	1921	TTCCAGAGAAAAGCTGATCCAGATCTTCCAAAGGCGATCAGGAGAGAGAAACCGAGGCCCTGGCA	1980
QY	2015	CTGCCCTACACTACCTCGGATCTCCCTCATTTGAGAAACAGTGTCTCATCTAAACATCTT	2074
Db	1981	CTGCCCTACACTACCTCGGATCTCCCTCATTTGAGAAACAGTGTCTCATCTAAACATCTT	2040
QY	2075	GGAGAAAGCAGTCTCTGTGTGATATAGAACTCTTTGACCATGCCCTCTCCAGGCTAAGTCC	2134
Db	2041	GGAGAAAGCAGTCTCTGTGTGATATAGAACTCTTTGACCATGCCCTCTCCAGGCTAAGTCC	2100
QY	2135	CGGTATGCTTCTCTCGGACAAACCAAGCCCATCTTTACACACACACACACACACACACACC	2194
Db	2101	CGGTATGCTTCTCTCGGACAAACCAAGCCCATCTTTACACACACACACACACACACACACC	2160
QY	2195	TAATAAAAATCGAAAACAGAAAACCTTAACTCCACAGAAAGGCAAGATCTCACACAGCAGA	2254
Db	2161	TAATAAAAATCGAAAACAGAAAACCTTAACTCCACAGAAAGGCAAGATCTCACACAGCAGA	2220
QY	2255	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCAGCTCTGATTAAACGGCTTTGCTGGTTT	2314
Db	2221	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCAGCTCTGATTAAACGGCTTTGCTGGTTT	2280
QY	2315	GCTTTGCTTTCTATTTCATTAACCATGACGCTTAACAGAAAGCAGACAGAAACCTGTTTAC	2374
Db	2281	GCTTTGCTTTCTATTTCATTAACCATGACGCTTAACAGAAAGCAGACAGAAACCTGTTTAC	2340
QY	2375	TGCAAAAAGCCACTGAGATCTCACCTCACCTGACACAAAAGSCAGCTATCATACAGGCTT	2434
Db	2341	TGCAAAAAGCCACTGAGATCTCACCTCACCTGACACAAAAGSCAGCTATCATACAGGCTT	2400
QY	2435	ATCAGAAACACAGGAATTTGTCCATCAAGCTTACCCTAGGTCCTAGTGCCTGAGCTAGG	2494
Db	2401	ATCAGAAACACAGGAATTTGTCCATCAAGCTTACCCTAGGTCCTAGTGCCTGAGCTAGG	2460
QY	2495	ACCTCACACTGGCATGCTTTAGCTTTGAGAAAGGATTAAGTGGAGTCAGGTACGAAAGAAA	2554
Db	2461	ACCTCACACTGGCATGCTTTAGCTTTGAGAAAGGATTAAGTGGAGTCAGGTACGAAAGAAA	2520
QY	2555	GGACAGGACGAAAGCATCGCTCCATGTGGAAGAACATATCTGCTCTTCAGATGACCCAGG	2614
Db	2521	GGACAGGACGAAAGCATCGCTCCATGTGGAAGAACATATCTGCTCTTCAGATGACCCAGG	2580
QY	2615	GTAGCTCACGCCATGTGTCTTAACTCCAGAGGTCCTAGTGGCCATGGAAGTCCCA	2674
Db	2581	GTAGCTCACGCCATGTGTCTTAACTCCAGAGGTCCTAGTGGCCATGGAAGTCCCA	2640
QY	2675	GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGGAATGGG	2734
Db	2641	GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGG-ATGGG	2699
QY	2735	CTGGAGAGATGGCTCAGCGGTTTAAAGAGCACTGACTGCTCTTCCAGAGATCTCTGAGTTCAA	2794
Db	2700	CTGGAGAGATGGCTCAGCGGTTTAAAGAGCACTGACTGCTCTTCCAGAGATCTCTGAGTTCAA	2759
QY	2795	TTCCAGCAACCAATGTGTGCTCAACCATCTGTATGGGATTCGATGCCCTCTTCTG	2854
Db	2760	TTCCAGCAACCAATGTGTGCTCAACCATCTGTATGGGATTCGATGCCCTCTTCTG	2819
QY	2855	GGTGTCTGTGAAGACGACAGTGTATGACATATATAAAATAAATAAATAAATAAATAAATAA	2914
Db	2820	GGTGTCTGTGAAGACGACAGTGTATGACATATATAAATAAATAAATAAATAAATAAATAA	2879
QY	2915	CAAAAACAGAGAGAGGAGCATGCTACCTTTCTACCTCACTTCTTCTCAAGGCCACCTT	2974
Db	2880	CAAAAACAGAGAGAGGAGCATGCTACCTTTCTACCTCACTTCTTCTCAAGGCCACCTT	2939
QY	2975	AAAGTGAATTTGTGAACCGAGTCCCTTTTGCAGAGAGTTAGAGATATTTCTCAAACTCTA	3034

Db 2940 AAAGTGAATTGTGAACCAAGTCCCTTTTGCAGAGAGTTAGAGATATTTCTCAAACTCTA 2999
 QY 3035 ATACCTTCACATCTAAATCAATCTTCATTCACAAATTTCCAAATTTTATATACACTCTC 3094
 Db 3000 ATACCTTCACATCTAAATCAATCTTCATTCACAAATTTCCAAATTTTATATACACTCTC 3059
 QY 3095 CAGTTTGTGGTGAGGGTGTGTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT 3154
 Db 3060 CAGTTTGTGGTGAGGGTGTGTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT 3119
 QY 3155 GTTTTTGATTTGTTTTTCTCTGTTTCAGACTCCATGACAGTTCAATTAATGTCAATAATG 3214
 Db 3120 GTTTTTGATTTGTTTTTCTCTGTTTCAGACTCCATGACAGTTCAATTAATGTCAATAATG 3179
 QY 3215 AGTTCAATCC 3224
 Db 3180 AGTTCAATCC 3189

RESULT 4

US-09-764-246-1
 ; Sequence 1, Application US/09764246
 ; Patent No. US20010046672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRASH, ALAN R.
 ; BOEGLIN, WILLIAM E.
 ; JISAKA, MITSUO
 ; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ARLES A. TAYLOR, JR.
 ; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
 ; CITY: DURHAM
 ; STATE: NORTH CAROLINA
 ; COUNTRY: USA
 ; ZIP: 27707
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
 ; COMPUTER: IBM PC/XT/AT compatible
 ; OPERATING SYSTEM: Windows 3.1
 ; SOFTWARE: WORD PERFECT 6.1 and ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/764,246
 ; FILING DATE: 17-Jan-2001
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: <Unknown>
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ARLES A. TAYLOR, JR.
 ; REGISTRATION NUMBER: 39,395
 ; REFERENCE/DOCKET NUMBER: 1242/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 493-8000
 ; TELEFAX: (919) 419-0383
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-764-246-1

Query Match 43.3%; Score 1395.2; DB 9; Length 2685;
 Best Local Similarity 79.8%; Pred. No. 0;
 Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;
 QY 7 GCAGTAGAGACTAAACT--GGTCAGGAGGATGGGAAATGCAGGGTGAGAGTATCCACG 64
 Db 42 GCCGTAGAGAGCTGACTTAGGCTGGCAGCATGGCCGAGTTTCAGGGTCAGGGTGTCCACC 101

QY 65 GGGAAAGCCTCTGGGCTGGCACAATGGGCAAAAGTGTCTGTCAACATCGTGGGAACCCAC 124
 Db 102 GGAAAGCCTCTGGGCTGGCACAATGGGCAAAAGTGTCTGTCAACATCGTGGGAACCCGG 161
 QY 125 GGAGAGAGCCCTTTAGTACCTCTGGACCATCTGGGCAAGGAGTTTCAGCGCCGGTGTCTGAA 184
 Db 162 GGAGAGAGCCCTTTAGTACCTCTGGACCATCTGGGCAAGGAGTTTCAGCGCCGGTGTGAG 221
 QY 185 GAAGACTTCAGAGTGAAGCTTCCCGGACGTAGGCACCTGTGTGATGTCTCGAGTCCAC 244
 Db 222 GAGGACTTCAGAGTGAAGCTTCCCGGACGTAGGCACCTGTGTGATGTCTCGAGTCCAC 281
 QY 245 AAAGCAACCCCGGAGAGTGTCCCTCCCGCTTATGTCTTCCGTTCTGTGATGTCTGTCTGC 304
 Db 282 AAGCGCCCTCTCTGCGGCTCTGTCTGCGGCTCTGTCTGCGGCTCTGTCTGTCTGCG 338
 QY 305 CGCTGGTTTCAGAGTGGAGTGTCTACCTGGGCTGTCACTTCCACTTCCCTCTGTATCAGTGG 364
 Db 339 CGCTGGTTTCAGAGTGGAGTGTCTACCTGGGCTGTCACTTCCACTTCCCTCTGTATCAGTGG 398
 QY 365 CTGGAAGGGCGGGGAGTGTGTCTGAGAGAGGAGCAGCAAAAGTGTCTCTGGAAGAC 424
 Db 399 CTGGAAGGGCGGGGAGTGTGTGTCTGAGAGAGGAGTGTGTCTGGAAGAC 458
 QY 425 CATCACCTTACACTGCAGGATCAGCGCCAGAGAGCTTGTGTCCAGCAGAGATGTATC 484
 Db 459 CACACCTTGTGTCTCCAGCAACAGCGCCAGAGAGCTTCTGAGGCTCTGAGGATGTATC 518
 QY 485 AGCTGGAAGACTTACATTTGAAGTGTGCTCTGCTCTGCTTACACAGAGACTGTGAAAGAC 544
 Db 519 CAGTGGAGGGTTTACACCCAGGTTGGCTCTCACTGCTGTGATGAAGAGACAGTGAAGAC 578
 QY 545 TTGACCTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTTTAAAGCCAC 604
 Db 579 TTGAGCTCAATATCAAAATCTCCACAGCCAAAGATGCCAACTTTTATCTCAAGCTGGC 638
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 Db 639 TCTGCTTTTGCAGAGATGAAATCAAGGGGTGTCTGACCCGCAAGGGGCTCTGAGGAGT 698
 QY 665 CTGAGGAGATGAGAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTGTGTGTT 724
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 Db 759 GAGCACTGGCAGGAGATGCTTCTTCCCTCCAGTTCCTGATGCTCTCAACCCGTCTC 818
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 QY 845 CCAGTGTGGGCTGGAAACAGTCTGAGGCTGAGTTGGAGAGGCTCCCTGCTCTTG 904
 Db 879 TCATTTGTTGGTCTTGGACAGCTTCAGGCTGAGCTAGAGAGGCTCTCTGCTCTTG 938
 QY 905 GTGATCATGGCATTTCTTCTGGAGTCCACCAACATCTCTCAATGAAAGCTCAGTTC 964
 Db 939 GTGATCATGGCATTTCTTCTGGAGTCCACCAACATCTCTCAATGAAAGCTCAGTTC 998
 QY 965 TCTGAGCCCGGATGACCTTGTACACAGAGTCTGAGGCTCGGAGCCCTGCTTCCCAT 1024
 Db 999 TCTGCGCCCAATGACCTGTCTATACAGAGCCAGGCTGCGGCGCTGCTGCTCTC 1058
 QY 1025 GCCATCCAGCTCAACAGACTCCCGGCGCAGACACCCCATCTTCTCCGCGCAGGATGAC 1084
 Db 1059 GCCATCCAGCTCAGCCAGACACCCCGGCGCAGACACCCCATCTTCTGCGCCACTGATGAC 1118
 QY 1085 ACCTGGGACTGTGTGGCAAGAGCTGGGTTCGCAATTCAGTGTATCATCCATGAG 1144
 Db 1119 AAGTGGGACTGTGTGGCAAGAGCTGGGTTCGCAATTCAGTGTATCATCCATGAG 1178
 QY 1145 GCTGTCAACATCTGTGTGATGCCCATCTGATTCAGAAAGTCTTTTGTGCTTGGCCACATTA 1204

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Db 1179 GGCCTCAGCCAGCTGTGCTCACTCACTGTGCTGCTGAGTCTTCCACCTGTGCTACCCTG 1238
Qy 1205 CGTACAGCTCCTAGGTGTGCTCACTCCTCTCTCAAGCTATTGATTCCTCACAATTCGGTACACA 1264
Db 1239 CGTACAGCTGCCCACTGCCACCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACC 1298
Qy 1265 CTGCACATCAACACGCTTCCCGCGGAGTGTCTGTTGCCCTTGGGAAGTTGATAGACAAG 1324
Db 1299 CTGCACATCAACACACTGCCCGCGGAGTGTCTTATCGTCCAGGGCAGGTGTGTGACAGG 1358
Qy 1325 TCCACAGGCTTGGCACTGGGGGATTCCTGTGACCTGATTAAGAGAAACATGAGAGCAGTGT 1384
Db 1359 TCCACAGGCTCGGCATTAAGGCTTCTGTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
Qy 1385 AACTACTCTGTCTGTCTCTCTGCTCCCTGAGATATCCGAGCCGAGGTGTGGAGACATCCCA 1444
Db 1419 AACTATTCTCTCTGTCTGTCTGCTGAGGATATCCCGACCCGAGGATTTGAAGACATCCCA 1478
Qy 1445 GGCTACTATTACCGAGATGATGGGATGACAGATCTTGGGGGCAATAAAGAGCTTTTGTCTCT 1504
Db 1479 GGCTACTACTACGATGATGGGATGACAGATTTGGGGTGCAAGTGGACGCTTTGTCTCT 1538
Qy 1505 GAAATAGTCAGCATCTACTATCAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCAG 1564
Db 1539 GAAATCATCGGTATCTACTACCAAGTGATGATCTGTCCAAGATGACAGAGAGCTCCAG 1598
Qy 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGGAGAAAGCTCAGGTATGCC 1624
Db 1599 GCCTGGGTGAGGAGATCTTCTTCCAAGGGCTTCTTAAACAGGAGAGCTCAGGTATCCCT 1658
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Db 1659 TCTCTACTGAGACCGGGAAGCCCTGTGTCAGTATGTCACCATGGTGATATTCACCTGC 1718
Qy 1685 TCAGCAGCATGCGGCTGTGAGTGAGGCGAGTTTGAATGATGATGATGATGATGATGATGAT 1744
Db 1719 TCAGCAGCATGCGGCTGTGAGTGAGGCGAGTTTGAATGATGATGATGATGATGATGATGAT 1778
Qy 1745 CTGCCACCTACCATGAGTACACACACTTCTCCAGAGGCGAGGCGGCGGCTGAGGT 1804
Db 1779 CTGCCACCTACCATGAGTACACACACTTCTCCAGAGGCGAGGCGGCGGCTGAGGT 1838
Qy 1805 TTATAGCAGCAGCTTCCAGCAGTTAATCGTCAAGTTATCAATCATTCCTCTCTGCGGTG 1864
Db 1839 TTATAGCAGCAGCTTCCAGCAGTTAATCGTCAAGTTATCAATCATTCCTCTCTGCGGTG 1898
Qy 1865 CTAAGCGCAGAACCTGGGACCAAGGCGGCTGGGCGCACTATCCAGATGAAACATTTACA 1924
Db 1899 CTGAGCAAGGAGGCTGGAGACCAAGGCGGCTGGGCGCACTATCCGATGAGCACTTACA 1958
Qy 1925 GAGGATGCCCCCGGCGAAGCGTGGCTTCCAGAGAAAGTATCCAGATCTCCAG 1984
Db 1959 GAGGATGCCCCCGGCGAAGCGTGGCTTCCAGAGAAAGTATCCAGATCTCCAG 2018
Qy 1985 GGATCAGGAGAGGAACCGAGGCTGGCACTGCGCTACACCTACCTGATCTTCCCTC 2044
Db 2019 GGATCAGGAGAGGAACCGAGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2078
Qy 2045 ATTGAGAACAGTGTCTTCCATCTTAACATCTTGGAGAGAGACAGTCTGTGTGACAT 2098
Db 2079 ATCGAGAACAGGCTCTCCATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAAT 2132
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RESULT 5
US-09-960-706-985
; Sequence 985, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; TITLE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US

; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 985
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 U78294
US-09-960-706-985

Query Match 43.3%; Score 1395.2; DB 10; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

Qy 7 GCAGTAGAGAGCTAAACT--GGTCAGAGAGATGGCGAAATGACGGGTGAGAGTATCCAG 64
Db 42 GCCGTAGAGAGCTGACTTAGCTGGCAGCATGGCCGAGTTCAGGGTCAGGGTGTCCACC 101
Qy 65 GGGGAAGCCTGTGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGAACCCAC 124
Db 102 GGAGAAGCCTTTCGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGGACCCGG 161
Qy 125 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCAGGCGCGGCTCTGAA 184
Db 162 GGAGAGAGCCCTTCCCTTGGCAATCTCGGCAAGGAGTTCAGTGGGGCGCTGAG 221
Qy 185 GAAGACTTCGAGGTGACGCTTCCCGAGGACGTAGGCACTGTGCTGATGTGCGAGTCCAC 244
Db 222 GAGGACTTCGAGGTGACGCTCCCGAGGACGTAGGCGGAGTGTCTGCTGCGCTGCAC 281
Qy 245 AAAGCACCCCGGAGTGTCCCTCCCGCTTATGTCTTTCCGTTTGTGATGCTGCTGCTGCTG 304
Db 282 AAGGCGCGCC--AGTGTGCTGCTGCTGCGGCGGCTGCGCGGAGTGTGCTGCTGCTGCTG 338
Qy 305 CGCTGTTTCGAGCTGAGTGTGCTACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
Db 339 CGCTGTTTCGAGCTGACACCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 398
Qy 365 CTGGAAGGCGGCGGCGGAGTGTGCTGAGAGAGGAGGAGCAAGAGTGTCTTGGCAAGAC 424
Db 399 CTGGAAGGCGGCGGCGGAGTGTGCTGAGAGAGGAGTGTGAGAGAGTGTCTGCGGAGAC 458
Qy 425 CATCACTTACACTGAGATCAGCGCAGAGAGGAGTGTGAGTCCAGGAGAGAGATGTAC 484
Db 459 CACCACCTGTGCTCAGCAACAGCGCCAGGAGGAGCTTCAGGCGCGGAGAGATGTAC 518
Qy 485 AGCTGGAAGACTTACATCAAGTACTCTGCGATGAAGAAATGCCAACTCTTCTTTAAAGCCAC 544
Db 519 CAGTGAAGAGGCTTACAAACCCAGGTTGGGCTCTACTGCTGATGAAGAAATGCCAACTCTT 578
Qy 545 TTGAGACCTCAACATCAAGTACTCTGCGATGAAGAAATGCCAACTCTTCTTTAAAGCCAC 604
Db 579 TTGAGAGCTCAATATCAATATCTCCACAGCAAGAAATGCCAACTCTTCTTTAAAGCTGC 638
Qy 605 TCCGCGTATACGAGACTGAAAGTCAAAAGGCTCTCTGGAGCCGACAGGACTCTGGAGGAGT 664
Db 639 TCTGCTTTTGCAGAGATGAAATCAAGGGGTGTGCTGGACCCGCAAGGGGCTCTGGAGGAGT 698
Qy 665 CTGAGGAGAGTGAAGGCTGTTTAACTTCCCAAGACTTCCAGAGACTCCAGAGAGATGTGTTT 724
Db 699 CTGAATGAGATGAAGAGATCTTCACTTCCGAGAGACCCAGAGAGCTGAGCAGCATTT 758
Qy 725 GCACACTGGCAGAGAGATGCTTCTTTCGCTTCCAGTTCCTTAATGGCATCAACCCGGTCT 784
Db 759 GAGCACTGGCAGAGAGATGCTTCTTTCGCTTCCAGTTCCTTAATGGCTCTCAACCCGCTG 818
Qy 785 CTGATTGCGCGCTGTGTCAGAGTCTCCCAACAACTTCCCGGCTCACTGATGAATGTGGCC 844

Db 819 CTGATCCGCGTGTCTCACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGTTGCC 878
QY 845 CCAGTGTGGGCGCTGGAAACCAAGTGTGCAAGGTGAGTTGGAGAGGGCTCCCTGTTCTTG 904
Db 879 TCAATTGTTGGTCTTGGGACCAAGTGTGCAAGGTGAGTTAGAGAGGGCTCCCTGTTCTTG 938
QY 905 GTGATCATGGCATTTCTTCTGAGTCCACCAACCAATCTCAATGGAAGGCTCAGTTC 964
Db 939 GTGGATCAGCGCATCTCTCTGGCATCCAGACCAATGTCATTAATGGAAGCGCAGTTC 998
QY 965 TCTGAGCGCCCGATGACCTCTTTACACAGAGCTCAGGGTCCGACCCCTGCTTCCCATTT 1024
Db 999 TCTGGCGCCCAATGACCTCTGTATACCAAGCCAGGCTGGGGCGGTGCTGCTCTC 1058
QY 1025 GCCATCCAGTCAAAACAGACTCCGGGCGAGACAAACCCCATTTCTGCCCCAGCGATGAC 1084
Db 1059 GCCATCCAGTCAAGCAGACCCCGCGCCCAACACAGCCCATCTTCTGCCCCACTGATGAC 1118
QY 1085 AGTGGGACTGTTCTGCGCAAGACCTGGGTTCCGAATCTGAGTTTACATCATGAG 1144
Db 1119 AAGTGGGACTGTTCTGCGCAAGACCTGGGTTCCGAATCTGAGTTTCTCTTCCATGAG 1178
QY 1145 GCTGTCAACATCTGCTGATGCCCATCTGTATTCAGAAAGTCTTTGCTTGGSCCACTTA 1204
Db 1179 GCCCTCAGCAGCTCTGCACTCATCTGCTGCTGAGGTTCTCACCTGCTGCTACCTG 1238
QY 1205 CGTCAAGTGCCTTAGTGTCAACCTCTCTTCAAGCTATTGATTCCTCACATTCGGTACACA 1264
Db 1239 CGTCAAGTGCCTTAGTGTCAACCTCTCTTCAAGCTGTGATCCCGCACACCCGATACAC 1298
QY 1265 CTGCAATCAACACAGCTTGGCGGAGCTGCTGTTGGCCCTGGAAAGTTGATGACAAAG 1324
Db 1299 CTGCAATCAACACAGCTTGGCGGAGCTGCTTATCGTCCAGGCGAGTGTGTGACAGG 1358
QY 1325 TCCAGAGCTTGGCACTGGGGGATCTCTGACCTGATAAAGAGAAACATGAGCAGCTG 1384
Db 1359 TCCAGAGCATCGGCATTTGAAGCTTCTGAGTTGATACAGAGAAACATGAAGCAGCTG 1418
QY 1385 AACTACTCTGCTCTGCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAAGACATCCCA 1444
Db 1419 AACTATTCTCTCTGCTGCTGCTGAGGATATCCGAGCCCGAGGAGTTGAAGACATCCCA 1478
QY 1445 GGCTACTATTACCGAGATGAGGATGAGATCTGGGGGGCAATAAAGCTTTGTCTCT 1504
Db 1479 GGCTACTACTACCTGATGAGGATGAGATTTGGGGTGCAGTGGAAACGCTTTGTCTCT 1538
QY 1505 GAAATAGTCAGATCTACTATCCAGTGCACATCCGTCACAGATGACCAAGAGCTCCAG 1564
Db 1539 GAAATCATCGGTATCTACTACCAAGTGTAGTCTGTCCAGATGACAGAGAGCTCCAG 1598
QY 1565 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGGCGGAGAAAGCTCAGGTATGCC 1624
Db 1599 GCCTGGGTGAGAGATCTTCTCTCAAGGGCTTCTTAACACAGGAGCTCAGGTATCCCT 1658
QY 1625 TCCTTTGTTGATACCCGGGAAGCCTGTGTCAGTATATCAACATGGTATATCACTTCG 1684
Db 1659 TCCTCACTGAGAGACCCGGGAAGCCTGTGTGAGTATGTCAACATGGTATATCACTTCG 1718
QY 1685 TCAGCAGATGACAGTGTGAGTTCAGGCGCAGTTCGACTCTTGTGTTGGATGCCCAAT 1744
Db 1719 TCAGCAGATGACAGTGTGAGTTCAGGCGCAGTTCGACTCTTGTGTTGGATGCCCAAC 1778
QY 1745 CTGCCACCTTACATGACGATACCAACCTACTTCTCAAGGCGCAGGCGCGGCTGAGAGT 1804
Db 1779 CTGCCACCTTACATGACGATGACCAACCTTCTCAAGGCGCTGCAACATGCGAGGCG 1838
QY 1805 TTCTAGCCAGCTCCCGAGAGTAAATTCGTCAGTATATCAATCATGCTCTCTGGCTG 1864
Db 1839 TTCTAGCCAGCTCCCGAGAGTAAATTCGTCAGTATATCAATCATGCTCTCTGGCTG 1898
QY 1865 CTAAGCGAGAACTGGGGACCAAGGCGCCCTGGGCCACTATCCAGATGAACATTTCACA 1924

Db 1899 CTGACCAAGGAGCCTGGAGACCAAGGCGCCCTGGGCACCTATCCGATGAGCACTTCACA 1958
QY 1925 GAGGATGCCCCCGCGCAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATTCCTCAAG 1984
Db 1959 GAGGAGGCGCCCTCGCGGAGCATGCGCACCTTCCAGAGCGCGCTCCAGATCTCGAGG 2018
QY 1985 GGCATCAGGAGAGGACCGGAGGCTGGCACTGGCCCTACACCTACCTGATCTCCCTC 2044
Db 2019 GGCATCCAGGAGCGGAAACCGGGGCTGTGTGCTGCTTACCTTACCTAGACCTCCCTC 2078
QY 2045 ATTGAGAACAGTGTCTCCATCTTAACATCTTGGAGAAAGCAGTCTCTGTGTGACAT 2098
Db 2079 ATCAGAAACAGCTCTCCATCTTAATCCAGGGGAAACACAGGCCCCAGATGACAT 2132

RESULT 6

US-09-873-319-642
; Sequence 642, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; FILE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; EARLIER FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 642
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 U78294
US-09-873-319-642

Query Match 43.3%; Score 1395.2; DB 10; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;
QY 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGGCAAAATCAGGGTCAGAGTATCCACG 64
Db 42 GCCGTAGAGAGCTGAGCTTAGCTGGCAGCATGGCCGAGTTTCAGGGTCAGGGTGTCCACC 101
QY 65 GGGGAAGCTGTGGGGCTGGCACAATGGCAAAAGTGTCTGTGAGCATGTGGGAACCCAC 124
Db 102 GGAGAGCTTTCGGGGCTGGCACAATGGCAAAAGTGTCTGTGAGCATGTGGGACCCGG 161
QY 125 GGAGAGAGCTTGTAGTACCTCTGACCATCTGGGCAAGGAGTTCAGGCGCGGTCTGAA 184
Db 162 GGAGAGAGCTTGTAGTACCTCTGACCATCTGGCAAAATCTCGGCAAGGAGTTCAGT 221
QY 185 GAACATCTCAGAGTGAGCTTCCCGAGAGCTAGGCACTGTGCTGATGCTCGAGTCCAC 244
Db 222 GAGGACTTCCAGGTGAGCTCTCCCGAGAGCTAGGCGGAGTGTGCTGCTGCGGCTGAC 281
QY 245 AAAGCAGCTTCCGAGAGTGTCTCCCGCTTATGTCTTTTCCGTTCTGATGCTGTTCTGC 304
Db 282 AAGCGCCCCC---AGTGTGCTGCTGCTGGGGCCCCCTGGCCCCCGGATGCTGTTCTGC 338
QY 305 CGCTGTTTCCAGCTGAGTGTGCTACCTTGGGGCTGCACTCCACTTCCCTCTGTTATCAGTGG 364
Db 339 CGCTGTTTCCAGCTGAGTGTGCACTCCCGCGGGGGCGGCCACCTCTCTTCTCCCTGTACAGTGG 398
QY 365 CTGGAAGGGGGGAGGAGTGTGCTGAGAGAGGAGCAGCAAGAGTGTCTCTGGCAAGAC 424
Db 399 CTGAGAGGGGGGGGAGCCCTGCTGAGAGAGGGTACAGCCAAAGGTGTCTCTGGGACAG 458

QY 425 CATCAACCTTACATGAGGATCAGGCCAGAGAGCTTGTGATCCAGGCAGAGATGTAC 484
DB 459 CACCAACCTGTGCTCCAGCAAAGCCGAGGAGGCTTCCAGGCCGCGAGAGATGTAC 518
QY 485 AGCTGGAAGATTACATTTGAAGTTGGCTCTCCCTGCTTGCCTGACAGAGACTGTGAAGAC 544
DB 519 CAGTGAAGGCTTACAAACCCAGGTTGGCTCTCACTGCTGGATGAAAGACATGTGAAGAC 578
QY 545 TTGGACCTCAACATCAAGTACTCTGGATGAAAGTCCAACTCTCTTTAAAGCCCAAC 604
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QY 605 TCCGGCTATACCGGATGAAAGCTTCAAGGCTCTTGGACCGCAGAGACTCTGGAGGAGT 664
DB 639 TCTGCTTTTGCAGAGATGAANAATCAAGGGTTGCTGGACCGCAAGGGCTCTGGAGGAGT 698
QY 665 CTGAGGAGATGAGAGGCTGTTTAACTTCCGCAAGACTCTCCAGCAGAGAGATGTGTTT 724
DB 699 CTGAATGAGATGAANAAGGATCTTCAACTTCCGAGGAGCCCAAGAGCTGAGCAACATTT 758
QY 725 GCACACTGCGAGAGATGCTTCTTCCGCTCCAGTTCCTAAATGGCATCAACCGGTC 784
DB 759 GAGCACTGCGAGAGATGCTTCTTCCGCTCCAGTTCCTAAATGGCATCAACCGGTC 818
QY 785 CTGAATGCGGCTGTGTCACAGTCTCCCAAAACAATTTCCGCTCACTGATGAATGGTGGC 844
DB 819 CTGATCCGCGCTGTCACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGGTGGC 878
QY 845 CGAGTCTCGGCGCTGAAACAGTCTGAGGCTGAGTTGAGAGAGGCTCCCTGTTCTTG 904
DB 879 TCATTGTTGGTCTTGGAGCAGCTTGCAGGCTGAGCTAGAGAAGGGCTCCCTGTTCTTG 938
QY 905 GTGGATCATGCAATTTCTGAGTCCACACCAATCTCAATGGAAGCTCAGTTTC 964
DB 939 GTGGATCAGGCGATCTCTCTGGCTCCAGACCAATGTCAATGGAAGCGGAGTTTC 998
QY 965 TCTGAGCCCCGATGACCTGTGTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAAT 1024
DB 999 TCTGCGCCCCAATGACCTGTGTATACAGAGCCAGGCTGCGGGCGCTGCTGCTCTC 1058
QY 1025 GCCATCCAGCTCAACAGACTCCGCGGCAGACACCCCATCTTCTGCGCCAGCATGAC 1084
DB 1059 GCCATCCAGCTCAGCCAGACCCCGGCCCAACAGCCCATCTTCTGCGCCATGATGAC 1118
QY 1085 AGTGGAGCTGTTGCTGCGCAAGACTGCTGCTGCAATTTCTGAGTTTACATCAATGAG 1144
DB 1119 AAGTGGAGCTGTTGCTGCGCAAGACTGCTGCTGCAATTTCTGAGTTTCTCTTCCATGAG 1178
QY 1145 GCTGTCCACATCTGCTGCATGCCATCTGATTCCAGAACTCTTTGCTTGGCCCATTA 1204
DB 1179 GCCCTCAGCACTGCTGCATCACAATCTGCTGCTGAGTCTTTCACCTGGCTACCCCTG 1238
QY 1205 CGTCACTGCTAGGTGTGACCTCTCTTCAAGCTATGATCTCACAATCTGATGATGAC 1264
DB 1239 CGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1298
QY 1265 CTGCATCAACAGCTTCCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
DB 1299 CTGCATCAACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1358
QY 1325 TCCACAGGCTTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
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QY 1385 AACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
DB 1419 AACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1478
QY 1445 GGTACTATTACCGAGATGATGGATGCGAGATCTGGGGGCAATAAGAGCTTTGCTCT 1504
DB 1479 GGCTACTACTACCGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 1538

QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTGACACATCCGTCGAAGATGACCAAGAGCTCCAG 1564
DB 1539 GAAATAGTCAGCATCTACTATCCAAAGTGATGAGTCTGTGTCGAAGATGACCAAGAGCTCCAG 1598
QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGCTTCTCGGCCGAGAAAGCTCAAGGTATGCC 1624
DB 1599 GCCTGGGTGAGGAGATCTTCTCTGAGGCTTCTTAAACAGGAGAGCTCAAGGTATCCCT 1658
QY 1625 TCCTTGTGGATACCCGGGAAGCCCTGCTCCAGTATATCAACATGGTGTATTTACCTGTC 1684
DB 1659 TCCTCACTGGAGACCCGGGAAGCCCTGCTGAGTATGTCAACATGGTGTATTTACCTGTC 1718
QY 1685 TCAGCAAGCATGAGCTGTGATTCAGGTCAGGTCAGTCTGCTGTTGGATGCCAAT 1744
DB 1719 TCAGCAAGCATGAGCTGTGATTCAGGTCAGGTCAGTCTGCTGTTGGATGCCAAT 1778
QY 1745 CTGCCACCTACCATGTCAGCTACCAACCTACTTCCAAAGGCCAGGCCCGGCTCGAGAT 1804
DB 1779 CTGCCACCATGTCAGCTGTCACCACTTCCAAAGGCCCTGGCAACATGCGAGGCG 1838
QY 1805 TTCTAGTCAGCTCCAGCAGTAAATTCGTCAAGTTATCAATCATTTGCTCTCTGGCTG 1864
DB 1839 TTCTAGTCAGCTCCAGCAGTAAATTCGTCAAGTTATCAATCATTTGCTCTCTGGCTG 1898
QY 1865 CTAGCGCAGAACCTGGGGACCAAGGCCCTGGGCCATCTCCAGATGACATTCACA 1924
DB 1899 CTAGCAAGGAGCTGGAGACCAAGGCCCTGGGCCATCTCCAGATGACATTCACA 1958
QY 1925 GAGGATGCCCCCGCGGAAGCTGCTGCTTCCAGAAAGCTGATCCAGATCTCCAAG 1984
DB 1959 GAGGAGGCCCTTGGCGGAGCATGCGCACCTTCCAGAGCGGCTGGCCAGATCTCGAGG 2018
QY 1985 GGCATCAGGAGAGAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2044
DB 2019 GGCATCAGGAGAGAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2078
QY 2045 ATTGAGAACAGTGTCTCCATCTAATCTTGGAGAGACAGTCTGCTGTCAT 2098
DB 2079 ATCGAGAACAGGCTCTCCATCTAAATCCAGGGGAACACAGGCCCGAGATGACAT 2132

RESULT 7

US-10-716-204-1
; Sequence 1, Application US/10716204
; Publication No. US20040137483A1
; GENERAL INFORMATION:

APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM E.
JISAKA, NITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARLES A. TAYLOR, JR.

STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

CITY: DURHAM

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/716,204

FILING DATE: 18-Nov-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2685 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-716-204-1

Query Match 43.3%; Score 1395.2; DB 19; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 416; Indels 5; Gaps 2;

QY	7	GCAGTAGAGCTAACT--GGTCAGGAGGATGGCGAATGCAGGGTCAGAGTATCCACG	64
DB	42	GCCGTAGAGAGCTGGACTTAGGCTGGCAGCATGGCCGAGTTTCAGGGTCAGGGTGTCCACC	101
QY	65	GGGGAAGCCTGTGGGGCTGGCACATGGGACAAAGTGTCTGTACGATCGTGGGAACCCAC	124
DB	102	GGAGAAGCCTTCGGGGCTGGCACATGGGACAAAGTGTCTGTACGATCGTGGGACCCCG	161
QY	125	GGAGAGCCCTTAGTACTCTTGACCAATCTGGGCAAGAGTTTCAGCGCCGGTGTGAA	184
DB	162	GGAGAGCCCCCACTGCCCTGGACAAATCTGGCAAGGAGTTCACTCGCGGGCGCTGAG	221
QY	185	GAAGACTTCGAGGTGACGCTTCCCAGGACGTAGGCACTGTGCTGATGCTGGAGTCCAC	244
DB	222	GAGGACTTCAGGGTAGCCTCCCGAGGACGTAGGCCGAGTGTCTGCTCGCGGTGCAC	281
QY	245	AAAGCACCCTCGAGGTGTCTCCCGCTTATGTCTTTCCGTTCTGATGCTCTGTTCTGC	304
DB	282	AAAGGCCCCC---AGTGTGCCCTGTCTGGGGCCCTTGGCCCGGATGCTGTCTGC	338
QY	305	CGCTGGTTCGAGCTGGAGTGTACTCTGGGGGTGCATCTCCATCTCCCTCTGTTATCAGTGG	364
DB	339	CGCTGGTTCAGCTGACACCGCGGGGGCGGCCACCTCTCTTCCCTGTCTACCACTGG	398
QY	365	CTGGNAGGGGGGGGAGCTGGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC	424
DB	399	CTGGAGGGGGGGGAGCCCTGTGTCTGAGGAGGGTACAGCAAGGTGTCTTGGGCGAC	458
QY	425	CATCACCTTACACTCGAGATCAGCGCCAGAGGAGCTTGAGTCCAGGCGAGAGATGTAC	484
DB	459	CACCACTGTGCTCCAGCAACAGCCCGAGAGGAGCTTCAGGCCCGGCGAGAGATGTAC	518
QY	485	AGCTGGAGAGCTTACATTTGAAGGTTGGCTCGCTGCTTGGACACGAGACTGTGAAAGAC	544
DB	519	CAGTGAAGGCTTACACCCAGGTTGGCTCACTGCTCTGGATGAAAGACAGTGGAAAGAC	578
QY	545	TTGACCTCAACATCAAGTACTCTCGGATGAAGATGCAAACTCTCTTTAAAGCCAC	604
DB	579	TTGGAGCTCAATATCAAAATCTCCACAGCAAGATGCAAACTTTTATCTCAAGCTGGC	638
QY	605	TCCGCTATACGAGCTCAAAAGTCAAGGGCTCTTGGACCGCAGAGGACTTGGAGGAGT	664
DB	639	TCTGCTTTTGAGATGAATAATCAGGGGTTGTCTGGACCGCAAGGGCTCTGGHAGAGT	698
QY	665	CTGAGGGAGATGAGAAGCTGTTTAACTTCCGCAAGACTTCCAGCAGCAGAGTATGTGTTT	724
DB	699	CTGAATGAGATGAAGGATCTTCAACTTCCGAGGACCCAGCAGCTGAGCAGCATTT	758
QY	725	GCAACTGGCAGGAAGATGCTTCTTCCGCTCCAGGTTCTTAAATGGCATCAACCCGCTC	784
DB	759	GAGCACTGGCAGGAGATGCTTCTTTCGCTCCCAAGTTCCTGAATGGTCTCAACCTGTC	818
QY	785	CTGATTCGCGCTGTCAAGTCTCCCAACACTTCCCGGTCACTGATGAATGGTGGCC	844
DB	819	CTGATTCGCGCTGTCTACTACTCTCCAAAGAACTTTCCCGCTCACTGATGCCATGGTGGCC	878

QY	845	CCAGTGTGGCCCTGGNAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG	904
DB	879	TCATTGTTGGGTCTGGGACCAGCTTGAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG	938
QY	905	GTGGATCATGGCATTTCTTCTGGAGTCCACCAACATCTCTCAATGGAAGGCTCAGTTC	964
DB	939	GTGGATCAGGCATCTCTCTGGCATCCAGACCAATGTCTATATGGAAGCGGAGTTC	998
QY	965	TCTCAGCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGAGCCCTGTTCCCAAT	1024
DB	999	TCTGGGCCCAATGACCTGTATACAGAGCCAGGCTGGGGCCGCTGCTGCTCTC	1058
QY	1025	GCCATCAGCTCAACAGACTCCCGGGCCACAAACCCATCTTCTTCCCGCCAGCATGAC	1084
DB	1059	GCCATCAGCTCAGCCAGACCCCGGCCCAACAGCCCATCTTCTTCCCGCCAGCATGAC	1118
QY	1085	ACGTGGGACTGTTGCTGGCCAAAGACTCTGGGTTCGCAATCTGAGTTTATCATTCATGAG	1144
DB	1119	AAGTGGGACTGTTGCTGGCCAAAGACTCTGGGTTCGCAATCTGAGTTTATCATTCATGAG	1178
QY	1145	GCTGTCAACATCTGCTGCATGCCCATCTGTATCCAGAACTCTTTCCTTGGCCACATTA	1204
DB	1179	GCCCTCAGCACCTGCTGCACTCATCTGCTGCTGAGTCTTTCACCTGGCTACCTG	1238
QY	1205	CGTCACTGCTAGGTGTCACCTCTCTTCAAGCTATTGATTCCTCACAATTTCGGTACACA	1264
DB	1239	CGTCACTGCTAGGTGTCACCTCTCTTCAAGCTATTGATTCCTCACAATTTCGGTACACA	1298
QY	1265	CTGCACATCAACACGCTTGGCCGGAGCTGCTGCTGCTGCTGGGAGTTGATGACAAAG	1324
DB	1299	CTGCACATCAACACGCTTGGCCGGAGCTGCTGCTGCTGCTGGGAGTTGATGACAAAG	1358
QY	1325	TCCACAGCCCTTGGCACTGGGGGATCTCTGACCTGTATAAAGAGAAACATGAGAGCTG	1384
DB	1359	TCCACAGCCCTTGGCACTGGGGGATCTCTGAGTTGATGATGAGAGAAACATGAGAGCTG	1418
QY	1385	AATCTCTGCTGCTGCTGCTGCTGAGATTCAGAGCCCGAGGTTGGAAGACATCCCA	1444
DB	1419	AATCTCTGCTGCTGCTGCTGAGATTCAGAGCCCGAGGTTGGAAGACATCCCA	1478
QY	1445	GGCTACTATTACCGAGATGAGGATGAGATCTGGGGGCAATAAAGAGCTTCTCTCT	1504
DB	1479	GGCTACTATTACCGAGATGAGGATGAGATTCAGAGCCCGAGGTTGGAAGACATCCCA	1538
QY	1505	GAATAGTTCAGCATCTACTATCCAAAGTACACATCCGTCCTCAAGATGACCAAGAGCTCCAG	1564
DB	1539	GAATAGTTCAGCATCTACTATCCAAAGTACAGTCTGTCCTCAAGATGACCAAGAGCTCCAG	1598
QY	1565	GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTTCCGCGGAGAAAGCTCAGGATGCCC	1624
DB	1599	GCCTGGGTGAGGAGATCTTCTTCCAAAGGCTTCTTAAACCAAGGAGAGCTCAGGATGCCC	1658
QY	1625	TCCCTGTTGGATACCCGGAGCCCTGCTCCAGTATATCACCATTGATATTCACCTGCG	1684
DB	1659	TCCCTGTTGGATACCCGGAGCCCTGCTCCAGTATATCACCATTGATATTCACCTGCG	1718
QY	1685	TCAGCCAAAGATGAGCTGTGAGTTTCAGGCTTCCAGCTCTTGTGTTTGGATGCCCAAT	1744
DB	1719	TCAGCCAAAGATGAGCTGTGAGTTTCAGGCTTCCAGCTCTTGTGTTTGGATGCCCAAT	1778
QY	1745	CTGCCACTTACATGAGCTACCAACCACTTCTTCCAAAGGCGAGGCCCGGCTCAGAGT	1804
DB	1779	CTGCCACTTACATGAGCTACCAACCACTTCTTCCAAAGGCGAGGCCCGGCTCAGAGT	1838
QY	1805	TTCTATGCGGCTCCAGCAGTTAATTCGTCAGTTATCATTATTCATCTCTCTGCTG	1864
DB	1839	TTCTATGCGGCTCCAGCAGTTAATTCGTCAGTTATCATTATTCATCTCTCTGCTG	1898
QY	1865	CTAAGCGCAGAACTCGGGACCAAGGCCCTCGGCCACTATCCGATGAGCACTTCACA	1924
DB	1899	CTAAGCGCAGAACTCGGGACCAAGGCCCTCGGCCACTATCCGATGAGCACTTCACA	1958

QY 1925 GAGGATGCCCCCGGGAAGCGTGGCTGCTTCCAGAGAAAAGTGAATCAGATCTCCAAAG 1984
Db 1959 GAGGAGGCCCTCGGCGGAGCATCGCCACTTCCAGAGCGGCTGGCCAGATCTCGAGG 2018
QY 1985 GCATCAGAGGAGGAACGAGGCTGGCACTGGCCCTACACCTACTGATCTCCCTC 2044
Db 2019 GGATCCAGAGGGAACCGGGGCTGGTGGCTGCCCCACACCTACTAGACCTCCCTC 2078
QY 2045 ATTGAGAACAGTGTCTCCATCTAAACATCTTGAGGAAGACAGTCTGTGTGACAT 2098
Db 2079 ATCGAGAACGGTCTCCATCTAAATCCAGGGGAACACAGGCCCCAGATGACAT 2132

RESULT 8
US-09-862-658-1
; Sequence 1, Application US/09862658
; Patent No. US20020137101A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-053001
; CURRENT APPLICATION NUMBER: US/09/862,658
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/205,675
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (459)...(2591)
US-09-862-658-1

Query Match 20.5%; Score 659.6; DB 9; Length 3320;
Best Local Similarity 63.9%; Pred. No. 9.6e-190;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAACTTACATTAAGAGTTGGCTGCTGCTGACGAGGAGTGTGAAAGA 543
Db 1013 CAGTGGGAATCGGTCTGCGCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 1072
QY 544 CTGGACCTCAACATCAAGTACTCTCGATGAGATGCCAACTCTCTTTAAAGCCCA 603
Db 1073 CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTGCTCTTCAATGCCAT 1132
QY 604 CTCGCGGTATACGAGCTGAAAGTCAAAGGCTCTCGGACCGCACAGGACTCTGGAGGAG 663
Db 1133 CCTGGCTCTTGGGAATGAAGCTTCGAGGCTGTTGGATCGCAAGGCTCTTGGAAAGA 1192
QY 664 TCTGAGGAGATGAGAAGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGTT 723
Db 1193 GCTGGATGATGATCAGAAACATCTCTGCTGCCATAAGACCTTCACGACAAAGTATGTCAC 1252
QY 724 TGCACACTGCGAGGAGATGCTCTTCTCGCTCCCAAGTTCTTAAATGGCATCAACCCGCT 783
Db 1253 AGAGCACTGGTGTGAAGATCACTTCTTGGGTACCAAGTACCTGAATGGTGTCAATCCCGT 1312
QY 784 CTTGATTCGCGCTGTACAGTCTCCCAACAACTTCCCGGTCACTGTATGATGAATGGTGGC 843
Db 1313 CATGCTCACTGATCTCTAGCTTGGCCAGCAGCTGCTGTACCAATGACATGTTGGC 1372
QY 844 CCCAGTCTGGGCCCTTGGAACCAAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTT 903
Db 1373 CCCCTTCTGGGACAGACACATGCTGCTGAGACAGAGCTAGAGAGGGGAAACATCTTCT 1432
QY 904 GGTGGATCATGGCATCTTCTCGAGTCCACACCAACATCCTCAATGGAAAGCCTCAGTT 963
Db 1433 AGCGGACTACTGATCCTGGCGGAGGCCCCCACTGCTTAAACGGCGCCGAGCAGTA 1492

QY 964 CTCTGCAGCCCGATGAGCCCTGTTACACAGAGCTCAGGTCCTCGAGCCCTGCTTCCCAT 1023
Db 1493 CTTGGCCGCCCCACTGTGCTGCTGCTGCTCAGCCCCCAG---GGGGGCGCTGGTCCCTT 1549
QY 1024 TGCCATCCAGTCAAAAGACTCCCGGGCCAGACAAACCCATCTTCTCTGCCAGCGATGA 1083
Db 1550 GGCCATCCAGTCAAGCAGACCCCGGGCCTGACAGCCCCATCTTCTTGGCCCATGACTC 1609
QY 1084 CACGTGGGACTGGTGTCTGGCCAGACCTGGGTTCGCAATCTTGAGTTTTCATCCATGA 1143
Db 1610 CGAATGGGACTGGTGTCTGGCCAGACCTGGGTGGCAACTCTGAGTTCTTGGTGCACGA 1669
QY 1144 GGCTGTCAACATCTGCTGCAATGCTGATTCAGATTCAGAGTTTTCATCCATCAT 1203
Db 1670 AAACAACACGCACTTCTGTGCAACGCTGCTGCGAGGCTTCGCCCATGGCCACGCT 1729
QY 1204 AGCTCAGCTGCTAGTGTCTCAACCTCTCTCAAGCTATTGATTCCTCAATTCGGGTACAC 1263
Db 1730 GGCCAGCTGCGCTCTGCCACCCCATCTACAAGCTCTCTACTCCCCCACACTCGATACAC 1789
QY 1264 ACTGCACATCAACACGCTTGGCCGGGAGCTGCTGCTTGGCCCTGGGAAAGTTGATAGACAA 1323
Db 1790 GCTGAGGTGAACACCATCGCGAGGGCCACGCTGCTCAACCCCGAGGGCTCTGTGACCA 1849
QY 1324 GTCCACAGGCTTGGCACTGGGGGATTCCTGACCTGATAAAGAGAAACATGGAGCAGCT 1383
Db 1850 GGTACAGTCCATCGGGAGGCAAGGCTCTATCTACCTCATGACACGGGCTTGGCCACAT 1909
QY 1384 GAACTACTCTGCTGCTGCTCTCCCTGAAGATATCGAGCCGAGGTGTGGAAGACATCC 1443
Db 1910 CACCTACACCAATTTCTGCTTCGGAACAGCTGCGGGCCCGGGCTCTGGCTATCCC 1969
QY 1444 AGGCTACTATTACCAGATGATGGGATCGAGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503
Db 1970 CAACTACCACTACCGAGACGAGGCTGAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC 2029
QY 1504 TGAATAGTCAAGATCTACTATCAAGTGACACATCTCGTCCAAAGATGACCAAGAGCTCA 1563
Db 2030 AGAAATCGTGGGCTACTATTATCCAGTGACGATCTGTGACAGCAGGATTCGAGAGTGA 2089
QY 1564 GSCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGSCCGAGAAAGCTCAGGTATGCC 1623
Db 2090 GSCCTGGACTGCGGAGATTTTGTCTCAGCGTTCCTGGCCGGGAAAGCTCAGGTTTCCC 2149
QY 1624 CTCTCTTGTGGATACCCCGGAAGCCCTGCTCCAGTATATCACCATGGTGATATCACCTG 1683
Db 2150 AAGCCGCTGTGCACCCCGAGGAGATGTTGAAGTTCTCTACTGCAATCATCTTCAATTG 2209
QY 1684 CTCAGCCAAAGCATGAGCTGTCTGAGGCGAGTTCAGCTCTTGTGTTGGATGCCCAA 1743
Db 2210 CTCTGCCAGCAGCTGCTGTCAACAGTGGGAGCATGATCTTGGGGCTGGATGCCCAA 2269
QY 1744 TCTGCCACTTACCATGACGCTACCAACCTACTTCCAAAGGCCAGGCCCGCTGAGAG 1803
Db 2270 TGCTCCATCATCATGAGCAGCCCCCAGACCAAGGGGACCCACCCCTGAAAGAC 2329
QY 1804 TTTCTATAGCCAGCTCCCAGCAGTTAAATTCGTCAAGTTATCATCATCTCTCTGGCT 1863
Db 2330 TTACCTAGACACCTTCCCTGAAGTGAACATCAGCTGTAACAACCTCTCTCTCTGGTT 2389
QY 1864 GCTAAGCGAGAACTGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTAC 1923
Db 2390 GGTAGCCAAAGAACCAAGGACAGAGGCCCTGGGGACCTTCCAGATGAGCATTTCAC 2449
QY 1924 AGAGGATCCCCCGGCGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
Db 2450 AGAGAGGCCCGCGAGCGGAGCATCGCGCTTTCAGAGCCCGCTGGCCAGATCTCAAG 2509
QY 1984 GGCCATCAGGGAGGAGAAACCGAGGCTGGCACTGGCTTACCTACCTGGATCTCTCCCT 2043
Db 2510 GGACATCCAGGAGCGGAACCGAGGCTGGCACTGGCTTACCTACCTGGACCTCCCT 2569
QY 2044 CATTGAGAAACAGTGTCTCCATCTAAC 2069


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Db      2570  CATTGAGAACAGTGTCTCTCAATCAAC 2595
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RESULT 9
US-10-175-696-22
; Sequence 22, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (459)...(2591)
US-10-175-696-22

Query Match      20.5%; Score 659.6; DB 14; Length 3320;
Best Local Similarity 63.9%; Pred. No. 9.6e-190;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

Qy      484  CAGCTGGAAGACTTACATTGAAGTGTGGCTTCGCTTGACCAAGAGACTGTGAAGA 543
Db      1013  CAGTGGGAATCGGTACCTGCGCGCTTCCCATGAAATTTGACATCCATCCCTGATGTA 1072
Qy      544  CTTGGACCTCAACATCAAGTACTCTGCGATGAAGAATGCCAACTCTTTTAAAGCCCA 603
Db      1073  CATGGAGCCCAATGTTTCGATACTCAGACCAACCAAGACGATCTCGCTGTCTTTCAATGCCAT 1132
Qy      604  CTCGCGGTATACGGAGCTGAAAGCTCAAGGGCTCCTGGACCGCACAGACTCTGGAGGAG 663
Db      1133  CCTTGCCTCTTGGGATGAAGCTTCGAGGGCTGTTGATCGAAGGGCTCTCTCGAAGAA 1192
Qy      664  TCTGAGGGAGATGAGAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGT 723
Db      1193  GCTGGATGATCATGCAGAACATCTTCTGCTGCCATAAGACCTTCACGACAAAGTATGTCAC 1252
Qy      724  TGCACACTGGCAGGAAGATGCTTCTTCGCCCTCCAGTTCCTAAATGGCATCAACCCGGT 783
Db      1253  AGAGCACTGGTGAAGATCACTCTTTTGGGTACCACTGATGCTGAATGGTGTCAATCCCGT 1312

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Qy	784	CTGTGATTCGGCCGTGTCA	CAGTCTCCCAAACAACTCTCCCGGTCACTGATGAATGTGGC	843
Db	1313	CATGCTCCA	CTGATCTCTAGCTTTGCCAGCAAGCTGCGCTGTCA	1372
Qy	844	CCCAAGTCTGGGCCCTTGGAA	CCAGTCTGCAGGCTGAGTTGGAGAAAGGGCTCCCGTGTCTT	903
Db	1373	CCCTTTGCTGGGACAGGAC	ACATGCTCTGACAGAGCTAGAGAGGGGGAACATCTTCCT	1432
Qy	904	GGTGGATCATGGCA	TCTTTTCTGGAGTCCACACCAACATCCTCAATTGGAAAGCCTCAGTT	963
Db	1433	AGCGGACTACTGGAT	CTCTGGCGAGGCCCCACCACTGCCTAAACGGCCCGCAGAGTA	1492
Qy	964	CTCTGAGCCCCGATGAC	CCCTGTGTTACACAGAGCTCAGGGTCCGAGACCCCTGTTGCCAT	1023
Db	1493	CGTGGCGGCCCACTGTG	CTGTGTGGCTCAGCCCCCAG--GGGGCGCTGGTGCCCTT	1549
Qy	1024	TGCGATCCAGCTCAAA	CAGACTCCCGGGCCAGACACCCCATCTTCTGCGCCAGCGATGA	1083
Db	1550	GGCCATTCAGCTCAG	CCAGACCCCGGGGCTGACAGCCCCCATCTTCTGCGCCACTGACTC	1609
Qy	1084	CACGTGGGACTGGTCT	GTGGCCAAAGACCTGGGTTCGCAATTTCTGAGTTTTACATCATGA	1143
Db	1610	CGAATGGGACTGCTG	CTGTGGCCAGACGTGGGTGCGCACTCTGAGTTCCTGGTGCACGA	1569
Qy	1144	GGCTGTCA	CACATCTCTCTGTGATGCCCATCTGATTCAGAAAGTCTTGGCTTGGCCACATTT	1203
Db	1670	AAACAAACCGCACTT	TTCTGTGACGCAATTTGTCTGCGAGGCCCTTCGCCATGGCCACGCT	1729
Qy	1204	ACGTGAGCTGCC	TAGGTGTCAACCTCTCTTCAAGCTATTGATTTCCTCACATTCGGGTACAC	1263
Db	1730	GGCCCAAGCTGCC	CGCTCTGCCACCCCCATCTACAAGCTCTACTCCCCCACACTCGATACAC	1789
Qy	1264	ACTGCACATCA	CACACCTTTGCCGGGAGCTGCTGCTTGCCCTGGGAAGTTGATAGACAA	1323
Db	1790	GCTGCAAGGTGA	ACCATCGAGGGCCACGCTGCTCAACCCGAGGGCCTCTGTGACCA	1849
Qy	1324	GTCCACAGGCC	CTTTGGCACTGGGGGATTTCTGTACCTGTATAAAGAGAAACATGAGCAGCT	1383
Db	1850	GGTCACGTCCAT	CGGAGCAAGGCCTCATCTACCTCATGAGCACGGGCTGGGCCACATT	1909
Qy	1384	GAACTACTCTGT	CTGTCTCGCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCC	1443
Db	1910	CACCTACACCAAT	TTTCTGCTTTCCGACAGACCTTGC	1969
Qy	1444	AGGCTACTATTAC	GAGATGATGGGATGCAGATCTCGGGGGCAATAAAGAGCTTTGTCTC	1503
Db	1970	CAACTACC	ACTACCGGAGACGCGCCTGAAGATCTCGGGCGGCCATTTGAGAGCTTTGTCTC	2029
Qy	1504	TGAAATAGT	CAGCATCTACTATCCAAAGTACACATCCGCTCCAAGATGACCAAGAGCTCCA	1563
Db	2030	AGAAATCGTGGG	CTACTATTATCCCAAGTACGCACTGTGTCAGCAGGATTCGAGAGTGCA	2089
Qy	1564	GGCCTGGGTGAG	GAGAGATCTTCTCTGAGGGCTTCTCGCGCCGAGAAAGCTCAGGATGACC	1623
Db	2090	GGCCTGGA	CTGCGAGATTTTGTCTCAGGCGTTCTTGGGCCCGGAAAGCTCAGGTTTCCC	2149
Qy	1624	CTCTCTGTTGG	ATACCCGGAGCCCTGCTCCAGTATATCACCATGGTGTATTTACCTG	1683
Db	2150	AAGCCGCTGTG	CAACCCCAAGGAGATGTTGTAAGTTCTCTCACTGCAATCATCTTCAATTG	2209
Qy	1684	CTCAGCAAGCA	GTGACGTGTGAGTTCAGGCCAGTTTCGACTCTTGTGTTGGATGCCCAA	1743
Db	2210	CTCTGCC	CAAGCAGCTGTCTGTCTCAAGTGGGAGCATGACTTTGGGCGCTGAGTGGCCAA	2269
Qy	1744	TTCTGCC	CACTTACATGACCTACCAACCACTACTTCCAAAGGCGCAGGCCCGGCTGAGAG	1803
Db	2270	TGCTCCAT	CATCCATGAGGCAGCCCCACCCACAGACCAAGGGGACCAACCCCTGAAGAC	2329
Qy	1804	TTTTCATAG	CCAGCTCCCAAGCAGTTAAATTTCGTCAAGTTATCATCATTTGCTCTCGGCT	1863
Db	2330	TTACCT	TAGACACCCCTCCCTGAAAGTGAACATCAGCTGTAAACACCTCCTCTCTTCTGGTT	2389
Qy	1864	GCTAAGCG	CAGAACCTTGGGGACCAAGAGGCCCTTGGGCCACTATCCAGATGAACACTTCAC	1923


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Db 2390 GGTAGCCAGAACCCAGGAGCAGAGGCCCCCTGGGCACTTACCCAGATGAGCACTTCAC 2449
Qy 1924 AGAGGATGCCCCCGCGGAAGGTGGCTCTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
Db 2450 AGAGGAGGCCCGAGCGGAGCATGCCGCCCTTCAGAGCCGCCCTGGCCAGATCTCAAG 2509
Qy 1984 GGGCATCAGGAGAGGAAACCGAGGCTGGCACTGGCCCTACAGCTACCTGGATCTCCCT 2043
Db 2510 GGACATCCAGGAGCGGAACAGGGTCTGGCACTGGCCCTACACTTGGACCCCTCCCT 2569
Qy 2044 CATTGAGAACAGTGTCTCATCTAAC 2069
Db 2570 CATTGAGAACAGTGTCTCATCTAAC 2595

RESULT 10
US-10-776-871-22
; Sequence 22, Application US/10776871
; Publication No. US20040132087A1
; GENERAL INFORMATION:
; APPLICANT: Gluckemann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/776,871
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/10/175,696
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (459)...(2591)
US-10-776-871-22

Query Match 20.5%; Score 659.6; DB 19; Length 3320;
Best Local Similarity 63.9%; Pred. No. 9.6e-190;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

Qy 484 CAGCTGGAAAGACTTACATTGAAGGTGGCTCGCTCCCTTGACACGAGACTGTGAAGA 543
Db 1013 CAGTGGGAATCGGTACTCGCCCGGCTTCCGCCATGAAATTGACATCCCATCCCTGATGTA 1072
Qy 544 CTTGGACCTCAACATCAAGTACTCTCGGATGAGATGCCAAACTCTTCTTTAAAGCCCA 603
Db 1073 CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTCTTCAATGCCAT 1132
Qy 604 CTCGCGTATACGGAGCTGAAAGTCAAAGGGCTCTCTGGACCGCACAGGACTCTGGAGGAG 663
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Db 1133 CCCTGCGCTCTTGGGAATGAAGCTTCGAGGGCTGTGTGGATCGCAAGGGCTCCTCGAAGAA 1192
Qy 664 TCTGAGGGAGATGAGAAGCTGTTTAACTTCGCGAAGACTCCAGCAGCAGAGTAGTGTGT 723
Db 1193 GCTGATGACATGCAAGACATCTTCTGTGTGCATAGACCTTCAGCAAAAGTAGTGTAC 1252
Qy 724 TGCACACTGGCAGGAGAGATGCTTCTTCCCTCCAGTTCCTTAAATGGCATCAACCCGGT 783
Db 1253 AGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCACTACCTGAATGGTGTCAATCCCGT 1312
Qy 784 CTTGATTCGCGCTGTCAAGTCTCCCAAAACAATTCGCGGTCACTGATGAATGGTGGC 843
Db 1313 CATGCTCCACTGCACTCTTAGCTTGGCCAGCAAGCTGCTGTCAACNAATGACATGGTGGC 1372
Qy 844 CCCAGTGTGGGCCCTGGAAACCAAGTCTCAGGCTGAGTTGGAGAGGGCTCCTCTGTCTT 903
Db 1373 CCCCTTGTGGACAGGACACATGCTGTGACAGAGCTAGAGAGGGGGAACATCTTCT 1432
Qy 904 GGTGATCATGGCATTTCTTCTGGAGTCCACACCAACATCTCTCAATGGAAGCCCTCAGTT 963
Db 1433 AGCGGACTACTGGATCTCTGGCGGAGGCCCCCACTGCTTAAACGCGCGCAGCAGTA 1492
Qy 964 CTCTGACGCCCCGATGACCTCTGTACACAGAGCTCAGGTTCCGACCCCTGCTTCCCAT 1023
Db 1493 CTTGGCCGCCCACTGTGCTGCTGTGGCTCAGCCCCCAG--GGGGCGCTGGTGCCCTT 1549
Qy 1024 TGCATCCAGTCAAAACAGACTCCCGGGCCAGACAACCCCATCTTCTGCCCCAGGATGA 1083
Db 1550 GGCCATCCAGCTCAGCCAGACACCCCGGCCCTGACAGCCCCCATCTTCTGCCCATGACTC 1609
Qy 1084 CACGTGGGACTGGTTGTGGCCAAAGACCTGGGTTCCGAAATCTTGATTTTACATCCATGA 1143
Db 1610 CGAATGGGACTGGCTGTGGCCAAAGACGTGGGTGGCAACTCTGAGTTCTCTGGTGCACGA 1669
Qy 1144 GGCTGTCAACATCTGCTGCAATGCCCATCTGATTCACAGAGCTTTTGGCTTGGCCACAT 1203
Db 1670 AAACAACACGCACTTCTGTGCACGCAATTTGTGTGCGAGGCTTCGCAATGGCCACGCT 1729
Qy 1204 AGCTCAGCTGGCTAGGTGTCACTCTCTTCAAGCTATTGATTCCTCAATTCGGTACAC 1263
Db 1730 GCGCCAGCTGCCGCTCTGCCACCCCATCTACAGCTCTCTTCCCCCACTCGATACAC 1789
Qy 1264 ACTGCACATCAACAGCTTTGCCCGGAGCTGTCTGTGCCCTCGGGAAGTTGATAGACAA 1323
Db 1790 GCTGCAGGTGAACACCATCGCGAGGGCCACGCTGTCAACCCCGAGGGCTCTGTGACCA 1849
Qy 1324 GTCACAGGCTTGGCACTGGGGGATTTCTTGACCTGATAAAGAAAACATGGAGAGCT 1383
Db 1850 GGTACAGTCCATCGGGAGGCAAGGCTCATCTACCTCATGAGCAGCGGCTTGGCCCATTT 1909
Qy 1384 GAACTACTCTGTCTGTCTCCCTGAAGATATCGAGCCCGAGGTGTGGAAGACATCC 1443
Db 1910 CACCTACACCAATTTCTGCCCTTCGGAACAGCTCGGGGCCCGCGGCTCTGGCTATCCC 1969
Qy 1444 AGGCTACTATTACCGAGATGATGGATGCAGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503
Db 1970 CAACTACCACTACCGAGACGCGGCTGAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC 2029
Qy 1504 TGAATAGTCAGCATCTACTATFCAAGTGACACATCCGTCCAGATGACCAAGAGCTCA 1563
Db 2030 AGAATTCGTGGGCTACTATTATCCAGTGACGCACTCTGTGCAGCAGGATTCGAGAGCTGA 2089
Qy 1564 GGCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGSCCGAGAAAGCTCAGGTATGCC 1623
Db 2090 GGCCTGGAGCTGCGAGATTTTGTCTCAGCGTTTCTTGGCCCGGAAAGCTCAGGTTTCC 2149
Qy 1624 CTCCTTTTGGATACCCCGGAAGCCCTGTCAGTATATCACCATGGTGATATTCACCTG 1683
Db 2150 AAGCCGGCTGTGCACCCCGAGGAGATGGTGAAGTTCTCTACTGCAATCATCTTCAATG 2209
Qy 1684 CTCAGCCAAAGCATGAGCTGTGTCAGTTCAGGTCAGTTCGACTCTGTGTGTGGATGCCAA 1743
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Db 2210 CTCTGCCAGCAGCGTCTGTCTCAACAGTGGGAGCATGACTTTTGGGGCCTGGAGTGCCTAA 2269
 Qy 1744 TCTGCCACTTACCATGACCTACCAACCACTTACTTCCAAAGGCCAGGCCCGGCTGAGAG 1803
 Db 2270 TGCTCCATCATCTCATGAGCAGCGCCCAACCCAGACCAAGGGGACCAACCACTGAAGAC 2329
 Qy 1804 TTTTCATAGCCAGCTCCAGCAGTTAAATTCGTCAAGTTATCATCATATGCTCTCTGGCT 1863
 Db 2330 TTACTTAGACACCCCTCCCTGAAGTGAACATCAGCTGTATAACAACCTCTCTCTCTGGTT 2389
 Qy 1864 GCTAAGCCAGAACTCTGGGACCAAAAGGCCCTGGGCCACTATCCAGATGAAACACTTTCAC 1923
 Db 2390 GGTTAGCCAGAACCAAGGACAGAGGCCCTTGGCACCTACCCAGATGAGCACTTTCAC 2449
 Qy 1924 AGAGGATCCCCCGCGGAAAGCGTGGCTCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
 Db 2450 AGAGGAGCCCGAGGCGGAGCATCGCGCCCTTCCAGAGCGGCTGGCCAGATCTCAAG 2509
 Qy 1984 GGGCATCAGGAGAGGAACCGAGGCTGGCACTGCCCTACCTACTCTGGATCCTCCCT 2043
 Db 2510 GGACATCCAGGAGCGGAACCAAGGCTGGCACTGCCCTACCTACTCTGGACCTCCCT 2569
 Qy 2044 CATTTAGAACAGTGTCTCCATCTAAC 2069
 Db 2570 CATTTAGAACAGTGTCTCCATCTAAC 2595

 RESULT 11
 US-10-422-264-29
 ; Sequence 29, Application US/10422264
 ; Publication No. US20030172391A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, C. Alexander, Jr.
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: NO. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
 ; FILE REFERENCE: 7705.0009-00000
 ; CURRENT APPLICATION NUMBER: US/10/422,264
 ; CURRENT FILING DATE: 2003-04-23
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 3384
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-422-264-29

 Query Match 20.5%; Score 659.6; DB 16; Length 3384;
 Best Local Similarity 63.9%; Pred. No. 9.8e-190;
 Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

 Qy 484 CAGCTGGAAGACTTACATTGAAGTTGGCTCGCTCGCTTGACCAGCAGACTGTGAAAGA 543
 Db 1053 CAGTGGGAATCGGTACTCGTCCCGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 1112

 Qy 544 CTTGGACCTCAACATCAAGTACTCTGCGATGAAGAAATGCCAAACTCTTCTTTAAAGCCCA 603
 Db 1113 CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTCTCTTCAATGCCAT 1172

 Qy 604 CTCGCGGTATACGGAGCTGAAGTCAAAAGGCTCCCTGGACCGCACAGGACTCTGGAGGAG 663
 Db 1173 CCCTGCGTCTTTGGGAATGAAGCTTCGAGGGCTGTTGGATCGCAAGGGCTCTCTGGAAGAA 1232

 Qy 664 TCTGAGGGAGATGAGAAGCTCTTTAACTTCGCGCAAGACTCCAGCAGCAGAGATGTGTT 723
 Db 1233 GCTGGATGACATGCAGAACATCTTCTGGTGCCATAGACCTTCACGACAAAGTATGTCAC 1292

 Qy 724 TGCACTGCGGAGGAAGATGCTTTCTTGCCCTCCCAAGTTCTTAAATGGCATCAACCCGGT 783
 Db 1293 AGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCACTGTAAGTGGTGTCAATCCCGT 1352

Qy	784	CTGTGATTCGGCCGTGTCA	CAGTCTCCCAAAACAACATCTCCGGGTCACTGATGAATGTGTGC	843
Db	1353	CATGCTCCACTGTCATCT	TAGCTTGGCCAGCAAGCTGCGCTGTCA	1412
Qy	844	CCCAAGTCTGGGCCCTGG	AACCAAGTCTGCAGGCTGAGTTGGAGAAAGGGCTCCCGTGTCTT	903
Db	1413	CCCTCTTGCTGGGACAG	ACAATGCTCTGACAGACAGAGCTAGAGAGGGGGAACAATCTTCCT	1472
Qy	904	GGTGGATCATGGCAATCT	TTTCTGGAGTCCACACCAACATCTCCTCAATGGAAAGCCTCAGTT	963
Db	1473	AGCGGACTACTGATCT	TGGCGGAGSCCCCACTGCTTAAACGGCGCCAGCAGTA	1532
Qy	964	CTCTGAGAGCCCGATG	ACCTCTGTTCACACAGAGCTCAGGGTCCGAGACCCCTGTGTTCCCAT	1023
Db	1533	CGTGGCGGCCCACTGT	GTGCTGTGTGGCTTCAGCCGCCCAAG--GGGGCGCTGGTGGCCCTT	1589
Qy	1024	TGCGATCCAGCTCAAA	CACAGACTCCCGGGCGACACACCCCATCTTCTCCGCCAGCCATGA	1083
Db	1590	GGCCATCCAGCTCAG	CCAGACCCCGGGGCTGACACGCCCATCTTCTCGGCCACTGACTC	1649
Qy	1084	CACGTGGGACTGTGCT	GTGGCCAAAGACCTGGGTTCCAAATCTTGAGTTTTCATCCATGA	1143
Db	1650	CGAATGGGACTGCTGT	GGCCAAAGACGTGGGTGCGCACTCTGAGTTCCTGGTGACAGA	1709
Qy	1144	GGCTGTACACACTCT	GCTGTGCATGCCCATCTGTATTCAGAAAGTCTTTGGCTTGGCCACATT	1203
Db	1710	AAACAACAGCACTTT	CTGTGACGCAATTTGCTGTGCGAGGCCCTTCCCATGSCCAGCT	1769
Qy	1204	AGTCAAGCTGCTAG	GTGTCAACCTCTCTTCAAGCTATTGATTTCTTACATTCGGGTACAC	1263
Db	1770	GCGCCAGCTGCCGCT	CTGCCACCCCACTACAGCTCTTACTCTCCCCACACTCGATACAC	1829
Qy	1264	ACTGCACTACAACAG	CTTGGCCGGAGCTGCTGCTTGGCCCTGGGAAGTTGATAGACAA	1323
Db	1830	GCTGCAAGTGAA	CAACATCGGAGGGCCACGCTGTCTAAACCCGAGGGCCTCGTGACCA	1889
Qy	1324	GTCCACAGGCTTTGG	CACCTGGGGGATTTCTCTGACCTGTATAAGAGAGAAAACATGAGCAGCT	1383
Db	1890	GGTCAGTCCATCGG	GAGCAAGGCCCTCATCTACCTCATGAGCACGGGCTGSCCAGCTT	1949
Qy	1384	GAATCTACTCTGTCT	GTCTGCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCC	1443
Db	1950	CACCTACACCAATTT	CTGTGCTTCCGACAGACCTTCCGGGCGCCGCGGCTCTGTGCTATCCC	2009
Qy	1444	AGGCTACTATTACG	AGATATGGGATGCAGATCTCGGGGGGCAATAAGAGCTTTTCTCTC	1503
Db	2010	CAACTACCACACTAC	CGAGACGAGCCTGGAAGATCTGGGCGGCCCATTTGAGAGCTTTGTCTC	2069
Qy	1504	TGAATATGTCAGCAT	CTACTATCCAAAGTGACACATCCGTCCAAAGATGACCAAGAGCTCCA	1563
Db	2070	AGAAATCGTGGGCTA	CTATTATCCAGTGAAGCATCTGTGACAGAGGATTCGGAGCTGCA	2129
Qy	1564	GGCTCGGTGAGGGAG	ATCTTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGATATGCC	1623
Db	2130	GGCTGGAATCGGAG	ATTTTGTCTCAGCGGTTCTCTGGGCGGGAAGCTCAGGTTTCCC	2189
Qy	1624	CTCCTTTGTTGGATA	CCCGGGAAGCCCTGTCTCAGTATATACCAATGGTGTATTCACCTG	1683
Db	2190	AAGCCGGCTGTGC	ACCCCAAGGAGATGTGTGAAGTTTCTCTACTGCAATCATCTTCAATTG	2249
Qy	1684	CTCAGCCAAGCATG	CAGCTGTTCAGTTTCAGSCCAGTTTCGACTCTTGTGTTTGGATGCCAA	1743
Db	2250	CTCTGCCAGCAGCCT	GTCTGTCAAGTGGGAGCATGACTTTTGGGSCCTGGATGCCCAA	2309
Qy	1744	TCCTGCCACCTTACC	ATGACGTACCAACCATCTACTTCCAAAGGCGAGGCCCGGCTCGAG	1803
Db	2310	TGCTCCATCATCC	ATGAGGACGCCCCCAACCCAGACCAAGGGACCAACCAACCTCGAAGAC	2369
Qy	1804	TTTTCATAGCCA	CGCTCCCAAGAGTTAAATTTGCTCAAGTTATACATCATTTCTCTGGCT	1863
Db	2370	TTAATCTAGACAC	CCCTCCCTGAGTGAACATCAGCTGTAAACCTCTCTCTCTCTGGTT	2429

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QY 1864 GCTAAGCCAGAACCTCTGGGGAACAAAGGCCCTCTGGGCCACTATCCAGATGAACACTTCAC 1923
Db 2430 GGTAGCCCAAGAACCCCAAGGACACAGAGGCCCTCTGGGCACTACCCAGATGAGCACTTCAC 2489
QY 1924 AGAGGATGCCCCCGCGAAGCGTGGCTGCTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
Db 2490 AGAGGAGGCCCGAGCGGAGGATCGCCGCTTCAGAGCCGCGCTGGCCAGATCTCAAG 2549
QY 1984 GGCATCAGGAGAGGAAACGAGGCCCTGGCACTGCCCTACACTTACCTGGATCTCCCTC 2043
Db 2550 GGACATCCAGAGCGGAACCGAGGCTGGCACTGGCCCTACACTTACCTGGACCTCCCTC 2609
QY 2044 CATTGAGAACAGTGTCTCCATTAAC 2069
Db 2610 CATTGAGAACAGTGTCTCCATTAAC 2635

RESULT 12
US-09-862-658-3
; Sequence 3, Application US/09862658
; Patent No. US20020137101A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 4638, A NOVEL HUMAN LIPOXYGENASE FAMILY
; FILE REFERENCE: 10448-053001
; CURRENT APPLICATION NUMBER: US/09/862,658
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/205,675
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-658-3

Query Match 20.4%; Score 658.6; DB 9; Length 2136;
Best Local Similarity 63.9%; Pred. No. 1.5e-189;
Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAAGACTTACATTGAAGGTGGCTCGCTGCTTGACCAAGACTGTGAAGA 543
Db 555 CAGTGGGAATCGGTACTCTGCGGCTTCCCATGAAAATTGACATCCCATCCCTGATGA 614
QY 544 CTGGACCTCAACATCAAGTACTCTCGATGAGATGCCAACTCTTTAAAGCCCA 603
Db 615 CATGGAGCCCAATGTTTCGATATCTAGCCCAAGACGATCTCGCTCTTCAATGCCAT 674
QY 604 CTCGGGTATACGAGCTGAAAGTCAAAGGGCTCTGGACCCGACAGGACTCTGGAGGAG 663
Db 675 CCTGGCTCTTGGGAATGAGCTTCGAGGGCTGTGGATCGAAGGGCTCTGGAGNA 734
QY 664 TCTGAGGAGATGAGAAGCTGTTAACTTCGCAAGACTCCAGCAGCAGAGATATGTGTT 723
Db 735 GCTGGATGATGACAGAACATCTCTGGTGCCTAAGACCTTCACGACAAAGTATGTCTAC 794
QY 724 TGCACACTGGCAGGAGATGCCTTCTTCGCTCCGATTCCTTAATGGATCAACCCGGT 783
Db 795 AGAGCACTGGTGTGAAGATGACATCTCTTGGTACCAATGATGAGTGTCAATCCCGCT 854
QY 784 CTGATTTCGCGCTGTACAGTCTCCCAAACTTCCCGGTCACTGTAGTAAATGGTGGC 843
Db 855 CATGTCCAATGATCTTAGTTCGCCAGCAAGCTGCTGTCAACATGACATGATGGTGGC 914
QY 844 CCCAGTCTGGGCCCTGGAAACAGTCTGCAGGCTGAGTTGGAGAAAGGGCTCCCTGTTCT 903
Db 915 CCCCTGTCTGGACAGGACACATGCTCGCAGACAGAGCTAGAGAGGGGAAACATCTTCT 974
QY 904 GGTGATCATGGATCTTCTTGGAGTCCACACCAACATCTCAATGGAAAGCCTCAGTT 963
Db 975 AGCGGACTACTGGATCTTGGGAGGGCCCCCACTGCTCCCTTAAACGGCCCGCAGGATGA 1034
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QY 964 CTCTGACGCCCGATGACCCCTGTTTACACAGAGCTCAAGGTCGAGACCCCTGCTTCCCAT 1023
Db 1035 CGTGGCCGCCCACTGTGCTGCTGAGCTCAGCCCCAG--GGGGCGCTGGTGCCCTT 1091
QY 1024 TGCCATCCAGCTCAAAAGACTCCGGGCGCAGACAAACCCCATCTCTCTGCCCGCAGATGA 1083
Db 1092 GGCCATCCAGCTCAGCCAGACCCCGGGCCTTACAGAGCCCATCTCTCTGCCCATGATCTC 1151
QY 1084 CACGTGGACCTGGTGTCTGGCCAAAGACCTGGTTTCGCAATTTCTGAGTTTATACATCAATGA 1143
Db 1152 CGAATGGAGCTGGCTGTCTGGCCAAAGACGTGGGTGGGCAACTCTGAGTTCTCTGGTGCACGA 1211
QY 1144 GGCTGTCAACATCTGTCTGCATGCCCATCTGATTTCCAGAACTTCTTGGCTTGGCCACATTT 1203
Db 1212 AAACAACACGCACTTTCTGTGCGAGCACTTGTCTGTGCGAGGCTTCGCGCATGGCCACGCT 1271
QY 1204 AGCTCAGCTGCTAGGTGTCAACCTCTCTTCAAGCTATTGATTTCTTCACTATCGGTACAC 1263
Db 1272 GCGCCAGCTGCGCTCTGTGCCACCCCATCTACAAGCTCTACTCTCCCCACACATCTCGATACAC 1331
QY 1264 ACTGCACATCAACACGCTTGGCCGGGAGCTGCTGCTTCCCTCGGGAAGTTGATAGACAA 1323
Db 1332 GCTGCAAGTGAACACCATCGCGAGGGCCACGCTGCTCAACCCCGAGGGCCTCGTGACCA 1391
QY 1324 GTCCAAGGCCCTTGGCACTGGGGGATTTCTTGACCTGATAAGAGAAAACATGGAGCAGCT 1383
Db 1392 GGTCAAGTCCATCGGGAGGCAAGGCTCATCTACCTCATGAGCAGCGGCTTGGCCCACTT 1451
QY 1384 GAACTACTCTGTCTGTCTCTCCCTGAAGATATCGAGCCCGAGGTGTGGAGAGATCCCT 1443
Db 1452 CACCTACACCAATTTCTGCTTCCGACAGGCTGCGGGCCCGCGGCGCTCTGGCTATCCCT 1511
QY 1444 AGGCTACTATTACCGAGATGATGGGATCGAGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503
Db 1512 CAATACCACTACCGAGAGCAGCGCTGAAGATCTGGGGGGCCATTTGAGAGCTTTGTCTC 1571
QY 1504 TGAATAGTCAAGCATCTATCCAAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCA 1563
Db 1572 AGAAATCGTGGGCTACTATTATCCAGTGACGCACTCTGTGACGACGAGTTCGGAGCTGCA 1631
QY 1564 GGCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGCAGAAAGCTCAGGTATGCC 1623
Db 1632 GGCCTGGAATCGCGAGATTTTGTCTCAGGCGTTCCTGGGCGGGAAAGCTCAGGTATCCC 1691
QY 1624 CTCTTGTGTGATACCGGGGAAGCCCTGCTCAGTATATCACCATGATGATATCACCTG 1683
Db 1692 AAGCGGCTGTGACCCCGAGAGAGATGGTGAAGTTCTCTCAATCAATCTTCAATTG 1751
QY 1684 CTCAGCCAAAGCATGCACTGTCAAGTTCAGGGCAGTTTCGACTCTTGTGTGATGCCCAA 1743
Db 1752 CTCTGCCCAGCAGCTGCTGTCAACAGTGGCAGCATGACTTTTGGGGCTTGGATGCCCAA 1811
QY 1744 TCTGCCACTTACATGCACTGACGCTACCAACCTACTTCCAAAGCCAGGCCCGCGCTGAGAG 1803
Db 1812 TGCTCATCATCATGAGGCGAGCCGCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1871
QY 1804 TTTTCATAGCCAGCTCCCGCAGAGTTAATTCGTCAGAGTTATCAATCATTTGCTCTCTGGCT 1863
Db 1872 TTACCTTAGACACCTCTCTCTGAAAGTGAACATCAGCTGTAAACCACTCTCTCTCTCTGTT 1931
QY 1864 GCTAAGCCAGAACTCTGGGAGCCAAAGGCCCTCTGGGCCACTATCCAGATGAACACTTCAC 1923
Db 1932 GGTTAGCCAAAGAACCAAGGACAGAGGCCCTCTGGGCACTTACCAGATGAGCACTTCAC 1991
QY 1924 AGAGATGCCCGCCCGCGAAGGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983
Db 1992 AGAGAGGCCCGCGAGGAGCATCGCGGCTTCCAGAGCGGCTTGGCCCGAGATCTCAAG 2051
QY 1984 GGGCATCAGGAGAGGAAACCGAGGCTCGGCACTGCGCTACACCTACCTGGATCTCCCTC 2043
Db 2052 GGACATCCAGAGCGGAACCAAGGGTCTGGCACTGCGCTTACCTACCTACCTGGACCTTCCCT 2111
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QY 2044 CATTGAGAACAGTGTCTCCATCTAA 2068
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Db 2112 CATTGAGAACAGTGTCTCCATCTAA 2136
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RESULT 13
US-10-175-696-24
; Sequence 24, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Gluckemann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-696-24

Query Match 20.4%; Score 658.6; DB 14; Length 2136;
Best Local Similarity 63.9%; Pred. No. 1.5e-189;
Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAAGACTTACATTGAAGTTGGCTCGCTGCTTACACAGAGACTGTGAAAGA 543
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Db 555 CAGTGGGAATCGGTACCTGCCGGCTTCCCCATGAATTGACATCCCATCCCTGATGA 614
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QY 544 CTGGAACCTCAACATCAAGTACTCTGCGATGAAGAAATGCAAACTCTTCTTTAAAGCCCA 603
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Db 615 CATGGAGCCCAATGTTGATGATCTAGCCACCAAGAGCATCTCGCTGCTCTTCAATGCCAT 674
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QY 604 CTCGCGGTATACGAGCTGAAGTCAAGGGCTCTGACCGCAGAGACTCTGGAGGAG 663
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Db 675 CCTCGCTCTTGGGAATGAAGCTTCGAGGGCTGTGGATCGCAAGGGCTCCTGGAAGA 734
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QY 664 TCTGAGGAGATGAGAAGCTGTTTAACTTCGCGAAGACTCCAGCAGCAGATATGTGT 723
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Db 735 GCTGATGATGACATGAGAACATCTCTGTTGATGATGAGACCTTTCAGACAAATGATGTAC 794
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QY 724 TGACACTGGCAGGAGATGCTCTCTGCGTCCCAAGTCTTAAATGGCATCAACCCCGT 783
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Db 795 AGAGCACTGGTGTGAAGATCACTCTCTTTGGGTACAGTACCTGAATGGTGTCAATCCCGT 854
|||||

QY 784 CTTGATTCGCCGCTGTACAGTCTCCCAAACTTCCGGTCACTGATGAATGGTGC 843
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Db 855 CATGCTCCACTGCATCTCTAGCTTGGCCAGCAAGCTGCTGTACCAATGACATGGTGGC 914
QY 844 CCCAGTGTGGGCCCTGGAACCACTGTGAGGCTGAGTTGGAGAAAGGCTCCCTGTTCTT 903
Db 915 CCCCTTGTGGGACAGGACACATGCTGACAGAGCTAGAGAGGGGGAACATCTTCCT 974
QY 904 GGTGATCATGGCATCTTTCTGGAGTCCACACCAATCTCTCAATGAAAGCTCAGTT 963
Db 975 AGCGACTACTGGATCTGGCGGAGGCCCCCACTGCCATTAACGGCCGCGCAGCAT 1034
QY 964 CTCTGCAGCCCCGATGACCTCTGTTTACACAGAGCTCAGGGTCCGAGACCCCTGCTTCCAT 1023
Db 1035 GGTGCGCGCCCACTGTGCTGCTGTGCTCAGCCCCCAG--GGGGGCTGGTGCCTT 1091
QY 1024 TGCCATCCAGCTCAAAAGACTCCGGGCGAGACAAACCCATCTCTGCGCCAGGATGA 1083
Db 1092 GGCCATCCAGCTCAGCCAGACCCCGGGCCTGACAGCCCCCATCTTCTGCGCCACTGATC 1151
QY 1084 CACGTGGGACTGTTGCTGGCCAAAGACTGGGTTGCAATTTCTGATTTTACATCATGA 1143
Db 1152 CGAATGGGACTGGCTGCTGGCCAAAGACTGGGTGGGCAACTCTGATTTCTGGTGACGA 1211
QY 1144 GGCTGTACACATCTGCTGCATGCCCATCTGAITTCAGAAAGTCTTTGCTTTGGCCACAT 1203
Db 1212 AAACAACAGCACTTTCTGTGCACGCAATTTGCTGTGGAGGCTTTCGCCATGGCCACGT 1271
QY 1204 AGTCACTGCTAGGTGTACCTCTCTTCAAGTATTGATTTCTTCACTTCGTTACAC 1263
Db 1272 CGGCAGCTGCGCTCTGCCACCCCATCTACAAGCTCTACTCTCCCCACACTCGATACAC 1331
QY 1264 ACTGCACATCAACAGCTTGGCCGAGCTGCTGTTGCGCCCTGGGAAGTTGATAGACA 1323
Db 1332 GCTGAGGTGAACACCACTGCGAGGGGCCACGCTGCTCAACCCCGAGGGCTCTGGTGACA 1391
QY 1324 GTCCACAGGCTTGGCACTGGGGGATTTCTTGACTGATAAAGAGAAACATGGAGCAGCT 1383
Db 1392 GGTCACTGCTAGTGGGAGGCAAGGCTCATCTCATGAGCAGCGGCTTGGCCACTT 1451
QY 1384 GAATCTCTGCTGCTGTCTCTGCTGAAGATATCGAGCCCGAGGTGTGGAAGACATCC 1443
Db 1452 CACCTACACCAATTTCTGCTTCCGGACAGCTGCGGGCCGCGGCTCTGGCTATGCC 1511
QY 1444 AGGCTACTATTACCGAGATGGATGAGTGCAGATCTGGGGGCAATAAGAGCTTTGTCTC 1503
Db 1512 CAATACCACTACCGAGACGCGCTGAAGATCTGGGCGGCTTGAAGAGCTTTGTCTC 1571
QY 1504 TGAATAGTCAAGCTACTACTCAAGTGACACATCCGTCCTCAAGATGACCAAGAGCTCCA 1563
Db 1572 AGAATCGTGGGCTACTATTATCCAGTGAGCATCTGTGACGAGGATTCGAGCTGCA 1631
QY 1564 GGCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGGAGAAAGCTCAGGTATGCC 1623
Db 1632 GGCTGGACTGCGAGATTTTGTCTCAGGCGTTCTGCGGCGGGAAGCTCAGGTATGCC 1691
QY 1624 CTCCTTGTGATACCCGGGAGCCCTGGTCCAGTATATACCATGATGATATTCACCTG 1683
Db 1692 AAGCCGCTGTGCAACCCAGGAGATGGTGAAGTCTCTACTGCAATCATCTTCAATG 1751
QY 1684 CTACGCAAGCATGAGCTGTGCTTCAAGGCTGCTGACTCTTGTGTTGGATGCCCAA 1743
Db 1752 CTCTGCCAGCAGCAGTGTCTGCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCNA 1811
QY 1744 TCTGCCACCTACATGAGCTACCAACCACTTCTTCCAAAGGCCAGGCCGCGCTGAGAG 1803
Db 1812 TGCTCCATCATCCATGAGGAGCCGCCCAACCCAGACCAAGGGGACCAACCCCTGAAGAC 1871
QY 1804 TTTCAATAGCAGCTCCAGCAGTTAATTCGTCAAGTTATCACATCATCTCTCTGCTGCT 1863
Db 1872 TTACTAGACACCTCCCTGAGTGAACATCAGCTGTAAACACCTCTCTCTCTCTGCTGTT 1931
QY 1864 GCTAAGCGCAGAACTGGGAGCAAGGCCCTTGGCCACTTATCCAGATGAACACTTCCAC 1923
Db 1932 GGTAGCCAGAACCCAAAGGACAGAGGCCCTTGGGACCTTACCCAGATGAGCACTTAC 1991
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1804 TTTATAGCCAGCTCCAGAGGTTAATTCGTAAGTTATACATCATTTGCTCTGSGCT 1863
1872 TTACCTAGACACCTTCCCTGTAAGTGAACATCAGCTGTATACCAACCTTCTTCTGGTT 1931
1864 GCTAAGCCGAGAACCTGGGGACCAAGGCCCTGGGCACTATCCAGATGAACACTTCCAC 1923
1932 GGTAGCCAGAACCAAGGACCAAGGCCCTGGGCACTATCCAGATGAACACTTCCAC 1991
1924 AGAGATCCGCCCGCGGAGCGTGGCTTCCAGAGAAAGCTGATCCAGATCCCAA 1983
1992 AGAGAGGCCCGGAGCGGAGCATGCCGCTTCCAGAGCGCGCTGGGCCAGATCTCAAG 2051
1984 GGGCATCAGGGAGGACCGAGGCTGGCACTGCGCTTACACCTACCTGGATCTCCCT 2043
2052 GGACATCCAGGAGCGGACCAAGGCTGGCACTGCGCTTACACCTACCTGGAGCCCTCCCT 2111
2044 CATTGAGAACAGTGTCTCCATCTAA 2068
2112 CATTGAGAACAGTGTCTCCATCTAA 2136

RESULT 15
US-10-422-264-5
; Sequence 5, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-422-264-5

Query Match 20.4%; Score 658; DB 16; Length 2236;
Best Local Similarity 63.9%; Pred No. 2,3e-189;
Matches 1013; Conservative 0; Mismatches 570; Indels 3; Gaps 1;

484 CAGCTGGAAGACTTACATTGGAAGGTTGGCTCGCTGGCTTGAACCAAGAGACTGTGAAGA 543
90 CAGTGGGAATCGGTACTGCTGCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 149
544 CTGGAACCTCAACATCAAGTACTCTGGATGAAGATGCCAACTCTCTTTAAAGCCCA 603
150 CATGGAGCCCAATGTTCGATATCTAGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT 209
604 CTCGCGTATACGAGCTCAAGGCTCAAGGCTCTGGACCGCACAGGACTCTGGAGGAG 663
210 CCTGCGCTTGGGAATGAAGCTTCGAGGGCTGTGGATCGAAGGGCTCCTGGAAGAA 269
664 TCTGAGGAGATGAAGAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGT 723
270 GCTGATGACATGCAGACATCTTCTGGTGCCATGAAGACTTCAGACAAAGATATGTCAC 329
724 TGCACACTGGCAGGAGATGCTCTTCCCTCCAGTTCCTTAATATGCGATCAACCCGGT 783
330 AGAGCACTGGTGTGAAGATCACTCTTTGGGTACCAAGTACCTGATGTGTCAATCCCGT 389
784 CTTGATTCGCGCTGTACAGTCTCCCAAACTTCCCGGCTCACTGATGAATGGTGGC 843
390 CATGCTCCACTGCTACTAGCTTGCCCGAGAGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983

844 CCAGTGTGGCCCTGGAAACCACTGTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTT 903
450 CCCCTTGTGGGACAGGACACATCCCTGCGACAGAGCTAGAGAGGGGAAACATCTTCT 509
904 GGTGGATCATGGCAATCTTTCTGAGTCCACACCAACATCTCAATGGAAAGCTTCAGTT 963
510 AGCGGACTACTGGATCTTGGGGAGGCCCCACCACTGCTCTTAACGGCCCGCAGCAGTA 569
964 CTCTGAGCCCCGATGACCTTGTACACAGAGCTCAGGGTCCGGAACCCCTGCTTCCCAT 1023
570 GGTGGCCGCCCACTGTGCTGCTGTGCTCAGGCCCCAG---GGGGCGCTGGTGGCTT 626
1024 TGCATCCAGCTCAACAGACTCCCGGGCCAGACAAACCCATCTTCTGCGCCAGCGATGA 1083
627 GGCATCCAGCTCAGCCAGAGACCCCGGGCTTGAAGCCCCATCTTCTGCGCCATGATC 686
1084 CACGTGGGACTGTGTGCTGGCCAAAGACTGGGTTTCGCAATTTCTGAGTTTTCATCCATGA 1143
687 CGAATGGGACTGGCTGTGCGCAAGACTGGGTGCGCAACTCTGAGTTCTTCTGGTGCA 746
1144 GGCTGTACACATCTGTGCAATGCCATCTGATTCAGAAAGTCTTGTGCTTGGCCACAT 1203
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807 GCGCAGCTGCGCTCTGCCACCACTTACAAAGCTTCTACTCCCCACACATCGATACAC 866
1264 ACTGCACATCAACACGCTTGGCCGGGAGTGTCTGTTGCCCTGGGAAGTTGATAGCAA 1323
867 GCTGAGGTGAACCACTGGGAGGGCCACGCTGCTCAACCCGAGGGCTCTGGGACCA 926
1324 GTCCACAGGCTTGGCACTGGGGGATTTCTTGAAGTGAACAGAAACATGGAGCAGCT 1383
927 GGTCAAGTCCATCGGAGGCAAGGCTCATCTACTCATGAGCAGGCTTGGCCACTT 986
1384 GAATCTCTGTCTGTCTTCTTCCCTGAAGATATCGAGCCCGAGGTGTGGAAGACATCC 1443
987 CACCTACACCAATTTCTGCTTCCGAGCAGCTGCGGGCCCGCGGCTGCTGGCTATCCC 1046
1444 AGGCTACTTATTCGAGATGATGGATGAGATCTGGGGGCAATAAGAGCTTGTGCTC 1503
1047 CAATACCACTACCGAGACGAGGCTTGAAGATCTGGGCGGCCATTTGAGAGCTTGTCTC 1106
1504 TGAATAGTCAGCATCTACTATCAAGTGAACATCCGTCGAAGATGACCAAGAGCTCCA 1563
1107 AGAATCGTGGGCTACTATTATCCAGTGAAGCATCTGTGAGCAGGATTCGGAGCTCA 1166
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1347 TGCTCCATCATCCATGAGGAGCCCGCCACCCAGACCAAGGGGACCAACCCCTGAGAC 1406
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1407 TTACTTAGACACCTTCCCTGAAAGTGAACATCAGCTGTAAACACCTCTCTCTTCTG 1466
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Job time : 1290.13 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:01:37 ; Search time 358.769 Seconds
(without alignments)
14704.042 Million cell updates/sec

Title: US-10-688-676A-3
Perfect score: 3224
Sequence: 1 cagcttcagtagagagcta.....gtcataaatgagttcattcc 3224

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3178	98.6	3205	US-09-061-768A-3	Sequence 3, Appli
2	3178	98.6	3205	US-09-764-246-3	Sequence 3, Appli
3	1398.4	43.4	2674	US-09-949-016-3041	Sequence 3041, Ap
4	1395.2	43.3	2685	US-09-061-768A-1	Sequence 1, Appli
5	1395.2	43.3	2685	US-09-764-246-1	Sequence 1, Appli
6	1395.2	43.3	2685	US-09-949-016-156	Sequence 156, App
7	659.6	20.5	3384	US-09-547-435-29	Sequence 29, Appli
8	658	20.4	2236	US-09-547-435-5	Sequence 5, Appli
9	658	20.4	2701	US-09-547-435-1	Sequence 1, Appli
10	657	20.4	2307	US-09-799-451-803	Sequence 803, App
11	657	20.4	2604	US-09-547-435-23	Sequence 23, Appli
12	565.8	17.5	2469	US-09-087-727-1	Sequence 1, Appli
13	565.8	17.5	2469	US-09-853-053-1	Sequence 1, Appli
14	565.8	17.5	2469	US-09-949-016-155	Sequence 155, App
15	466.2	14.5	1383	US-09-547-435-11	Sequence 11, Appli
16	466.2	14.5	1848	US-09-547-435-9	Sequence 9, Appli
17	466.2	14.5	2316	US-09-547-435-27	Sequence 27, Appli
18	440.6	13.7	2497	US-09-023-655-1155	Sequence 1155, Ap
19	440.6	13.7	2497	US-10-071-411A-3	Sequence 3, Appli
20	440.6	13.7	2497	US-09-949-016-109	Sequence 109, App
21	440.2	13.7	2496	US-09-949-016-5821	Sequence 5821, Ap
22	407.2	12.6	1441	US-09-547-435-13	Sequence 13, Appli
23	335.6	10.4	2343	US-09-641-638-652	Sequence 652, App
24	335.6	10.4	2343	US-10-170-097-652	Sequence 652, App
25	308.6	9.6	1005	US-09-547-435-7	Sequence 7, Appli
26	308.6	9.6	1470	US-09-547-435-3	Sequence 3, Appli
27	308.6	9.6	1938	US-09-547-435-25	Sequence 25, Appli

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29	215.4	6.7	588	4	US-09-547-435-19	Sequence 19, Appli
30	188.4	5.8	898	4	US-09-547-435-21	Sequence 21, Appli
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ALIGNMENTS

RESULT 1
US-09-061-768A-3
; Sequence 3, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NONE
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
US-09-061-768A-3

Query Match 98.6%; Score 3178; DB 3; Length 3205;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 2

US-09-764-246-3

; Sequence 3, Application US/09764246

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; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-246-3

Query Match 98.6%; Score 3178; DB 4; Length 3205;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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D 121 CTGGGCAAGAGGTTGAGCGCCGGTGTGAAGAACTTTGAGGTTGAGCTTCCCGAGGAC 180
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D 241 ATGTCTTTCCGTTCTGATGCTCGTGTTCGCGCTGGTTTCGAGCTGGAGTGGCTACTGGG 300
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Dd	361	GAGGAGCAGCAAAAGGTGTCTTGGCAAGACCATCACCTACACTGCAGGATCAGCGCCAG	420	QY	1535	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTTGGGTGAGGAGATCTTCTCTGAGGCG	1594
QY	455	AAGGAGCTTGAGTCCAGGCAGAGAGATGTACAGCTGGAAGACTTACATTCGAAGTTGGCT	514	Dd	1501	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTTGGGTGAGGAGATCTTCTCTGAGGCG	1560
Dd	421	AAGGAGCTTGAGTCCAGGCAGAGAGATGTACAGCTGGAAGACTTACATTCGAAGTTGGCT	480	QY	1595	TTCTCTGGCCGAGAAAGCTCAGGTATGCCCTCTTCTTGTGGATACCCGGGAAGCCCTGTGTC	1654
QY	515	CGCTGGCTTTGACCAACAGAGACTGTGAAAGACTTTGGACCTCAACATCAAGTACTCTGCGATG	574	Dd	1561	TTCTCTGGCCGAGAAAGCTCAGGTATGCCCTCTTCTTGTGGATACCCGGGAAGCCCTGTGTC	1620
Dd	481	CGCTGCTTTGACCAACAGAGACTGTGAAAGACTTTGGACCTCAACATCAAGTACTCTGCGATG	540	QY	1655	CAGTATATCACCATCGTGTATTTCACTGTCTCAGCAAGCAAGCATGAGTGTCTAGTTTCAGCG	1714
QY	575	AAGATGCCAAACTCTTTTAAAGCCCACTCCGCGTATACGGAGCTGAAAGTCAAGGG	634	Dd	1621	CAGTATATCACCATCGTGTATTTCACTGTCTCAGCAAGCAAGCATGAGTGTCTAGTTTCAGCG	1680
Dd	541	AAGAAATGCCAAACTCTTTTAAAGCCCACTCCGCGTATACGGAGCTGAAAGTCAAGGG	600	QY	1715	CAGTTTCGACTCTTGTGTGTGGATGCCCAATCTGCCACCTTACCATGCAGTCAGCTACCAACCT	1774
QY	635	CTCTCGACCGCACAGACTCTCGAGAGTCTGAGGAGATGAGAAGGCTGTTTAACTTC	694	Dd	1681	CAGTTTCGACTCTTGTGTGTGGATGCCCAATCTGCCACCTTACCATGCAGTCAGCTACCAACCT	1740
Dd	601	CTCTCGACCGCACAGACTCTCGAGAGTCTGAGGAGTCTGAGGAGATGAGAAGGCTGTTTAACTTC	660	QY	1775	ACTTCCAAAGGCGCGCCGCTGAGAGTTTTCATAGCCACGCTCCAGCAGTAAATTCG	1834
QY	695	CGCAAGACTCCAGCAGCAGATATGTGTTTGCACTGCGCAGGAAGATGCTTCTTCGCC	754	Dd	1741	ACTTCCAAAGGCGCGCCGCTGAGAGTTTTCATAGCCACGCTCCAGCAGTAAATTCG	1800
Dd	661	CGCAAGACTCCAGCAGCAGATATGTGTTTGCACTGCGCAGGAAGTGCCTTCTTCGCC	720	QY	1835	TCAGTGTATCATCATCTTCTCTGGCTGTAAAGCGCAGACCTGGGACCAAGGCC	1894
QY	755	TCCAGTCTCTAAATGGCATCAACCCGGTCTCTGATTCGCGGCTGTACAGTCTCCCAAC	814	Dd	1801	TCAGTGTATCATCATCTTCTCTGGCTGTAAAGCGCAGACCTGGGACCAAGGCC	1860
Dd	721	TCCAGTCTCTAAATGGCATCAACCCGGTCTCTGATTCGCGGCTGTACAGTCTCCCAAC	780	QY	1895	CTGGGCCACTATCCAGATGAACAACATTTACAGAGGATGCCCCCGCGGAAGCGTGTGCC	1954
QY	815	AACCTCCCGTCACTGATGAATGTGTGGCCCAAGTCTGGGCCCTGGAAACCAAGTCTGCAG	874	Dd	1861	CTGGGCCACTATCCAGATGAACAACATTTACAGAGGATGCCCCCGCGGAAGCGTGTGCC	1920
Dd	781	AACCTCCCGTCACTGATGAATGTGTGGCCCAAGTCTGGGCCCTGGAAACCAAGTCTGCAG	840	QY	1955	TTCCAGAGAAAGCTGATCCAGATCTCAGAGGTCATCAGGAGAGGAAACGAGGCTTGGA	2014
QY	875	GCTGAGTTGGAGAAGGCTCCCTGTCTTGTGTGGATCATGGCATCTTCTTGAGTCCAC	934	Dd	1921	TTCCAGAGAAAGCTGATCCAGATCTCAGAGGTCATCAGGAGAGGAAACGAGGCTTGGA	1980
Dd	841	GCTGAGTTGGAGAAGGCTCCCTGTCTTGTGTGGATCATGGCATCTTCTTGAGTCCAC	900	QY	2015	CTGCCCTACACTCTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCAATCTAAACATCTT	2074
QY	935	ACCAACATCTCAATGGAAGCTCAAGTCTTGAGAGCCCGATGACCTGTTCACACAG	994	Dd	1981	CTGCCCTACACTCTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCAATCTAAACATCTT	2040
Dd	901	ACCAACATCTCAATGGAAGCTCAAGTCTTGAGAGCCCGATGACCTGTTCACACAG	960	QY	2075	GGAGAAGCAGTCTCTGTGTGACATATAGAACTCTTTGACCATGCCCTCTCCAGGCTTAAGTCC	2134
QY	995	AGCTCAGGGTCCGAGCCCTGCTCCATTTGCCATCCAGTCAACAGACTCCCGGGCCA	1054	Dd	2041	GGAGAAGCAGTCTCTGTGTGACATATAGAACTCTTTGACCATGCCCTCTCCAGGCTTAAGTCC	2100
Dd	961	AGCTCAGGGTCCGAGCCCTGCTCCATTTGCCATCCAGTCAACAGACTCCCGGGCCA	1020	QY	2135	CGGTATGCTTCTCTGGACAACCAAGCCCATCTTTACACACACACACACACACAC	2194
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Dd	1021	GACAAACCCATCTTCTGCCCCAGCGATGACACGTGGGACTGTGTGCTGGCCAAAGACTCG	1080	QY	2195	TAATAAATCGAAACAGAAACCTTAACTCCACAGAGGCAAGATCTCACACAGCAGA	2254
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Dd	1081	GTTCCGAATCTGAGTTTTACATCAATGAGGCTGTACACATCTGCTGATGCCATCTG	1140	QY	2255	GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTCAGCTCTGATTAAACGGCTTTTGTGTTT	2314
QY	1175	ATTCCAGAGTCTTTGCTTTGGCCACATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1234	Dd	2221	GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTCAGCTCTGATTAAACGGCTTTTGTGTTT	2280
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Dd	1261	CTCGTTGCCCTGGGAAGTTGATGAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1320	QY	2435	ATCAGGAACACAGGAATTTGTCCAATCAAGGCTTACCCTAGGTCCTAGTGCCTACG	2494
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Dd	1381	ATCCGAGCCCGAGGTGTGGAAGACATCCCAAGGCTACTATTACCGAGATGATGGGATG	1440	QY	2555	GGACAGGAGGAGGATGCTCATGTGAAGAAACATATCTCTCTTCCAGATGACACG	2614
QY	1475	ATCTGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGATCTACTATCAAGTGAC	1534	Dd	2521	GGACAGGAGGAGGATGCTCATGTGAAGAAACATATCTCTCTTCCAGATGACACG	2580
Dd	1441	ATCTGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGATCTACTATCAAGTGAC	1500				

QY 2615 GTAGCTCAGCCATGTGTCTTAACTCCAGAGGTCTCTAGTGGCCATGAAGACTCCA 2674
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QY 2581 GTAGCTCAGCCATGTGTCTTAACTCCAGAGGTCTCTAGTGGCCATGAAGACTCCA 2640
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QY 2675 GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATATCTTTTAAAGAGAGAGGAATGGG 2734
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QY 2735 CTGGAGAGATGGCTCAGCGGTTAAAGAGACAGTACTGCTCTCCAGAGATCTCTGAGTTCAA 2794
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QY 2855 GCGTCTCTGAAGACAGCAGCAGTGTATGCATATATAAAATAAAATCTTTTAAAAA 2914
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RESULT 3

US-09-949-016-3041
; Sequence 3041, Application US/09949016
; Patent No.: 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3041
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3041

Query Match 43.4%; Score 1398.4; DB 4; Length 2674;

Best Local Similarity 79.9%; Pred. No. 0; Mismatches 416; Indels 5; Gaps 2;
Matches 1673; Conservative 0;

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QY 1060 GCCATCAGCTCAGCCAGAGACCCCGGCCCAAGAGCCCATCTCTCTGCCCCACTGATGAC 1119
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QY 1985 GGCATAGGAGAGAAACCGAGGCTTGGCACTGCGCTTACACTTACCTGATGCTTCCCTC 2044
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RESULT 5

US-09-764-246-1

; Sequence 1, Application US/09764246

; Patent No. 6649355

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; JIISAKA, MITSUO

; BOEGLIN, WILLIAM E.

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/764,246

; FILING DATE: 17-Jan-2001

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395

; REFERENCE/DOCKET NUMBER: 1242/5


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;
; TELSCOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-764-246-1

Query Match      43.3%; Score 1395.2; DB 4; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY      7 GCAGTAGAGCTAACT--GGTCAGGAGATGGGGAATGCAGGGTGAGATGCCAG 64
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QY      185 GAAGACTTCGAGGTGAGCGCTTCCCAGGAGCTAGGCACTGTGCTGATGCTGCGAGTCCAC 244
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QY      365 CTGGAGGGCGGGGAGCTGTGCTGAGAGGGAGCAGCAAGGTGCTTGGCAAGAC 424
DB      399 CTGGAGGGCGGGGAGCCCTGTGTCTCGAGGGGTACAGCCAAAGTGTCTTGGGCAGAC 458
QY      425 CATCACCTACACTGCAGGATCAGCCAGAAAGAGCTTTCAGTCCAGGCGAGAGATGTAC 484
DB      459 CACCACCTGTGCTCAGCAACAGCCGACAGGAGAGCTTCAGGCCCGGCGAGAGATGTAC 518
QY      485 AGCTGGAAGACTTACATTGAAGTTGGCTCGCTTGCCTTGAACAAGAGACTGTGAAAGAC 544
DB      519 CAGTGGAAAGCTTACAAACCCAGGTTGGCTCTCACTGCTGGATGMAAAGACAGTGGAAAGAC 578
QY      545 TTGGACCTCAACATCAAGTACTTCGCGATGAGAAATGCCAAACTCTCTTTAAAGCCCA 604
DB      579 TTGGAGCTCAATATCAAAATCTCCACAGCCAAAGAAATGCCAACTTTTATCTAAGAGTGC 638
QY      605 TCCGCTATACGAGCTGAAAGTCAAAAGGCTCCTGGACCGCACAGACTCTTGGAGGAGT 664
DB      639 CTGCTTTTCAGAGATGAAATCAAGGGTGTCTGGACCGCAAGGGGTCTTGGAGGAGT 698
QY      665 CTGAGGGAGATGAAAGGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGAGATATGTGTTT 724
DB      699 CTGAATGAGATGAAAGGATCTTCAACTTCGAGGAGACCCAGCAGCTGAGCAGCGCATTT 758
QY      725 GCACACTGGCAGAGATGCTCTTCGCTCCAGTTCCTAAATGGCATCAACCCGGTC 784
DB      759 GAGCACTGGCAGGAGATGCTCTTTCGCTCCAGTTCCTGAATGCTCTCAACCCCTGTC 818
QY      785 CTGATTTCGCGCTGTACAGCTGTCCCAAAACAATCTCCCGGTCACTCATGAAATGGTGGCC 844
DB      819 CTGATCGCGCGCTGTCACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGTGTGGCC 878
```

```
QY      845 CCAGTGTGGCCCTGGAAACCAAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904
DB      879 TCATTGTTGGGTCTTGGGACCAAGTTCGAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938
QY      905 GTGATCATGCAATCTTTCTGGAGTCCACCAACATCCTCAATGGAAGAGCTCAGTTTC 964
DB      939 GTGATCAGGCATCTCTCTGGCATCCAGACCAATGTCAATTAATGGGAGCCGAGTTTC 998
QY      965 TGTGAGCCCGATGAGCCCTGTTACACAGAGCTCAGGGTCGGGACCCCTGTTCCCAATT 1024
DB      999 TCTGGGCCCCAAATGACCTCTGTATACAGAGCCAGGCTGCGGGCCGCTGTGCTCTCTC 1058
QY      1025 GCCATCAGCTCAACACAGACTCCCGGGCGACACACCCATCTTCTCCCGCAGCGATGAC 1084
DB      1059 GCCATCCAGCTCAGCAGACACCCCGGCCAAACAGCCCCATCTTCTGCGCCACTGATGAC 1118
QY      1085 ACGTGGGACTGTTGCTGCGCAAGACTCTGGGTTCGCAATCTTGAGTTTTACATCCATGAG 1144
DB      1119 AAGTGGGACTGTTGCTGCGCAAGACTCTGGGTGCGCAATGCCGAGTTCTCTTCCATGAG 1178
QY      1145 GTGTACACATCTGCTGCATGCCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204
DB      1179 GCGCTCAGCGACTGCTGCACCTCACTCTGCTGCTGAGGTCTTCACTGCTGCTACCTCTG 1238
QY      1205 GGTGAGCTGCTAGGTGTCACTCTCTCAAGCTATTGATTCCTCACTTCGGTACACA 1264
DB      1239 GGTGAGCTGCCCCACTGCGCACCTCTTCAAGCTGTGATCCCGCACACCCGATACACC 1298
QY      1265 CTGCACATCAACACGCTTTGCCGGGAGCTGCTGCTGCTGCGGGAAGTTGATAGACAAG 1324
DB      1299 CTGCACATCAACACACTCGCCCGGAGTGTCTATCTGTCGCGAGGAGGTGGTGACAGG 1358
QY      1325 TCCACAGCCTTGGCACTGGGGGATTTCTGCACTGTATAAAGAGAAACATGAGAGAGTGG 1384
DB      1359 TCCACAGCATCGGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAAACATGAAGCAGTGG 1418
QY      1385 AACTACTCTGCTGTGCTCCCTGCAAGATATCCGAGCCGAGGTGTGGAGACATCCCA 1444
DB      1419 AACTATTCTCTGCTGTGCTGCTGAGGATATCCGAGCCGAGGAGTTGAAGACATCCCA 1478
QY      1445 GGTACTATTACCGAGATGATGGAGTGCAGATCTCTGGGGGCAATAAAGAGCTTTCTCTCT 1504
DB      1479 GGTACTACTACCGTATGATGGGATGCAGATTTGGGGTGCAGTGAACGCTTTGCTCTCT 1538
QY      1505 GAAATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
DB      1539 GAAATCATCGGTATCTACTACCAAGTGTAGTCTGTCCAAAGATGACAGAGAGCTCCAG 1598
QY      1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCTCGGCGGCAAGCTCAGGTATGCC 1624
DB      1599 GCCTGGGTGAGAGAGATCTTCTCAAGGGCTTCTCTCAAGGGCTCAGGTATCCCT 1658
QY      1625 TCCTTGTGGAATACCCGGGAAGCCCTGTGTCCAGTATATCACCATGTGTATATTCACCTGC 1684
DB      1659 TCCTCACTGGAGACCCGGGAGCCCTGTGTGAGTATGTCAACATGGTATATTCACCTGC 1718
QY      1685 TCAGCAAGAGATGACAGCTGTCTGAGTTCAGGCCAGTTTCGACTCTTGTGTTGGATGCCAAT 1744
DB      1719 TCAGCAAGAGATGCGGCTGTCTGAGTTCAGTTCAGTTCAGTTCGCTGCTGATGCCAAC 1778
QY      1745 CTGCCACCTACCATGAGCTACCACTTCTTCCAAAGGCGAGGCCCGGCTGAGAGT 1804
DB      1779 CTGCCACCGAGATGAGCTGCGCACCCACCTCCAAAGGGCTCGGCAACATGCGAGGGC 1838
QY      1805 TTTATAGCAGCTCCAGCAGTTAAATTCGTCAAGTTATACATCATCTCTCTCTGCTG 1864
DB      1839 TTTATAGCACCTCCACCTGTCAATGGCAGATGTGATGTCTCTCTCTCTCTCTGCTG 1898
QY      1865 CTAAGCGCAGAACTCTGGGACCAAGGGCCCTGGGCCACTATCCAGATGAACATCTTCA 1924
DB      1899 CTGAGCAAGGAGCTGGAGACCAAGGGCCCTGGGCCACTATCCGATGAGCACTTCA 1958
QY      1925 GAGGATGCCCCCGGGGAAGCGTGGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAG 1984
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Db 1959 GAGGAGGCCCCCTCGGGGAGCATCGCCACTTCCAGAGCCGCTGGCCAGATCTCGAGG 2018
Qy 1985 GGCATCAGGAGGAGAACCGAGGCTGGCACTGCCCTACACTACTCTGATCTCCCTC 2044
Db 2019 GGCATCCAGGAGCGGAACCGGGGCTGGTGTCTGCTACACCTACTAGACCTCCCTC 2078
Qy 2045 ATTGAGACAGTGTCTCCATCTAAATCTTGGAGAGACAGTCTGTGTGACAT 2098
Db 2079 ATCGAGACAGGCTCTCCATCTAAATCCAGGGGAACACAGGCCCCAGATGACAT 2132

RESULT 6

US-09-949-016-156
; Sequence 156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-156

Query Match 43.3%; Score 1395.2; DB 4; Length 2685;

Best Local Similarity 79.8%; Pred. No. 0;

Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

Qy 7 GCAGTAGAGGCTAACT--GGTCAGGAGGATGGCGAATGACAGGTGAGATATCCACG 64
Db 42 GCCGTAGAGCTGACCTTAGGCTGGCAGCTGGCGGAGTTCAGGGTCAGGTGTCAC 101
Qy 65 GGGGAAGCTGTGGGCTGGCAGTGGGACAAAGTGTCTGTCAGCATCGTGGGAACCCAC 124
Db 102 GGAGAGCTTCGGGGCTGGGACATGGGACAAAGTGTCTGTCAGCATCGTGGGACCCGG 161
Qy 125 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTCAGGCGCGGTGCTGAA 184
Db 162 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTCAGTGGGCGCTGAG 221
Qy 185 GAAGACTTCAGGTGACGCTTCCGAGGAGCTAGGACGTGCTGATGCTGGGAGTCCAC 244
Db 222 GAGGACTTCAGGTGACGCTTCCGAGGAGCTAGGCGGAGTCTGCTGCTGGCGCTGAC 281
Qy 245 AAAGCAGCCCGGAGTGTCTTCCGCTTATGTCTTTCCGTTCTGATGCTGCTGCTGCTG 304
Db 282 AAGGCGCCCC--AGTGTGCCCCCTGCTGGGGCCCCCTGGCCCCGGATGCTTGTCTG 338
Qy 305 CGCTGGTTCGAGCTGGAGTGGCTACCTGGGGGCTGCATCTCACTTCCCTGTTTATCAGTGG 364
Db 339 CGCTGGTTCGAGCTGACACCGCGGGGCGGCCACCTCTCTTCCCTGCTTACAGTGG 398
Qy 365 CTGGAAAGGGGGGGGAGTGTGTCTGAGAGGAGGAGGAGCAAGGTGTCTTGGCAAGAC 424
Db 399 CTGGAGGGGGGGGAGCCCTGCTGTGTCAGAGGGGTACAGCCAAAGGTGTCTTGGGAG 458
Qy 425 CATCACTTACATGTCAGGATCAGCGCCAGAGAGGAGTGTGATCCAGGCGAGAGATGTAC 484
Db 459 CACCACCTTGTCTCCAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGGAGAGATGTAC 518

Qy 485 AGCTGGAGAGCTTACATTGAAAGGTTGGCTCGCTCGCTTGACCCAGAGACTGTGAAAGAC 544
Db 519 CAGTGGAGAGGCTTAAACACCCAGGTTGGCTCAGTCCCTGGATGAAAGACAGTGGAAAGAC 578
Qy 545 TTGACCTTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTCTTTAAAGCCAC 604
Db 579 TTGAGCTCAATATCAAAATCTCCACAGCCAAAGATGCCAACTTTATCTACAGAGCTGGC 638
Qy 605 TCCGGTATACGGAGCTGAAAGTCAAAGGGCTCTCGGACCCGACAGGACTCTGGAGGAGT 664
Db 639 TCTGCTTTTGAGAGATGAAATCAAGGGGTGTCTGGACCCGAAAGGGGCTCTGGAGGAGT 698
Qy 665 CTGAGGAGATGAGAAGGCTGTAACTTCCGCAAGACTCCAGCAGCAGAGATATGTGTTT 724
Db 699 CTGATGAGATGAAGAGATCTTCACTTCCGGAGGACCCAGCAGCTGAGCAGCATTT 758
Qy 725 GCACATGGCAGGAGATGCTTCTTCCGCTCCAGTTCTTAAATGGCATCAACCCGGT 784
Db 759 GAGCAGTGGCAGGAGGATGCTTCTTCCGCTCCAGTTCTTGAATGGTCTCAACCTGTC 818
Qy 785 CTGATTCGCGCTGTCAAGTCTCCAAACAACTTCCCGGTCACTGATGAATGCTGGCC 844
Db 819 CTGATTCGCGCTGTCACTACTCTCCAAAGAACTTCCCGGTCACTGATGCTGATGGTGC 878
Qy 845 CCAGTGTGGGCTGGAAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904
Db 879 TCATTGTTGGTCTTGGGACAGCTTGCAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938
Qy 905 GTGATCATGGCATTTCTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCCTCAGTTC 964
Db 939 GTGATCAAGCATCTCTCTGGCATCCAGACCAATGTCTAATATGGGAAGCGCAGTTC 998
Qy 965 TCTGAGCCCGGATGACCTCTTACACAGAGCTCAGGTCGGGACCCCTGTTCCCATTT 1024
Db 999 TCTGCGGCCCAATGACCTCTATACAGAGCCAGGCTCGGGCCGCTGCTGCTCTC 1058
Qy 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGACACCCATCTTCTCCGCCAGCATGAC 1084
Db 1059 GCCATCCAGCTCAGCAGAGACCCCGGGCCAAACAGCCCATCTTCTCCGCCACTGATGAC 1118
Qy 1085 ACGTGGGAGCTGTTGCTGGCCAAAGACCTGGGTTCGCAATCTGAGTTTTTACATCCATGAG 1144
Db 1119 AAGTGGGACTGTTGCTGGCCAAAGCTGGGTGGCAATGCGAGTTCTCTTCCATGAG 1178
Qy 1145 GCTGTCAACATCTGTCATGCCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204
Db 1179 GCCCTCAGCAGCTGTGCACTCATCTGCTGCTGAGGTCTTCACTGCTGCTGCTGCTG 1238
Qy 1205 GTCAGCTGCTAGGTGTCACTCTCTTCAAGCTATTGATTCCTCACAATTCGGTACACA 1264
Db 1239 GTCAGCTGCCCCCATGCCCCCTCTTCAAGCTGCTGATCCCGCACACCCGATACACC 1298
Qy 1265 CTGACATCAACACGCTTGGCCGGAGCTGCTGCTGGCCCTGGGAAGTTGATAGACAAG 1324
Db 1299 CTGACATCAACACACTGCCCCGGAGGCTGTATCTGTCAGCAGGCGAGGTGGTGCAGG 1358
Qy 1325 TCCAGAGCCCTTGGCAGCTGGGGGATCTCTCACTCTGATTAAGAGAAACATGGAGCAGT 1384
Db 1359 TCCAGAGCATCGGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
Qy 1385 AACTACTCTGCTGCTGCTCTTCCCTGAAGATATCCAGCCCGAGGCTGTGGAGACATCCCA 1444
Db 1419 AACTATTTCTCTCTGCTGCTGCTGAGGATATCCGGACCCGAGGAGTTGAAAGACATCCA 1478
Qy 1445 GGCTACTATTACCAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTTCTCT 1504
Db 1479 GGCTACTACTACCTGATGATGGGATGAGATTTGGGGTGCAGTGGAAAGCTTTTCTCT 1538
Qy 1505 GAAATAGTTCAGCATCTACTTCCAAAGTGAACATCTCCGTCCTCAAGATGACCAAGAGCTCCAG 1564
Db 1539 GAAATCATCGGTACTACTACTCCCAAGTGAATGAGTCTGTCCTCAAGATGACAGAGAGCTCCAG 1598
Qy 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTTCCGGCCGAGAAAGCTCAGGTATGCC 1624

[illegible]

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RESULT 7
US-09-547-435-29
; Sequence 29, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-29

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	Query Match	20.5%	Score 659.6	DB 4	Length 3384
	Best Local Similarity	63.9%	Pred. No. 2e-187		
	Matches 1014	Conservative 0	Mismatches 569	Indels 3	Gaps 1
Qy	484	CAGCTGGAAGACTTACATTGAAGTTGGCCTCGCTTTGACCAACGAGACTGTGAAGA	543		
Db	1053	CAGTGGGAATCGGTACCTGCGCGGCTCCCCATGAAAATTGACATCCCATCCCTGATGTA	1112		
Qy	544	CTTGGACCTCAACATCAAGTACTCTGCGATGAAGAATGCCAAACTCTTTCTTTAAAGCCCA	603		
Db	1113	CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT	1172		
Qy	604	CTCGCGCTATACCGGAGCTGAAAGTCAAAGGGCTCTCGACCGCACAGGACTCTTGGAGGAG	663		

1173	CCCTGCGTCTCTTGGGAATGAAGCTTCGAGGGCTGTGTTGATTCGCAAGGGCTCTCTGGAAGAA	1233
Qy		
664	TCCTGAGGAGATGAGAAGGCTGTTTAACTTCGCCAAGACTCCACGACGACGAGTATGTGTT	723
Db		
1233	GCTGGATGACATGCAGAAATCTTCTGGTGGCCATAGACCTTCAACGACAAAGTATGTCAAC	1292
Qy		
724	TGCACACTGGCAGGAAGATGCCTTCTTCGCTCCCAAGTTCCTAAATGGCANATCAACCCGGT	783
Db		
1293	AGAGCACTGGTGTGAAGATCACTTCTTGGGTACCACTACCTGAATGGTGTCAATCCCGT	1352
Qy		
784	CCTGATTGGCCGCTGTCAAGTCTCCAAACAATCTCCCGGTCACTGATGAATATGGTGGC	843
Db		
1353	CATGCTCCAATGATCTCTAGCTTGGCCAGCAAGCTGCTGTCAACAAATGACATGTTGGC	1412
Qy		
844	CCCAGTCTGGGCCCTGGAAACAGTCTGCAAGGCTGAGTTGGAGAAGGGCTCCCGTGTCTT	903
Db		
1413	CCCCCTTGTGGNACAGACACATGCTCTGACAGAGCTAGAGAGGGGNAACATCTTCCT	1472
Qy		
904	GSTGGATCATGGCAATCTTTTGTGAGTCCACACCAATCTCTCAATGGAAAGCCTCAGTT	963
Db		
1473	AGCGGACTACTGATCTCTGGCGAGGCCCCACCCACTGCCTAAACGGCGCCAGCAGTA	1532
Qy		
964	CTCTGACAGCCCCGATGACCTGTATTACACAGAGCTCAGGGTCGGGACCCCTGTCTCCCAT	1023
Db		
1533	CGTGGCCGCCCACTGTGCTCTGTGGTCTCAGCCCCCAG--GCGGCGCTGGTGGCCCTT	1589
Qy		
1024	TGCCATCTCAGCTCAAAACAGACTCCCGGGCGACACAACCCCATCTCTCTGCCACAGCGATGA	1083
Db		
1590	GGCCATCTCAGCTCAGCCAGACCCCGGGGCTGACAGCCCAATCTTCTGCCCACTGACTC	1649
Qy		
1084	CACGTGGGACTGGTGTCTGGCCAAAGACTCTGGGTTGCAATCTGAGTCTTTACATCCATGA	1143
Db		
1650	CGAATGGGACTGCTGCTGGCCAAAGCGTGGGTGCGCAACTCTGAGTTCCTGGTGACAGA	1709
Qy		
1144	GGCTGTCAACATCTGCTGTGATGCCCATCTGATTCAGAAAGTCTTTGGCTTGGCCACATTT	1203
Db		
1710	AAACAACAGCGCACTTCTCTGTGACGCAATTTGCTGTGCGAGGCCCTCGCCATGCGCCACGT	1769
Qy		
1204	ACGTACAGTGCCTAGTGTGACCCCTCTCTTCAAGCTATTGATTCCTACATTCGGGTACAC	1263
Db		
1770	GCGCCAGCTGCCGCTGTGCCACCCCAATCTACAGCTCTTACTCCCCCACTCGATACAC	1829
Qy		
1264	ACTGCACATCAACACGCTTTCGCCGAGCTGCTGTTGCCCTCTGGGAAGTTGATAGACAA	1323
Db		
1830	GCTGCAAGGTGAACACCATCGAGAGGCCACGCTGCTCAACCCCGAGGCGCTCGTGACCA	1889
Qy		
1324	GTCACAGGCTTGGCACTGGGGGATCTCTGACCTGATAAGAGAAAACATGAGACAGCT	1383
Db		
1890	GGTCAGTCCATCGGGAGGCAAGSGCTCATCTACCTCATGAGCACGGGCGCTGGCCCACTT	1949
Qy		
1384	GAACTACTGTCTGTGCTCTCCCTCAAGATATCCGAGCCCGAGGTTGGAAGACATCCC	1443
Db		
1950	CACCTACACAAATTTCTGCCCTTCCGACAGCCTGCGGGGCCCGGGCGTCTGTGCTATCCC	2009
Qy		
1444	AGGCTACTATTACCGAGATGATGGGATGACAGTCTGGGGGGCAATAAAGAGCTTTGTCTC	1503
Db		
2010	CAACTACCACTACCGAGACGACGGCCCTGAAGATCTGGCGGCCATTTGAGAGCTTTGTCTC	2069
Qy		
1504	TGAAATAGTCAGCATCTATATCAAGTGAACATCCGTCCAAAGATGAACAGAGCTCCA	1563
Db		
2070	AGAAATCGTGGGCTACTATTATCCCACTGACGCAATCTGTGACAGCAGGATTCGGAGCTGCA	2129
Qy		
1564	GGCTCGGTGAGGGAGATCTTCTCTAGGGCTCTCTCGGCCGAGGAAGCTCAGGTATGCC	1623
Db		
2130	GGCCTGGACTGGCGAGATTTTGTCTCAGGCGTTCTCTGGCGGGGAAAGCTCAGGTTTCCC	2189
Qy		
1624	CTCCTTGTGTGGATACCCCGGGAAGCCCTGGTCCAGTATATCAACCATGGTGATATTCACCTG	1683
Db		
2190	AAGCCGCTGTGCAACCCAGGAGAGTGTGAAGTTCTCACTGCAATCATCTTCAATTG	2249
Qy		
1684	CTCAGCCAAAGCATGCACTGTCTAGTTTCAGCCACAGTTCGACTCTTGTGTTTGGATGCCCAA	1743
Db		
2250	CTCTGCCACAGCAGCTGTCTGTCAACAGTGGGACAGCATGACTTTGGGGCTGGATGCCCAA	2309

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QY 1744 TCTGCCACTTACATGACAGTACCACCACTACTTCCAAAGCCAGGCCCGCCCTGAGAG 1803
Db 2310 TCTCCATCATCATGAGCAGCCGCCACCCAGACCAAGGGGACACACCCCTGAAGAC 2369
QY 1804 TTTTATAGCCAGCTCCCAAGAGTAAATTCGTCAAGTTATCATCATTCATTCCTCTGCT 1863
Db 2370 TTACCTAGACACCTCCCTGAGTGAACATCAGCTGTAAACACCTCTCTCTCTGCT 2429
QY 1864 GCTAGCGCAGAACCTGGGGACAAAGGCCCTGGGCCACTATTCAGATGAACATTCAC 1923
Db 2430 GGTAGCCAAAGAACCAAGGACAGAGGCCCTGGGCACTTACCCAGATGAGCACTTCA 2489
QY 1924 AGAGGATGCCCCCGGAGAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCA 1983
Db 2490 AGAGGAGGCCCGAGCGGAGCATCGCGCTTCCAGAGCCCGCTGGGCCAGATCTCAAG 2549
QY 1984 GGGCATCAGGAGAGGAACCGAGGCTGGCACTGCCCTACACCTACCTGGATCTCCCT 2043
Db 2550 GGACATCCAGGAGCGGACCGAGGCTGGCACTGGCACTGGCACTGGCACTGGCACT 2609
QY 2044 CATTGAGAACAGTGTCTCATTAAC 2069
Db 2610 CATTGAGAACAGTGTCTCATTAAC 2635
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RESULT 8

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US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-5
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Query Match 20.4%; Score 658; DB 4; Length 2236;
Best Local Similarity 63.9%; Pred. No. 4.6e-187;
Matches 1013; Conservative 0; Mismatches 570; Indels 3; Gaps 1;

QY 484 CAGCTGGAAGACTTACATGAGGTTGGCTCGCTCGCTTGCACCAAGAGTGTGAAGA 543
Db 90 CAGTGGGAATGGTACCTGCCCGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 149
QY 544 CTGAGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTCTTTAAAGCCCA 603
Db 150 CATGAGGCCATGTTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 209
QY 604 TTCGCGTATACGAGCTGAAAGTCAAGGGCTCTGGACCGCAAGGAGTCTGGAGGAG 663
Db 210 CCTCGCTCTTGGGAATGAAGTTCGAGGGCTGTGGATCGAAGGGCTCTGGGAAGA 269
QY 664 TCTGAGGAGATGAGAGGCTTTAACTTCGCAAGACTCCAGCAGCAGATGATGTT 723
Db 270 GCTGATGATGACGAGAAATCTTCTGCTGCGCATTAAGACCTTTCAGCAAAATGATGTCAC 329
QY 724 TGCACACTGGCAGGAGATGCTCTTCTGCGCTCCAGTTCCTTAAATGGCATCAACCCGCT 783
Db 330 AGAGCACTGGTGAAGATCACTTCTTTGGGTACCACTGATGATGATGATGATGATGAT 389
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QY 784 CTTGATTCGCGCTGTCTACAGTCTCCCAACAACTTCCCGGTCACTGATGAATGTTGTC 843
Db 390 CATGCTCCACTGCACTCTAGCTTGGCCAGCAAGCTGCTGTCAACAATGATGATGTTGTC 449
QY 844 CCCAGTGTGGGCCCTGGAACCAAGTCTCAGGCTGAGTTGGAGAAAGGGCTCCCTGTTCTT 903
Db 450 CCCCTTGTGGGACAGGACACATGCTTCGACAGACAGCTAGAGAGGGGAAACATCTTCT 509
QY 904 GGTGATCATGGCACTTTCTTCTGAGTCCACCAACATCTCTCAATGAAGACCTCAGTT 963
Db 510 AGCGACTACTGGATCTCTGGGAGGCCCCCACCACCTGCTTAAACGCGCGCAGCAGTA 569
QY 964 CTCTGACGCCCGATGACCTGTTACACAGAGCTCAGGTCCTCGGACCCCTGCTTCCCAT 1023
Db 570 CTGCGCCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
QY 1024 TGCATCCAGTCAAAACAGACTCCCGGCCAGACAAACCCCATCTTCTGCCCCAGGATGA 1083
Db 627 GGCCATCCAGTCCAGCAGACCCCGGCTGACAGCCCCCATCTTCTGCCCCCAGCTGACT 686
QY 1084 CAGTGGAGTGTGTTCTGGGCAAGACCTGGGTTGCAATTTCTGAGTTTATCATCATGA 1143
Db 687 CGAATGGGACTGGCTGCTGGGCAAGACGTTGGGTGCGCAACTCTGAGTTCTCTGGTGA 746
QY 1144 GCTGTACACATCTGCTGATGCCATCTGATCCAGAGTCTTGTGCTTGGCTTGGCCACAT 1203
Db 747 AAACACACGCACTTCTGTGACGCACTTGTGTGAGGCTTTCGCCCATGGCCACGCT 806
QY 1204 ACCTCAGCTGCTAGTGTCACTCTCTTCAAGCTATTGATTTCTTCACTTCGGTACAC 1263
Db 807 GCGCAGCTGCGCTGCTGCAACCCCATCTACAGCTCTCTTCTCCCACTCGATACAC 866
QY 1264 ACTGCATCAACAGCTTGGCCCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
Db 867 GCTGAGGTGAACACCACTGCGAGGCGCACGCTGCTCAACCCCGAGGCTCTGCTGACCA 926
QY 1324 GTCCACAGGCTTGGCACTGGGAGTCTCTGAGCTGATGAAGAAACATGGAGAGCT 1383
Db 927 GGTCACTGCTTCCAGGAGGAGGCTCTTCTGAGCTGATGAAGAAACATGGAGAGCT 986
QY 1384 GAACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
Db 987 CACTACACCAATTTCTGCTTCCGACAGCTGCGGCGCTGCGGCGCTCTGCTGCTGCT 1046
QY 1444 AGGCTACTATTACCGAGATGATGGATGATGATGATGATGATGATGATGATGATGATG 1503
Db 1047 CACTACCACTACCGAGACGCGCTGAAAGATCTGCGGCGCTGCTGCTGCTGCTGCTGCT 1106
QY 1504 TGAATAGTCAAGATCTACTATCAAGTACACATCCGTCCAGATGACCAAGACTCCA 1563
Db 1107 AGAATCGTGGGCTACTATTATCCAGTGAAGCTCTGTCAGCAGGATTCGGAGCTGCA 1166
QY 1564 GGCCTGGTGAAGGAGATCTTCTCTGAGGCTTCTCGGCGGAGAAAGCTCAGGTATGCG 1623
Db 1167 GGCCTGAGTGGAGATTTTGTCTCAGCGCTTCTGCGCGGAGAAAGCTCAGGTATGCG 1226
QY 1624 CTCTTGTGATACCGGGAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683
Db 1227 AAGCGCTGTGCAACCCAGGAGAGATGTTGAGTCTCTCTCTCTCTCTCTCTCTCTCT 1286
QY 1684 CTAGCAGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
Db 1287 CTCTGCGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1346
QY 1744 TCTGCCACTTACCATGAGCTTACCAACCTTCTTCCAAAGGCGCGGCGCTGAGAG 1803
Db 1347 TGCTCCATCATTCATGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1406
QY 1804 TTTTATAGCCAGCTCCCGAGGATTAATTCGTCAAGTTTATCAGATCATTCATTCCTG 1863
Db 1407 TTACTTAGACACCTTCCCTGAGTGAACATCAGCTGTAACAACTCTCTCTCTCTCTCT 1466
QY 1864 GCTAAGCGCAGAACCTGGGGAACCAAGGCGCTGCGGCGCTTATTCAGATGAACATTC 1923
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Db	1467	GGTTAGCCAAAGACCCAGAGGCCCTTGGGCACTTACCAGATGAGCACTTAC	1526
Qy	1924	AGAGGATGCCCGCGGAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA	1983
Db	1527	AGAGGAGCCCGAGGCGGAGCATCGCGCTTCCAGAGCGGCTGGCCCAAGTCTCAAG	1586
Qy	1984	GGGCATCAGGAGAGAAACGAGGCGCTGGCACTGCCCTACACTCTGGATCTCCCTT	2043
Db	1587	GGACATCCAGGAGCGAAACGAGGCTGGCACTGGCTTACCTACCTAGTGGACCTCCCT	1646
Qy	2044	CATTGAGACAGTGTCTCCATCTAAC	2069
Db	1647	CATTGAGAACAGCGTCTCCATCTAAC	1672
RESULT 9			
US-09-547-435-1			
; Sequence 1, Application US/09547435			
; Patent No. 6582957			
; GENERAL INFORMATION:			
; APPLICANT: Turner, C. Alexander, Jr.			
; APPLICANT: Zambrowicz, Brian			
; APPLICANT: Nehls, Michael			
; APPLICANT: Friedrich, Glenn			
; APPLICANT: Sands, Arthur T.			
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides			
; TITLE OF INVENTION: Encoding the Same			
; FILE REFERENCE: 7705, 0009-00000			
; CURRENT APPLICATION NUMBER: US/09/547,435			
; CURRENT FILING DATE: 2000-04-12			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 1			
; LENGTH: 2701			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-547-435-1			
Query Match 20.4%; Score 658; DB 4; Length 2701;			
Best Local Similarity 63.9%; Pred.No.5.3e-187;			
Matches 1013; Conservative 0; Mismatches 570; Indels 3; Gaps 1;			
Qy	484	CAGCTGGAAAGACTTACATTGAAGGTTGGCTCGCTCGCTGGACCGAGACTGTGAAGA	543
Db	555	CAGTGGGAATCGGTACTCTGCCCGGCTTCCCATGAAAAATTGACATCCCATCCCTGATGA	614
Qy	544	CTTGGACCTCAACATCAAGTACTCTCGGATGAAGATGCGAAACTCTTCTTTAAAGCCCA	603
Db	615	CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTCTCTTCAATGCCAT	674
Qy	604	CTCCGGGTATACGGAGCTGAAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAG	663
Db	675	CCCTGGCTCTTGGGAATGAAGCTTCGAGGGCTGTGGATCGCAAGGGCTCTTGGGAAGAA	734
Qy	664	TCCTGAGGAGATGAGAAGGCTGTTTAACTTCCCAAGACTCCAGCAGCAGAGATGATGTT	723
Db	735	GCTGGATGACATGCAGAACATCTTCTGGTGGCATAAGACCTTCACGACAAAGTATGTAC	794
Qy	724	TGCACACTGGCAGGAAGATGCTTTCTTTCGCTCCCAAGTTCCTTAATGGCATCAACCCGCT	783
Db	795	AGAGCACTGGTGTGAAGATCACTTCTTGGTACCAGTACCTGAATGGTGTCAATCCCGT	854
Qy	784	CTGATTTCGCGCTGTACAGTCTCCCAACACTTCCCGGTCACTGTAGTGAATGGTGGC	843
Db	855	CATGCTCCATGTCACTCTTGTAGTTGCCAGCAGCTGCTGTGTCACCAATGACATGGTGGC	914
Qy	844	CCCAAGTCTGGGCGCTCGAACCAGTCTGCAAGGTGAGTGGAGAGGGCTCTCTGTTCTT	903
Db	915	CCCTTGTCTGGACAGACACATGCTCTGCAGACAGAGCTAGAGAGGGGNAACATCTTCT	974
Qy	904	GGTGGATCATGGCATCTTCTTGGAGTCCACACCAACATCTCTCAATGGAAAGCCTCAGTT	963

Db	975	AGCGACTACTGGATCTCTGGCGGAGGCCCCACCACTGCCCTAAAGCGCGCCAGCAGTA	1034
Qy	964	CTCTCCAGCCCGCATGACCTCTGTTTACACAGAGCTCAAGGTCGGAACCCCTGCTTCCCAT	1023
Db	1035	CGTGGCGCGCCACCTGCTGCTGTGGCTAGCCCCCAG--GGGGGGCTGGTGCCCTT	1091
Qy	1024	TGCCATCAGCTCAAAACAGACTCCCGGGCCAGAACCCCATCTTCTCTGCCCCAGCATGA	1083
Db	1092	GGCCATCCAGCTCAGCCAGACCCCGGGCTTACAGCCCCCATCTTCTCTGCCCACTGACTC	1151
Qy	1084	CACGTGGGACTGGTGTCTGGCCAGACCTGGGTTCGCAATCTGAGTATTCTGATTTTATCAT	1143
Db	1152	CGAATGGGACTGGCTGCTGGCCAGACGCTGGGTGGCGCACTCTGAGTTCCTGGTGCAGCA	1211
Qy	1144	GGCTGTACACATCTGCTGCTGCCCATCTGATTCAGAAAGCTTTTGGCTTTGGCCACATTT	1203
Db	1212	AAACAACACGCACTTTCTGTGTCAGCAATTTGCTGTGCGAGGCTTTCGCCATGGCCACGCT	1271
Qy	1204	AGTCACTGCTTAGTGTGCTACCTCTCTTCAAGCTATTGATTCTCTCATATTCGGTACAC	1263
Db	1272	GGCCAGCTGCGCTCTTGCACCCCATCTACAAGCTCCTACTCCCCCACCACACTCGATACAC	1331
Qy	1264	ACTGCACATCAACACGCTTGGCCGGGAGCTGCTCGTTCGCTCGCTGGGAAAGTTGATAGACA	1323
Db	1332	GCTGAGGTGAACACCATCGGAGGGCCACGCTGCTCAACCCCGAGGGGCTCTGTGACACA	1391
Qy	1324	GTCCAAGGCTTGGCACTGGGGGATTTCTTGACCTGATAAAGAGAAACATGGAGCAGCT	1383
Db	1392	GGTCAAGTCCATCGGAGGCAAGGCTCATCTACCTCATGAGCAGGGGCTTGGCCACATTT	1451
Qy	1384	GAATCTCTGCTGCTGCTTCCCTGTAAGATATCCGAGCCGAGGTGTGGAAGACATCCC	1443
Db	1452	CACCTACACCAATTTCTGCTTCCGAGACGCTCGGGCCCGCGGCTCTTGGCTATCCC	1511
Qy	1444	AGGCTACTATTACCGAGATGATGGATCGAGATCTGGGGGGCAATAAAGAGCTTTGTCTC	1503
Db	1512	CAACTACCACATCCGAGAGCAGCGCTGAAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC	1571
Qy	1504	TGAATAGTCAAGCATCTACTATCCAAAGTGAACACATCCCGTCCAAGATGACCAAGAGCTCA	1563
Db	1572	AGAAATCGTGGGCTACTATTATCCAGTGACGCATCTGTGACAGCAGGATTCGAGCTGCA	1631
Qy	1564	GGCTTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGGAGAAAGCTCAGGTATGCC	1623
Db	1632	GGCTTGGATCCGCGAGATTTTGTCTCAGGCGTTCCTGGGCGGGAAAGCTCAGGTATGCC	1691
Qy	1624	CTCCTTGTGGATACCGGGAGCCCTGTCAGTATATCACCATGCTGATATCACCTG	1683
Db	1692	AAGCGGCTGTGACCCCGAGGAGATGGTGAAGTTCCTCACTGCAATCATCTTCAATTG	1751
Qy	1684	CTCAGCCAAAGCATGCACTGTCTCAGTTCAGGGCAGTTCGACTCTTGTGTTGGATGCCCAA	1743
Db	1752	CTCTGCCAGACGCTGTCTCAACAGTGGGAGCATGACTTTTGGGGCTTGGATGCCCA	1811
Qy	1744	TCTGCCACTTACATGCACTACCAACCACTATCTTCCAAAGGCCAGGCCCGGCTGAGAG	1803
Db	1812	TGCTCCATCATCATGAGCAGCCCCCAGACCAAGGGGACCAACCCCTGAAAGC	1871
Qy	1804	TTTCTAGCAGCTCCCGAGCAGTTAATTCGTCAGTTATCACATCATTTGCTCTTGGCT	1863
Db	1872	TTACCTAGACACCTTCCCTGAGTGAACATCAGCTGTAAACAACTCTCTCTTCTTGGTT	1931
Qy	1864	GCTAAGCGCAGAACTGGGGACAAAGGCCCTGGGCCACTTCCAGATGAACACTTAC	1923
Db	1932	GGTTAGCCAGAACCAAGGACAGAGGCCCTTGGGACCTTACCCAGATGAGCACTTAC	1991
Qy	1924	AGAGGATCCCCCGCGGAGCGTGGCTGCCCTTCAGAGAAAGTGAATCCAGATCTCCAA	1983
Db	1992	AGAGGAGGCCCGGAGCGGAGCATCGCGCTTCCAGAGCCGCTGGGCCAGATCTCAAG	2051
Qy	1984	GGGCTACAGGAGAGAACCGGCGCTGGCACTGGCTACACTACCTACCTGCTTCCCT	2043
Db	2052	GGACATCCAGGAGCGGAACCAAGGGTCTGGCACTGCCCTACACTACCTGAGACCTTCCCT	2111

QY 2044 CATTGAGAACAGTGTCTCCATCTAAC 2069
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Db 2112 CATTGAGAACAGCGTCTCCATCTAAC 2137

RESULT 10

US-09-799-451-803
; Sequence 803, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 803
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (172)..(2304)
US-09-799-451-803

Query Match 20.4%; Score 657; DB 4; Length 2307;
Best Local Similarity 63.8%; Pred. No. 9.4e-187;
Matches 1012; Conservative 0; Mismatches 570; Indels 3; Gaps 1;
QY 484 CAGCTGGAGAGCTTACATTGAAGGTTGGCTCGCTGCTGACACGAGACTGTGAAAGA 543
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Db 726 CAGTGGGAATCGGTACCTGCCCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 785
QY 544 CTGAGACCTCAACATCAAGTACTCTGCGATGAGAAATGCCAAACTCTTCTTTAAAGCCCA 603
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Db 786 CATGGAGCCCAATGTTTCGATACTACGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT 845
QY 604 CTCGCGGTATACGAGCTGAAGTCAAAGGGCTCTGACCGCACAGGACTCTGGAGGAG 663
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Db 846 CCCTCGCTCTTGGGAATGAAGCTTCGAGGGCTGTGGATCGAAGGGCTCTCGAAGAA 905
QY 664 TCTGAGGAGATGAGAAGGCTGTTTAACTTCGCAAGACTCCAGACGACAGATGATGTT 723
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Db 906 GCTGGATGACATGCAGAACATCTCTGTTGTCATTAAGACCTTCACGACAAAGTATGTAC 965
QY 724 TGCACTGGCAGGAGATGCTCTTCTGCTCCAGTTCCTAAATGGGATCAACCCGGT 783
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Db 966 AGAGCACTGGTGAAGATCACTTCTTGGGTACCACTACCTGAATGGTGTCAATCCCGT 1025
QY 784 CTGATTCGCGCTCTCACAGTCTCCCAACAACTTCCGGTCACTGATGAATGGTGGC 843
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Db 1026 CATGCTCACTGCATCTCTAGTCTGCCAGCAAGCTGCTGTCACTCAATGACATGGTGGC 1085

QY 844 CCCAGTGTGGGCCCTGGAAACCACTCTGAGGCTGAGTTGGAGAAGGCTCCCTGTTCTT 903
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Db 1086 CCCCTTGTGGGACAGGACACATCCCTGACAGAGAGCTAGAGAGGGGAAACATCTTCT 1145
QY 904 GGTGATCATGGCATTCTTTCTGAGTCCACACCAATCCTCAATGGAAGACCTCAGTT 963
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Db 1146 AGCGGACTACTGGATCTGGGGAGGCCCCACCACTGCTTAAACGGCCGACGACTA 1205
QY 964 CTCTGACGCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1023
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Db 1206 CGTGGCCGCCCACTGTGCTGCTGTGGCTCAGCCCCCAG--GGGGCGCTGGTGGCCCTT 1262
QY 1024 TGCCATCCAGCTCAAAAGACTCCGGGGCCAGACAAACCCATCTTCTGCCCGGAGTGA 1083
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Db 1263 GGCCATCCAGCTCAGCCAGACCCCGGGCTGACAGGCCCCATCTTCTGCCCCACTGACTC 1322
QY 1084 CACGTGGGACTGTTGCTGGCCAAAGACTGCGGTTGCAATCTCTGAGTTTATCATCATGA 1143
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Db 1323 CGAATGGGACTGGCTGTGGCCAAAGACTGGGTGGCNACTCTGAGTTCCTGGTGCAGA 1382
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QY 1204 ACCTCAGTGTGCTAGGTGTCACTCTCTTCAAGCTATTGATTCTCTCATATTGGTACAC 1263
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Db 1443 GCGCCAGTGTGCTGTGCCCCACCCATCTTCAAGCTCTTCTCCCCACACTCGGATACAC 1502
QY 1264 ACTGCATCAACACGCTTGGCCGGGAGCTGCTGTTGCCCTCGGMAAGTTGATAGACAA 1323
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Db 1503 GCTGAGGTGAACACATCGCGAGGGCCACGCTGCTCAACCCGAGGGCTCTGTGACCA 1562
QY 1324 GTCCACAGGCTTGGCCTGCGGAGTCTCTGACCTGATAAAGAGAAACATGGAGCAGCT 1383
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Db 1563 GGTCACTGTCCATCGGGAGGCAAGGCTCATCTACTCATGAGCAGGGCTCTGGCCACTT 1622
QY 1384 GAATCTCTGCTGTCTCTCTCTGAGATATCGAGCCCGAGGTGTGGAGACATGCC 1443
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Db 1623 CACCTACACCAATTTCTGCTTCCGAGCAGCTCTGGGGCCGCGGCTCTGGCTATCCC 1682
QY 1444 AGGCTACTATTACCGAGATGATGGATGACATCTGGGGGCAATAAAGAGCTTTGTCTC 1503
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Db 1683 CAATACCACTACCGAGACGAGGCTGGAAGATCTGGGGGCGCATTGAGAGCTTTGTCTC 1742
QY 1504 TGAATATGTCAGCATCTACTATCCAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCA 1563
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Db 1743 AGAATCGTGGCTACTATTATCCAGTACGATCTGTGAGCAGGATTCGGAGCTGCA 1802
QY 1564 GGCCTGGGTGAGGAGATCTTCTCTGAGGGTCTCTCGGCCGAGAAAGCTCAGGTATGCC 1623
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Db 1803 GGCCTGGAATGCGCAGATTTTGTCTCAGGCGTCTCTGGGGCGGAAAGCTCAGGTTTCCC 1862
QY 1624 CTCCTTGTGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGATGATATTCACCTG 1683
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Db 1863 AAGCGGCTGTGACCCCGAGGAGATGGTGAAGTTCCTCACTGCAATCATCTTCAATG 1922
QY 1684 CTACGCAAGCATCAGCTGTGCTCAGGCGCAGTTCGACTCTTGTGTTGGATGCCCAA 1743
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Db 1923 CTCTGCCAGCAGCCTGCTGTCAACAGTGGGACAGTACTTTGGGGCTTGATGCCCAA 1982
QY 1744 TCTGCCACCTACCATGAGCTACCAACCACTTCTTCCAAAGCCAGGCCCGGCTGAGAG 1803
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Db 1983 TGCTCCATCATPCCATGAGGACGCCCCACCCAGACCAAGGGGACACACCCCTGAAGAC 2042
QY 1804 TTTTATAGCAGCTCCCGCAGGTTAATTCTGTAAGTTATCAGATCATTTGCTCTCTGCT 1863
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Db 2043 TTACTAGACACCTCTCTGTAAGTGAACATCAGCTGTAAACCACTCTCTCTCTCTGCT 2102
QY 1864 GCTAAGCGCAGAACTCTGGGACCAAGGCCCTCTGGGCCACTTATCCAGATGAACACTTCC 1923
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Db 2103 GGTAGCCAGAACCCAGGACGAGGCCCTCTGGGACCTTACCCAGATGAGCACTTCC 2162
QY 1924 AGAGGATGCCCCCGGCGAAGCGTGGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983

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Db      2163  AGAGGAGGCCCCGAGGGCGGAGCATCGCGCGCTTCAGAGCGCGCTGGCCCGCATCTCAAG 2222
Qy      1984  GGGCATCAGGAGGAGGAAACGAGGCGCTGGCACTGCCCTACACCTTACCTGGATCTCTCCCT 2043
Db      2223  GGACATCAGAGCGGGAACAGGGTCTGGCACTGCCCTACACCTTACCTGGACCTCCCT 2282
Qy      2044  CATTGAGAACAGTGTCTCCATCTAA 2068
Db      2283  CATTGAGAACAGCGTCTCCATCTAA 2307

RESULT 11
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 2604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-23

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Query Match	20.4%;	Score 657;	DB 4;	Length 2604;
Best Local Similarity	63.8%;	Pred. No. 1e-186;		
Matches 1012;	Conservative 0;	Mismatches 570;	Indels 3;	Gaps 1;
Qy	484	CAGCTGGAAGACTTACATTTGAAGGTTGGCCTTCGCTGCTTGCACCAAGAGACTGTGAAGA	543	
Db	1023	CAGTGGGAATCGGTACCTGCTCCCGGCTTCCCATGAAAATTGACATCCATCCCTGATGA	1082	
Qy	544	CTTGGACCTCAACATCAAGTACTCTGCGATGAAGAAATGCCAAAATCTTCTTTAAAGCCCA	603	
Db	1083	CATGGAGCCAAATGTCGATACTCAGACCAACCAAGACGATCTCGCTGCTCTTCAATGGCAT	1142	
Qy	604	CTCGCGTATACGGAGCTGAAAGTCAAGGGCTCTCGACGGCACAGACTCTCTGGAGGAG	663	
Db	1143	CCCTGCGTCTCTGGGAATGAAGCTTCGAGGGCTCTTGATCGAAGGGCTCTCTGGAAGA	1202	
Qy	664	TCTGAGGGAGATGAAGAAGGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGATATGTGT	723	
Db	1203	GCTGGATGATGCAGAAACATCTTCTGTGCCATAAGACCTTCACGACAAGTATGTCAC	1262	
Qy	724	TGCACACTGGCAGGAAGATGCTTCTTTCGCCCTCCAGGTTCTTAATGGCATCAACCCGT	783	
Db	1263	AGAGCACTGGTGAAGATCACTCTTTTGGGTACCACTACCTGAATGGTGTCAATCCCGT	1322	
Qy	784	CTTGATTTCGGCGGTGCACAGTCTCCCAAAACAACTTCCCGGTCACTCATGAATAATGGTGGC	843	
Db	1323	CATGCTCACTGATCTCTAGCTTGCCAGCAAGCTGCTGTCAACCAATGACATGTTGGC	1382	
Qy	844	CCCAGTCTGGGCCCTGGAACCACTGTGCAAGGTGAGTTGGAGAAGGGCTCCCTGTTCCT	903	
Db	1383	CCCCCTTGTGGACAGGACACATGCCTGCACAGAGAGTAGAGAGGGGGAAACATCTTCCT	1442	
Qy	904	GGTGGATCATGGCAATTTCTTCTGGAGTCCACACCAACATCCTCAATGGAAGCCTCAAGT	963	
Db	1443	AGCGGAATACGTGGATCTCTGGCGGAGGGCCCCACCACCTGCTTAAACGGCCGCCAGCAGTA	1502	
Qy	964	CTCTGCAAGCCCCGATGACCCCTGTTTACACCAAGAGCTCAGGGTTCGGGACCCCTGCTCCCAT	1023	

1503	CGTGGCGGCCCACTGTGCGCTGTGTGTGCTCAGCCCCCAG---GGGGCGCTGTGTGGCCCTT	1555
1024	TGCCATTCAGGCTCAAAACAGAGCTCCCGGGCCAGACAACCCCATCTTCCTGCCCCAGCGATGA	1083
1560	GGCCATCCAGCTCAGCCAGAGACCCCGGGCTGTGACAGCCCATCTTCCTGTGCCCACTGACTC	1619
1084	CAGGTGGAGCTGGTTGCTGGCCAAAGACTTGGGTTCCGAATTCCTGAGTTTTCATCCATGA	1143
1620	CGAATGGGACTTGGCTGTGTGGCCAAAGACGTGGGTGGCGAACTCTGAGTTTCTGGTGGACGA	1679
1144	GGCTGTCCACATCTGTGTGCATGCCCATCTGATCTCCAGAAAGTCTTTGCTTGGCCACATT	1203
1680	AAACAACAGCAGCTTTCTGTGCGACGCAATTTGCTGTGCGAGGCTTCGCGCATGGCCAGCT	1739
1204	AGCTCAGCTGCTAGTGCTCACCCCTCTCTTCAAGCTATTGATTCCTCACTTCGATTCGATAC	1263
1740	GGCCAGCTTGCCTCTGCCACCCCATCTACAGCTCTCTACTCCCCACACTCGATACAC	1799
1264	ACTGCACATCAACAGCTTTGCCCGGGAGCTGTCTGTTGCCCCCTGGGAAGTTGATAGACAA	1333
1800	GCTGCAGGTGAACACCATCGCGAGGGCCAGCTGTCTCAACCCCGAGAGGCGCTCGTGGACCA	1859
1324	GTCCACAGGCTTGGCATCTGGGGAGTTCTCTGACCTGTATAAGAGAAACATGGAGCAGCT	1383
1860	GGTCAGCTGCATCGGGAGGCAAGGCTCTATCTACCTCATGACGACGGGCTTGCCCCACTT	1919
1384	GAACACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCGAGGCTGTGGGAAGACATCCC	1443
1920	CACCTACACCAATTTCTGCCCTTCGGACAGCTGCGGGCCCGGGCGTCTGGCTATCCC	1979
1444	AGGCTACTATTACCGAGATGATGGATGCGAGATCTCGGGGGCAATAAAGAGTTTGTCTC	1503
1980	CAACTACCACTACCGAGACGACGCGCTGAAGATCTGGCGGCGCAATTGAGAGCTTTGTCTC	2039
1504	TGAATAGTCAGCATCTACTATCCAAGTGCACATCCGTCGAAGATGCCAAGAGCTCCA	1563
2040	AGAAATCGTGGGCTACTATTATCTCCAGTGCATCTGTGCGAGCAGGATTCGAGGCTGCA	2099
1564	GGCTGGGTGAGGAGATCTTCTCTGAGGGCTTCCTCGGCCGAGAAAGCTCAGGTATGCC	1623
2100	GGCTTGACTGGCGAGATTTTGTCTAGGGGTTCTGGGCGGGAAAGCTCAGTTTCCC	2159
1624	CTCTTTTGTGGATACC GGGAAGCCCTGGTCCAGTATATCACCATGGTGATTCACCTG	1683
2160	AAGCGGCTGTGCACCCCGAGGAGATGGTGAAGTTCTCTCATGCAATCATCTTCAATTG	2219
1684	CTCAGCAAGCATGACGCTGTCAAGTCAGGCGATTCGAGCTCTGTGTTTGGATGCCCA	1743
2220	CTTGCCCGACGACGCTGTGTCAACAGTGGGCGACATGATCTTTGGGGGCTTGGATGCCCA	2279
1744	TC TGCCACCTACCATGCACTPACCACCACTACTTCCAAAGCGAGGCGCGGCTGAGAG	1803
2280	TGCTCATCATCTAGCGAGCCCCACCCAGACCAAGGGGACCAACAACCTGAGAC	2339
1804	TTTCTAGCCAGCTCCGAGCAGTTAATTCGTCAAGTTATCATCATTTGCTCTTGCTGCT	1863
2340	TTACTTAGACACCTCCCTCTGAAGTGAACATCAGCTGTAAACAACCTCCTCTTCTGCTG	2399
1864	GCTAAGCGCAGAACTCGGGGACAAAGGCCCCCTGGGCGCATATCCAGATGAACACTTCAC	1923
2400	GGTTAGCCAAAGAACCAAGAGCACGAGGCCCCCTGGGCGACTTACCCAGATGAGCACTTCAC	2459
1924	AGAGGATGCCCCCGGCGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAA	1983
2460	AGAGGAGCCCCGAGGGGAGCATCGCCGCTTCCAGAGCGGCTTGGCCGAGTCTCAAG	2519
1984	GGGCATCAGGGAGAGAAACCGAGGCTTGGCACTGCCCTACACTACCTGGATTCCTCCCT	2043
2520	GGACATCCAGGCGGAACACGAGGTCTGGCACTGCCCTACACTACCTGGACCCCTCCCT	2579
2044	CATTGAGAACAGTGTCTCCATCTAA	2068
2580	CATTGAGAACAGCGTCTCCATCTAA	2604

RESULT 12
US-09-087-727-1
; Sequence 1, Application US/09087727A
; Patent No. 6103496
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and
; FILE OF INVENTION: Nucleic Acids
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (260)..(2362)
US-09-087-727-1

Query Match 17.5%; Score 565.8; DB 3; Length 2469;
Best Local Similarity 60.3%; Pred. No. 3.1e-159;
Matches 955; Conservative 0; Mismatches 627; Indels 3; Gaps 1;

QY	488	TGGAAGACTTACATTGAAGTTGGCTCGCTGCTTACCAGGACACTGTGAAGACTTG	547
DB	788	TGGAATGGCTATATTCGGGATTCCTCAATTCATCAACTTAAAGGCCACCAAGTTCCTG	847
QY	548	GACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTCTTTAAAGCCCACTCC	607
DB	848	AACCTTAATCTCCGCTACTCTCTCTCAAGCGGCTCTCTCTCTCGTCCGCTGGGGCC	907
QY	608	CGGTATACGGAGCTGAAGTCAAGGGCTCTCGGACCGCAGGACTCTGGAGGAGTCTG	667
DB	908	ATGGCACTGGCTTTCAAGTTCGGGCTGTGGACTGCAAACTTCGTGGGAAGAGGCTG	967
QY	668	AGGGAGATGAGAGGCTGTAACTTCGCGAAGACTCAGCAGAGAGATGTGTTGCA	727
DB	968	AAGGACATTAGGAAATTTCCCTGGCAAGAAATCTGCTGCTCCGAGTACGTGGCCGAG	1027
QY	728	CAGTGGCAGGAGATGCTCTTTCGCTCCCAAGTTCTTAAATGGCATCAACCGGTCTG	787
DB	1028	CAGTGGCAGGAGACACTTCTTTGGGTACCAAGTACCTCAACGGGCTCAACCCCGGCTG	1087
QY	788	ATTCGCCGCTGTCAAGTCTCCCAACAACTTCCCGGTCACTGATGAAATGGTGGCCCA	847
DB	1088	ATCCGCCGCTGCACCGGATCCAGCAAGTTCCCGGTCAAGACGACATGGTGGCTCG	1147
QY	848	GTGCTGGGCGCTGGAAACAGTCTGAGGTGAGTGGAGAGGGCTCCCTGTTCTGTTG	907
DB	1148	TTCTCTGGGCGAGGAAACGTGTTGCAAGCGAGCTGGAGAGGGGAAATTTACCTGGCC	1207
QY	908	GATCATGCAATCTTTCTGGAGTCCACACCAATCTCTCAATGGAAAGCTCAGTTCTCT	967
DB	1208	GACTACCCGATCATGGAGGGGATCCCAACCGTGGAGCTCAGCGCGGGAAGCACCAC	1267
QY	968	GCAGCCCGGATGACCTGTGTACACAGAGCTCAGGGTCCGAGCCCTGCTCCCAATGCC	1027
DB	1268	TGCGCCCCCTCTGCTGCTGACATTTTGACCCGAG---GGCAAGATGATGCCATCGCC	1324
QY	1028	ATCCAGCTCAAAACAGATCTCCGGGGCCAGAACCCCATCTTCTCTGCCCGAGATGACG	1087
DB	1325	ATCCAGCTCAGCAGACCCCTGGGCGAGATTTGCCCATCTTCTCTGCCCGAGTCTGAG	1384
QY	1088	TGGAGCTGGTCTGGCAAGACCTGGGTTGCAATTTCTGATTTTACATCATGAGGCT	1147
DB	1385	TGGGACTGGCTAGGCCAAGACGTGGGTACGCTATGCGGAGTTCTCAGGCCACGAGCC	1444

QY	1148	GTACACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGGCTTGGCCACATTACGT	1207
DB	1445	ATCGCCCACTGCTGGAGACACACTCATTTGCTGAGGCTTTCTGCTGGCTTGTGAGG	1504
QY	1208	CAGCTGCTAGTGTACCCCTCTCTTCAAGTATTTGATTTCTCATTTCGGGTACACACTG	1267
DB	1505	AACCTGCCATGTGCCACCCCTCTCAAGTCTCTCATCCCCATACCCGATACACCGTC	1564
QY	1268	CACATCAACAGCTTGGCCGGAGCTGCTGCTGGCCCCCTGGGAAGTTGATAGAACGTC	1327
DB	1565	CAGATCAACAGCAATTTGGCCGGGCGTCTCTCAATGAGGGGGGCTCTCTGCCAAGGC	1624
QY	1328	ACAGCCCTTGGCACTGGGGGATTTCTTGACCTGTAAAGAGAAACATGGAGCAGTGAAC	1387
DB	1625	ATGCTCCCTGGGCGTGGAAAGGCTTTGCTGGGGTGTGTGACGGGCTCTCTCGAGGCTACC	1684
QY	1388	TACTCTGTCTGTCTCTCCCTGAAAGATATCCGAGCCCGAGGTGTGGAAGACATCCAGGC	1447
DB	1685	TATGACAGCTCTTACCTCCCAATGACTTTGTGAGCGTGGGTCCAGGACTGCTGCTGA	1744
QY	1448	TACTATTACGAGATGATGGGATCAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA	1507
DB	1745	TATTACTACCGGATGACAGCTTGGCGGTGTGGAATGCACCTGGAGAACTATGTGACGAG	1804
QY	1508	ATAGTCAGCATCTACTATCCAGTGAACATCCGTCAGATGACATCCGTCAGATGACCAAGAGCTCCAGGCC	1567
DB	1805	ATCATCACCTATTATTATCCCGAGTGACGACCGCTGGAGGGTGTATCCGGAATTCAGTCT	1864
QY	1568	TGGGTGAGGAGATCTTCTCTGAGGGCTCTCTCGCGGAGAAAGCTCAGGTATGCGCTCC	1627
DB	1865	TGGGTGAGGAGATCTTCTCTGAGGGCTCTCTCGCGGAGAGAGCTCAGGTATGCGCTCC	1924
QY	1628	TTGTTGGATACCCGGGAGCCCTGCTCCAGTATATCACCATGTTGATATTCACCTGTCTCA	1687
DB	1925	TGCTTGGCAACCGTCCCTGAGTGTATCGATATGTCACTATAGTCACTACACCTGTCT	1984
QY	1688	GCAAGCATGAGCTGTGCTGAGTTCAGGCGAGTTCGACTCTTGTGTTGGATGCCAATCTG	1747
DB	1985	GCCAAGCAGCTGTGTCTCAACACAGGCGAGATGGAGTTTCCCGCTGGATGCCAATCTC	2044
QY	1748	CCACTACCATGACAGTACCAACCTACTTCCAAAGSCCAGGCCCGCTGAGAGTTTC	1807
DB	2045	CCAGCTCATGCGGAATCCACCGATTCAGACTAAGGGGCTGACCACTCTGGAGACCTTC	2104
QY	1808	ATAGCCAGCTCCAGCAGTTAAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTGCTA	1867
DB	2105	ATGACAGCTTGCCTGGATGTGAACACCACTGTCATCAGCTGCTGGTCTCTGGACCTTC	2164
QY	1868	AGCGAGAACTGGGGGCAAAAGCCCTTGGGCCACTATCCAGATGAACACTTTCACAGAG	1927
DB	2165	AGCGAGAGCTGACGACAGCGCGCCCTGGGACACTTCCCGGACATTCACCTTCGTGGAG	2224
QY	1928	GATGCCCGCGGCAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGC	1987
DB	2225	GAGCCCGCGGAGAGAGATAGAGCGTTCGCCAGCGCCCTGAAACAGATCTCACACGAC	2284
QY	1988	ATCAGGAGAGAGAACCGAGGCTGCGCTGCGCTTACACTTACCTGGATCTCCCTCAT	2047
DB	2285	ATCCGCGAGCAACAGTGCCTTCCCATCCCTTACTACTTGGACCCCGGTGCTGAT	2344
QY	2048	GAGAACAGTGTCTCCATCTAACATC	2072
DB	2345	GAGAACAGCATTTCTATTAGGAGC	2369

RESULT 13
US-09-853-053-1
; Sequence 1, Application US/09853053
; Patent No. 656964
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan
; APPLICANT: Boeglin, William

Query Match	17.5%	Score 565.8	DB 4	Length 2469
Best Local Similarity	60.3%	Pred. No. 3.1e-159		
Matches 955	Conservative 0	Mismatches 652	Indels 3	Gaps 1
Qy	488	TGGAAGACTTTACATTGAAGGTGGCGCTCGCTCGCTTGACACAGAGACTGTGAAGAAGACTTG	547	
Db	788	TGGAATGGCTATATTCCGGGATTTCCCAATTCTCATCAACTTTAAGGCCACCAAGTCTCTG	847	
Qy	548	GACCTCAACATCAAGTACTCTGCGATGAAGAATGCCAAACTCTTTCTTTTAAAGCCCCACTCC	607	
Db	848	AACTTAAATCTCGCTACTCTCTTCTCAAGACGCGCTCTCTTCTTCGTCCGCTGGGGCCC	907	
Qy	608	CGGTATACGAGCTGAAGTCAAAAGGCTCTTGACGCGCACAGAGACTCTCGAGGAGTCTG	667	
Db	908	ATGGCACTGGCTTTCAAAGTCCGGCGCTGTGGAGTGCAAAACATTCGTGGGAAGAGGCTG	967	
Qy	668	AGGGAGATGAAGAAGCTGTGTTAACTTCGCGAAAGACTCCAGCAGCAGAGTATGTGTTGCA	727	
Db	968	AAGACATTAGGAATAATTTTCCCTGGCAAGAAATCTGTCTCTCCGAGTACGTGGCCGAG	1027	
Qy	728	CACGTGGCAGGAAGTGCCTTTCTGCGCTCCGAGTTCCTAAATGGCATCAACCCGCTCCTG	787	
Db	1028	CACGTGGGCAGAGACACTCTTCTTTGGGTACGAGTACCTCAACGCGCTCAACCCCGGCGCTG	1087	
Qy	788	ATTTCGCGCGTGTCAACAGTCTCCAAACAACTTCCCGGTCACTGATGAAATGSGTGGCCCCA	847	
Db	1088	ATCGCGCGCTGCAGCGGATCCACAGACAGTTTCCCGTTCACAGACGACATGGTGGCTCCG	1147	
Qy	848	GTGCTGGGCGCTGGAAACAGTCTGCAGGCTGAGTTGGAGAAGGCTCCCTGTTCTTTGGTG	907	
Db	1148	TTCTGGGCGAGGGAACGTGCTTGCAAGCGAGCTGGAGAAGGGAACATTTACCTGGCC	1207	
Qy	908	GATCATGGCATTTCTTCTGAGTCCACACAAACATCTCTCAATGGAAGACCTCAGTTCTCT	967	
Db	1208	GACTACCGCATCATGGAGGCGATCCCCACCGTGGAGCTCAGCGCGCGGAAGCAGCACAC	1267	
Qy	968	GCAGGCCGATGACCCCTGTTTACACACAGACTCAGGGTCCGAGCCCTGCTTCCCATGCCC	1027	
Db	1268	TGCGCCCCCTCTGCGCTGCTGCATTTTGGACCCGAG--GGCAAGATGATGCCCATGCC	1324	
Qy	1028	ATCAGCTCAAAACAGACTCCCGGCGCAGACAAACCCCATCTTCTTGCCCGCAGATGACAG	1087	
Db	1325	ATCAGCTCAGCCAGACCCCTGGGCGCAGATTGCCCCATCTTCTGCGCCAGTGATTTCTGAG	1384	
Qy	1088	TGGAGCTGGTTGCTGGCCAGACCTGGGTTCCGAATTTCTAGTTTTCATCTCCATGAGGCT	1147	
Db	1385	TGGAGCTGGCTGTAGCCCAAGACGTGGGTACGTTATGCGGAGTTCTACAGCCACGAGGCC	1444	
Qy	1148	GTCAACATCTGCTGCAATGCCCATCTCATTTCCAGAACTCTTTGCTCTGGGCCACATTAAGT	1207	
Db	1445	ATCGCCACCTGCTGGAGACACACCTCATTTGCTGAGGCCCTTCTGCTGGCCTTGTCTGAGG	1504	
Qy	1208	CAGCTGCTAGGTGTACCCCTCTCTTCAAGTATTGATTCCCTCACTTCGGTACACACTG	1267	
Db	1505	AACTTGCCCATGTGCCACCCCTCTACAAGCTCCTCATCCCCCATACCCGATACACCGTCT	1564	
Qy	1268	CACATCAACACGCTTGCCCGGAGCTGCTGTTGSCCCCTGGGAAGTTGATAGACAAGTCC	1327	

NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-155

Query Match 17.5%; Score 565.8; DB 4; Length 2469;
Best Local Similarity 60.3%; Pred. No. 3.1e-155;
Matches 955; Conservative 0; Mismatches 627; Indels 3; Gaps 1;

QY 488 TGGAGAGCTTACATGAAAGTTGGCTCGCTCGCTTGACACGAGACTGTGAAGACTTG 547
DB 788 TGGATGCTATATCCGGATTCCTCAATTCATCAACTTAAAGCCACCAAGTTCTG 847
QY 548 GACCTCAACATCAAGTACTCTCGATGAAGATGCCAAACTCTCTTTAAAGCCCACTCC 607
DB 848 AACTTAAATCTCCGCTACTCTCTTCAAGACGGCTCTCTTCTCGTCCGCTGGGGCC 907
QY 608 GGTATACGGAGCTGAAAGTCAAGGGCTCTCGHACCGACAGGACTCTGGAGGAGTCTG 667
DB 908 ATGGCACTGGCTTCAAGAGTCGGCGCTGTGGACTGCAAAACATTCGTGGAAGAGGCTG 967
QY 668 AGGAGATGAGAGCTGTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA 727
DB 968 AAGGACATTAGGAAATTTTCCCTGGCAAGAAATCTGTCTCGAGTACGTGGCCGAG 1027
QY 728 CACTGGCAGGAGATGCTCTTCTCCCTCCAGTTCTTAATGGCATCAACCCGCTCCTG 787
DB 1028 CACTGGCAGGAGACACTTCTTTGGGTACCGTACTCAAGGGGTCAAACCCGCTG 1087
QY 788 ATTGCGCGCTGTCAAGTCTCCCAACAACTTCCCGGTCACTGATGAATGGTGCCCA 847
DB 1088 ATCCGCGCTGTCAAGAGTCCAGACAAAGTTCCCGGTCAAGACGACATGTGGCTCG 1147
QY 848 GTGCTGGCCCTGGAGCAGTCTGAGCTGAGTTGGAGAGGGCTCCCTGTTCTTGGT 907
DB 1148 TTCTTGGCGAGGAACTGTGTGAAGCGAGCTGGAGAGGGGAAATTTACCTGGCC 1207
QY 908 GATCATGCTATCTTCTGAGTCCACCAACATCTCAATGGAAGCCCTCAGTTCTCT 967
DB 1208 GACTACCGCATATGGAGGATCCCAACCGTGGAGCTCAGCGCGGGAAGCAGCAC 1267
QY 968 GAGCGCCGATGACCTGTATACAGAGCTCAGGGTCCGACCCCTGCTCCCATGGCC 1027
DB 1268 TGGCGCCCTCTGCTGTGCTTGGACTTGGACCGAG--GGCAAGATGATGCCATGCC 1324
QY 1028 ATCCAGCTCAACAGACTCCCGGCGCAGACACCCATCTTCTGCGCAGGATGACAG 1087
DB 1325 ATCCAGCTCAGCAGACCCCTGGGCGCATTTGCCCATCTTCTGCGCCAGTATCTGAG 1384
QY 1088 TGGAGTGGTGTGCGCAAGACCTGGGTTCGCAATCTGAGTTTACATCATGAGCT 1147
DB 1385 TGGAGTGGTGTGCTAGCAGAGCTGGGTAGCTATGCGGAGTCTACAGCAGAGGCC 1444
QY 1148 GTCACATCTGCTGATGCCCATCTGATTCAGAAAGTCTTGGCTGGCCACATTCGT 1207
DB 1445 ATCGCCCACTGTGGAGACACACCTCATTTGTGAGGCTTCTGCTGCTGCTGAGG 1504
QY 1208 CAGTGGCTAGGTGTCACCTCTCTTCAAGTATGATTCCTACATTCGGTACACATG 1267
DB 1505 AACCTGGCCATGTGCGACCCCTCTACAAAGTCTCTATCCCCCATACCCGATACAC 1564
QY 1268 CACATCAACAGCTTGGCGGAGCTGTGCTGCTGCGGAGTGTGATGACAGATCC 1327
DB 1565 CAGATCAACAGATTTGGCGGCGCTTCTCTCAATGAGGGGGCTCTCTGCCAGGGC 1624
QY 1328 ACAGGCTTGGCACTGGGGGATTTCTGACCTGTATAAGAGAAACATGGAGCAGCTGAAC 1387
DB 1625 ATGTCCCTGGGCGTGAAGGCTTTGCTGGGGTGTGATGACGGGCTCTGCGAGCTCAC 1684
QY 1388 TACTGTCTGTGTCTCTCCCTGAAGATATCCAGAGCCCGAGGTGTGGAAGACATCCAGGC 1447

DB 1685 TATGACAGCTTACTCTACCTCCCCAATGACTTTGTGAGCGTGGGGTCCAGAGCTGCTGGA 1744
QY 1448 TACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA 1507
DB 1745 TATTACTACCGGATGACAGCTTGGCGGTGTGAATGCACTGGAGAAAGTATGTGACGGAG 1804
QY 1508 ATAGTACGATCTACTATCCAAAGTGACACATCCGTCCAAAGATGACCAAGAGCTCCAGGCC 1567
DB 1805 ATCATCACTATTATATCCCGAGTGACGACGCGCTGGAGGGTGTATCCGGAATTCAGTCT 1864
QY 1568 TGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGGAGAAAGCTCAGGTATGCTCTCC 1627
DB 1865 TGGGTGAGGAGAAATTTAAAGAGTGTCTCTCGGCGGAGAGCTCAGGCTTCCCTAGG 1924
QY 1628 TTGTTGATACCCGGGAAAGCTTGTTCAGATATACCATATGATGGTGTATATCACTGTCTCA 1687
DB 1925 TGCTTGGAAACCGTGTGAGCTGATCCGATATGATATAGTATCATACACCTGTCTCT 1984
QY 1688 GCCAAGCATGCGCTGTCTGAGGCGCTTCCAGTCTTCTGTTTGGATGCCAATCTG 1747
DB 1985 GCCAAGCAGCTGTCTGTCACACAGGCGCAGATGGAGTTTCCGCTGGATGCCAATCTC 2044
QY 1748 CCACCTACCATGAGCTTACCAACCTACTTCCAAAGGCCAGGCCCGCTGAGAGTTTC 1807
DB 2045 CCAGCTTCATCGGAATCCACCGATTCAGACTAAGGGGTGACCACTCTGGAGACCTTC 2104
QY 1808 ATAGCCACGCTCCAGCAGTTAAATTCGTCAAGTTTATCACATCATTTGCTCTCTGGCTGTA 1867
DB 2105 ATGGACACGTTTCCGGATGTGAAGACACAGCTGCATCAGCTGTGCTCTGGACCTTC 2164
QY 1868 AGCCAGAACTTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACACTTTCACAGAG 1927
DB 2165 AGCCGAGAGCTGACGACGAGCGGCCCTTGGGACACTTCCCGGACATTCACCTCTGTTGGAG 2224
QY 1928 GATCCCGCCGGGGAAGCGTGTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGCG 1987
DB 2225 GAGCCCGCGGAGAGCATAGAGCGTTCGCGCAGCGCTGAAACAGATCTCACACGAC 2284
QY 1988 ATCAGGAGAGGAAACCGAGGCTTGGCCTGCTGCTTACCTTACCTTGGATCTTCCCTCAT 2047
DB 2285 ATCCGCGAGCGCAACAAGTGTCTTCCCATCCCTTACTTACTTGGACCCGCTGCTGAT 2344
QY 2048 GAGAACAGTGTCTCCATCAATC 2072
DB 2345 GAGAACAGCATTTCTATTAGGAGC 2369

RESULT 15

US-09-547-435-11
; Sequence 11, Application US/09547435
; Patent No. 6582957

GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander, Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
FILE REFERENCE: 7705.0009-00000
CURRENT APPLICATION NUMBER: US/09/547,435
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
US-09-547-435-11

Query Match 14.5%; Score 466.2; DB 4; Length 1383;
Best Local Similarity 61.4%; Pred. No. 2.2e-129;

Matches		766;	Conservative	0;	Mismatches	478;	Indels	3;	Gaps	1;
QY	484	CAGCTGGAAAGACTTACATTTAAAGTTGGCTCGCTGCTTGACACAGAGACTGTGAAGA	543							
Db	90	CAGTGGAAATCGTACCTCGCCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA	149							
QY	544	CTTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTTTAAAGCCCA	603							
Db	150	CATGGAGCCCAATGTTTCGATACTCAAGCCACCAAGACGATCTCGCTCTCTCAATGCCAT	209							
QY	604	CTCCGGTATACGGAGCTCAAAAGTCAAAAGGGCTCTGGACCCACAGGACTCTGGAGGAG	663							
Db	210	CCCTGGCTCCTTGGGAATGAAGCTTCGAGGGCTGTTGGATCGAAGGGCTCTGGAAGAA	269							
QY	664	TCTGAGGGAGATGAGAAGCTGTTTAACTTCCGGAAGACTCCAGCAGCAGAGATATGTGTT	723							
Db	270	GCTGGATGACATGCAGAACATCTTCTGGTGCCTAAGACCTTTCACGACAAAGTATGTAC	329							
QY	724	TGACACTGGCAGGAAGATGCCTTCTTCCCTCCCAAGTTCCTTAATGGCATCAACCCGGT	783							
Db	330	AGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCAAGTACCTGAATGGTGTCAATCCCGT	389							
QY	784	CTGTATTCCCGCTGTACAGTCTCCAAACAACTTCCCGGTCACTGTATGAAATGTTGGC	843							
Db	390	CATGCTCCACTGCATCTCTAGCTTGCCCAAGCTGCCCTGTCCCAATGACATGGTGGC	449							
QY	844	CCAGTGTGGGCCCTGGAAACAGCTCTGCAGGCTGAGTTGGAGAAAGGGCTCCCTGTTCT	903							
Db	450	CCCTTGTCTGGNACAGGACACATGCTGTCAGACAGAGCTAGAGAGGGGAAACATCTTCT	509							
QY	904	GGTGGATCAATGGATTTCTTGGAGTCCACACCAACATCTCTCAATGGAAAGCCTCAGTT	963							
Db	510	AGCGGACTACTGGATCCTGGCGAGGCCCCACCCACTGCTTAAACGGCCGCGCAGCAGTA	569							
QY	964	CTCTCAGCCCCGATGACCTGTTACACAGAGCTCAGGGTCGGGACCCCTGTTCCCAT	1023							
Db	570	CGTGGCCGCCCTCACTGTGCTGTGCTGAGCCCCAG---GGGGCGCTGGTGGCCCTT	626							
QY	1024	TGCCATCCAGCTCAAAACAGACTCCCGGGCCAGACACCCCATCTTCTGCCCAGCGATGA	1083							
Db	627	GGCCATCCAGCTCAGCCAGACCCCGGGCTGACAGCCCCATCTTCTGCCCACTGACTC	686							
QY	1084	CAGTGGGACTGGTTGCTGGCAAGACCTGGGTTGCAATTTCTGAGTTTTCATCCATGA	1143							
Db	687	CGAATGGGACTGGCTGCTGCGCAAGACGTGGGTGCGCAACTCTGAGTTCTGTGTGCACGA	746							
QY	1144	GGCTGTACACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCTTGGCCACATTT	1203							
Db	747	AAACAAACGCACTTTCTGTGACGCAATTTGTGTGGAGGGCTTCGCCATGGCCACGCT	806							
QY	1204	AGTCAAGCTGCCCTAGGTGTACCCCTCTTCAAGCTATTGATTTCTTCATTCGGTACAC	1263							
Db	807	GGCCAGCTTGGCTGTGCCACCCCATCTACAGCTCCTACTCCCCCACTCGATACAC	866							
QY	1264	ACTGCACATCAACACGCTTCCCGGAGGTGCTGTTGGCCCTGGGAAAGTTGATAGCAA	1323							
Db	867	GCTGCAGGTGAACACCATCGGAGGGCCACGCTGCTCAACCCCGAGGGCTCGTGGACCA	926							
QY	1324	GTCCACAGGCTTGGCACTGGGGGATTCTGACCTGATTAAGAGAAACATGGAGCGCT	1383							
Db	927	GGTACGCTCATCGGAGGCAAGGCCCTCATCTACCTCATGAGCACGGGCTTGCCCACTT	986							
QY	1384	GAACTACTCTGCTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCCC	1443							
Db	987	CACCTACCAATTTCTGCTTCCGACAGCTGCGGGCCCGGGCTCTGGCTATCCC	1046							
QY	1444	AGGCTACTATTACCGAGATGATGGGATGAGATCTCGGGGGCAATAAAGAGCTTTGTCTC	1503							
Db	1047	CAACTACCACTACCGAGACGACGGCCCTGAAGATCTGGGGGCCATTGAGAGCTTTGTCTC	1106							
QY	1504	TGAAATAGTCAGCATCTACTATCCAGTGCACATCCGTCCAAGATGACCAAGGCTCCA	1563							
Db	1107	AGAAATCGTGGGCTACTATTATCCCAAGTACCGCATCTGTGCAGAGGATTCGAGGTGCA	1166							

Search completed: July 19, 2005, 21:32:02
Job time : 364.769 secs

QY	1564	GGCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTATGCC	1623							
Db	1167	GGCCTGGGACTGGCGAGATTTTGTCTCAGGCGTTCTGGGCCGGGAAAGCTCAGGTTCCC	1226							
QY	1624	CTCCTTGTGTGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTG	1683							
Db	1227	AAGCGGCTGTGCACCCCGAGGAGATGTTGAAGTTCCTCACTGCAATCTTCAATTG	1286							
QY	1684	CTCAGCCCAAGCATGTCAGCTGTCTCAGTTTCAGGCCAGTTTCGACTCTTTGTG	1730							
Db	1287	CTCTGCCCAGCACGCTGCTGTCAACAGTGGGCGAGGACGGCAGAGGTG	1333							

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 18, 2005, 21:49:42 ; Search time 28.3348 Seconds
(without alignment)
2298.893 Million cell updates/sec

Title: US-10-688-676A-4
Perfect score: 3604
Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTLDPPLIENSVISI 677

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No., is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451.5	40.3	674	2	arachidonate 5-lip
2	1442.5	40.0	674	1	arachidonate 5-lip
3	1429	39.7	670	1	arachidonate 5-lip
4	1249	34.7	663	1	arachidonate 12-lip
5	1224	34.0	663	1	arachidonate 12-lip
6	1192	33.1	663	1	arachidonate 12-lip
7	1187	32.9	663	2	arachidonate 12-lip
8	1186.5	32.9	662	1	arachidonate 15-lip
9	1177	32.7	663	1	arachidonate 12-lip
10	1176	32.6	663	2	arachidonate 12-lip
11	1164	32.3	663	1	arachidonate 12-lip
12	1144	31.7	663	1	arachidonate 15-lip
13	1044.5	29.0	1066	2	arachidonate 8-lip
14	592	16.4	685	2	probable lipoxigen
15	555	15.4	914	2	probable lipoxigen
16	541	15.0	862	2	lipoxigenase (EC 1
17	540	15.0	926	2	probable lipoxigen
18	538	14.9	908	2	lipoxigenase (EC 1
19	537.5	14.9	862	2	lipoxigenase (EC 1
20	536	14.9	876	2	probable lipoxigen
21	531	14.7	861	2	lipoxigenase (EC 1
22	523.5	14.5	876	2	lipoxigenase (EC 1
23	521	14.5	839	2	lipoxigenase (EC 1
24	521	14.5	853	2	lipoxigenase (EC 1
25	520	14.4	856	2	lipoxigenase (EC 1
26	519.5	14.4	858	2	lipoxigenase (EC 1
27	519.5	14.4	859	1	lipoxigenase (EC 1
28	518	14.4	853	2	lipoxigenase (EC 1
29	516.5	14.3	864	2	lipoxigenase (EC 1

30	513.5	14.2	857	2	S01864	lipoxigenase (EC 1
31	513	14.2	864	1	S07075	lipoxigenase (EC 1
32	511.5	14.2	599	2	S18612	lipoxigenase (EC 1
33	511.5	14.2	864	2	S13381	lipoxigenase (EC 1
34	509.5	14.1	741	2	S18906	lipoxigenase (EC 1
35	506	14.0	917	2	B96699	probable lipoxigen
36	505.5	14.0	859	2	T06429	lipoxigenase (EC 1
37	505	14.0	517	2	T06274	probable lipoxigen
38	505	14.0	936	2	T06190	lipoxigenase (EC 1
39	503.5	14.0	861	1	S01142	lipoxigenase (EC 1
40	502.5	13.9	877	2	T10085	lipoxigenase (EC 1
41	500.5	13.9	865	2	T11852	lipoxigenase (EC 1
42	498	13.8	868	2	S56655	lipoxigenase (EC 1
43	495.5	13.7	878	2	S74207	lipoxigenase (EC 1
44	495	13.7	862	2	S22153	lipoxigenase (EC 1
45	495	13.7	865	1	DASYL1	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1
149479
arachidonate 5-lipoxigenase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49479
R:Chen, X.S.; Naumana, T.A.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.
J. Biol. Chem. 270, 17993-17999, 1995
A:Title: cDNA cloning, expression, mutagenesis, intracellular localization, and gene chr
A:Reference number: A57186; MUID:95355399; PMID:7629107
A:Accession: I49479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-674 <RES>
A:Cross-references: UNIPROT:P48999; GB:L42198; NID:g886332; PIDN:AAC37673.1; PID:g886333
C:Genetics:
A:Gene: Alox5
C:Superfamily: arachidonate 5-lipoxigenase

Query Match 40.3%; Score 1451.5; DB 2; Length 674;
Best Local Similarity 42.3%; Pred. No. 3.8e-105; Indels 15; Gaps 6;
Matches 289; Conservative 133; Mismatches 246;

Qy	1	MAKCRVRVSTGEACGAGTWDKVSIVGTGHSPLVDH-LGKEFSAGASEDFEVTLPQ	59
Db	1	MPSYTVVATGSGWQFAGTDDYVILSLIGSAGSEKHLDDKAFYNDFERGAVDSYDVTVDE	60
Qy	60	DVGTVMLRVHKAPPEVSLPLMSFRSDFWFELEWLPAAALHFPYQWLEGAGELVL	119
Db	61	ELGSIYLVKIEKR-----KYWLHDDWLYKTYTLKTPHGDYIEFFPCYRWITGEIVL	112
Qy	120	REGAAKVSODDHPHTLQDQKQELSRQKMSWNTYIEGWPRCLDHTVTKDLNLKYS	179
Db	113	RDGRALARDQDQIHLKHQRKRELEAKQQRWMEWNPGLSLDAKCHKLPDRDIQFDS	172
Qy	180	MNAKLFKAHSAYTELKVKGLDR-TGLMRSLEMRRLNFRKTPKPAEYVFAHWQEDAF	238
Db	173	EKGVDVFLNYSKAMENLFINRFMEFSSWHDFADEKIFVKISNTISERVKHWQEDLM	232
Qy	239	FASFLNGINPVLIRRHCHSLPNPFPVTDEMVAAPVLPGTSLQAEKGSLSFLVDHGIISG	298
Db	233	FGYQFLNGCNPLIKRCTALPKPLPVTTEWMECSLERQLSLEQVEQEGNIIFVDYELDG	292
Qy	299	VHTNILING-KPQFSAAWTLHQSSGSPLLPIALQKQTPGDPNPILPSSDDTDWDLA	357
Db	293	IDANKTDFCTHQFLAAPICLLYKNL-ANKIVPIAQLNQTPGNSPIPLPDSKYDWDLA	351
Qy	358	KTWVRNSEFYTHEAVTHLLHAHLIPEVFALATLQRLPRCHPLFKLLIPHIYTHLINTLA	417
Db	352	KIWRSDGFHVHQITHLLRHLVSEVFGIANYQLPAVHPLFKLLVAHVAFTHINTYKA	411
Qy	418	RELLVAFKGLDKSTGLGTGFSDLIKRNMBSQLNSVLCPLPEDIRARGV---EDIPGY	474

Db 412 REQLICEYGLFKANATGGGGHVQVQRAVODLTYSLCLFPEAIRKARGMDSTEDMPFYFY 471
QY 475 RDGHWQIWAISFVSEIYIYPSDTSVDDQELQAWREIFSGFLGRSSGMPSLDD 534
Db 472 RDGLGLWEAIRQSFTEVVSIIYENDQVVEEDELQDFVKDVIYVGMKGKAGSPKSIK 531
QY 535 TREALVQYITWVITFCSAKHAASVSGQFDSVVMNPLPPTMQLPPPTSGQARPSFIAT 594
Db 532 SREKLSLEYLTIVIFASQAHAANFGQYDWCWIPNAPTMEAPPTAKGVVTIQIVDT 591
QY 595 LPAVNSSVHIITALLMULLSAEPGQDRPLGHPYDEHFTEDAPRRSVAAPORKLIQISKIRE 654
Db 592 LPDRGRSCHLGAVALSQFQENELFLGMYPEEHFTEKPVKEAMIRFRKNLEAIIISVIAE 651
QY 655 RNRLGLALPYTLDPLPIENSVSII 677
Db 652 RNKKKKLPYYLSPDRIPNSVAI 674

RESULT 2

DAHUAL

arachidonate 5-lipoxygenase (EC 1.13.11.34) [validated] - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence revision 03-May-1996 #text_change 09-Jul-2004
C:Accession: A28117; A37017; A28397; A32104; A38410
R:Dixon, R.A.F.; Jones, R.E.; Diehl, R.E.; Bennett, C.D.; Kargman, S.; Rouzer, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 416-420, 1988
A:Title: Cloning of the cDNA for human 5-lipoxygenase.
A:Reference number: A28117; MUID:88124852; PMID:3422434
A:Accession: A28117
A:Molecule type: mRNA
A:Residues: 1-674 <DIX>
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.
Adv. Prostaglandin Thromboxane Leukot. Res. 19, 466-469, 1989
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.
A:Reference number: A37017; MUID:89320027; PMID:2526519
A:Accession: A37017
A:Molecule type: mRNA
A:Residues: 1-674 <WATS>
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 26-30, 1988
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.
A:Reference number: A28397; MUID:88124804; PMID:2829172
A:Accession: A28397

A:Molecule type: mRNA

A:Residues: 1-535, 'PVGVPRDLRLPARRGQLRPVRLVLLDQCAPNHASPATDQ', 581-674 <RF1>
A:Note: parts of the sequence, including the amino end, were confirmed by protein sequen
A:Note: this sequence report appears to contain a frameshift error
R:Funk, C.D.; Hoshiko, S.; Matsumoto, T.; Radmark, O.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 86, 2587-2591, 1989
A:Title: Characterization of the human 5-lipoxygenase gene.
A:Reference number: A32104; MUID:89202374; PMID:2565035
A:Accession: A32104
A:Molecule type: DNA
A:Residues: 1-50 <FUN>
R:Hoshiko, S.; Radmark, O.; Samuelsson, B.
Proc. Natl. Acad. Sci. U.S.A. 87, 9073-9077, 1990
A:Title: Characterization of the human 5-lipoxygenase gene promoter.
A:Reference number: A38410; MUID:91067649; PMID:2251250
A:Accession: A38410
A:Molecule type: DNA
A:Residues: 1-11 <HOS>
A:Cross-references: GB:M38191
C:Comment: This calcium- and ATP-requiring enzyme catalyzes the first two steps in the h

A:Gene: GDB:ALOX5

A:Cross-references: GDB:132453; OMIM:152390
A:Map position: 10q11.2-10q11.2
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: iron; leukotriene biosynthesis; metalloprotein; oxidoreductase

F:2-674/Product: arachidonate 5-lipoxygenase #status experimental <MAT>
F:368,373,551,555,674/Binding site: iron (His, His, His, Aen, Ile) #status predicted
Query Match 40.0%; Score 1442.5; DB 1; Length 674;
Best Local Similarity 42.6%; Pred. No. 1.9e-104;
Matches 292; Conservative 126; Mismatches 248; Indels 19; Gaps 7;

QY 1 MAKCRVRVSTGEACAGTWDKVSIVSVITHGESPLVPLDH-LGKBFSAGAEEDFVETLPQ 59

Db 1 MPSYTVTVATGSQWFAAGTDDYVLSLVGSAGCSEKHLDDKPFYNDFERGAVDSYDVTVD 60

QY 60 DVGTVLMRVHAKPEVSLPLMSFRSDAFCRWFELEWLPGAALHPFCYOWLEGAGELVL 119

Db 61 ELGEIQLVRIEKR-----KYLNDNDWLYKIITLKTPHGDIYIEFPCYRWITGVVEVL 112

QY 120 REGAAKVSQDHHPTQDROKELSRQKMTYSWKTYIEGWPRCLDHTVTKOLDLNIKYSA 179

Db 113 RDGRAKLARDQIHLKHRRKELETRQKQYRWENWFGFPLSIDAKCHKDLPRDIQFDS 172

QY 180 MNAKLFPFKAHSAYTELKVGGLDDR-TGLWRSLSREMRLEFNPRKTPAAYVFAHWQEDAF 238

Db 173 EKVDFVLNYSKAMENLFINRFMEHMFQSSWDFADFEKIFVKISNTISERVVMNHQEDLM 232

QY 239 PASQFLNGINPVILRRCHSLPNNPVTDEMVAFLPGTSLQAELEKSLFLVDHGIISG 298

Db 233 FGYPFLNGCNFVILRRCTELPEKLPVITTEMVECSLERQLSLEQEQOQNIFFVDFELLDG 292

QY 299 VHTNILNGKP--QPSAAPMTLLHQSSGGPLLPALQIKOTPGDNPFIPLPSDDTDWL 355

Db 293 IDAN--KTDPCQLQPLAAPICLLYKNL--ANKIVPAIQNLPGDENIFILPSDAKYDWL 349

QY 356 LAKTWVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLPKLLIPIHRYTLHINT 415

Db 350 LAKIWRSSDFHVHTIITHLRLTHLVSEVFGIAMYRLQPAVHPIFKLLVAHVRFITAIN 409

QY 416 LARELLVAPGKLIKSTGLGTGGSDLIKRWMEQLNYSVLCPLPEDIRAGV---EDIPGY 472

Db 410 KAREQLICEGLDFKANATGGGHVQVQRAVKOLTYASLCFPEAIKARGMESKEDIPIY 469

QY 473 YRDDGQIWAISFVSEIYIYPSDTSVDDQELQAWREIFSEGLGRESGMPSL 532

Db 470 FYRDDGLGLWEAIRFTFAEVVDIYIEGQVVEEDPELQDFVNDVYVYVWGRKSSGFPKS 529

QY 533 LDTREALVQYITWVITFCSAKHAASVSGQFDSVVMNPLPPTMQLPPPTSGQARPSFI 592

Db 530 VKSRELSEYLTIVIFASQAHAANFGQYDWCWIPNAPTMRAPPTAKGVVTIEQIV 589

QY 593 ATLPVNSSVHIITALLMULLSAEPGQDRPLGHPYDEHFTEDAPRRSVAAPORKLIQISKI 652

Db 590 DTLPRGRSCHLGAVALSQFQENELFLGMYPEEHFTEKPVKEAMARFRKNLEAIVSVI 649

QY 653 RERNGLALPYTLDPLPIENSVSII 677

Db 650 AERNKKKLPYYLSPDRIPNSVAI 674

RESULT 3

A30882

arachidonate 5-lipoxygenase (EC 1.13.11.34) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A30882

R:Balcarek, J.M.; Theissen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, M.V.

J. Biol. Chem. 263, 13937-13941, 1988

A:Title: Isolation and characterization of a cDNA clone encoding rat 5-lipoxygenase.

A:Reference number: A30882; MUID:86330933; PMID:3417684

A:Accession: A30882

A:Molecule type: mRNA

A:Residues: 1-670 <BAL>

A:Cross-references: UNIPROT:P12527; GB:J03960; NID:G205228; PIDN:AAA41538.1; PID:G205229

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: oxidoreductase

Biochem. Biophys. Res. Commun. 172, 1230-1235, 1990
A:Title: Molecular cloning and expression of human arachidonate 12-lipoxygenase.
A:Reference number: A36246; MUID:91058562; PMID:2244907

A:Accession: A36246

A:Molecule type: mRNA

A:Residues: 1-188, 'PCLH', 193-260, 'Q', 262-321, 'S', 323-344, 'C', 346-663 <YOS>

A:Cross-references: GB:M62982; NID:9177106; PIDN:AAA51533.1; PID:9177107

R:Funk, C.D.; Furci, L.; FitzGerald, G.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 5638-5642, 1990

A:Title: Molecular cloning, primary structure, and expression of the human platelet/erythrocyte membrane 12-lipoxygenase.

A:Reference number: A35953; MUID:9032636; PMID:2377602

A:Accession: A35953

A:Molecule type: mRNA

A:Residues: 1-260, 'Q', 262-321, 'S', 323-388, 'P', 390-663 <FUN>

A:Cross-references: GB:M35418; NID:9189773; PIDN:AAA60056.1; PID:9189774

R:Husain, H.; Shornick, L.P.; Shannon, V.R.; Wilson, J.D.; Funk, C.D.; Pentland, A.P.; Am. J. Physiol. 266, C243-C253, 1994

A:Title: Epidermis contains platelet-type 12-lipoxygenase that is overexpressed in germinal vesicles.

A:Reference number: I51906; MUID:94136572; PMID:8304420

A:Accession: I51906

A:Molecule type: mRNA

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-427 <RES>

A:Cross-references: GB:S68587; NID:9545223; PIDN:AAD14020.1; PID:94261720

A:Experimental source: skin, epidermal cells

A:Accession: I64836

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-396, 'V', 398-427 <RE2>

A:Cross-references: GB:S68588; NID:9545222; PIDN:AAD14021.1; PID:94261721

C:Genetics:

A:Gene: GDB:ALOX12

A:Cross-references: GDB:127547; OMIM:152391

A:Map position: 17p13.1-17p13.1

C:Function:

A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,10E,14Z) - (12S) - 12-H

A:Pathway: leukotriene biosynthesis

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidoreductase

F:360,365,540,544,663/Binding site: iron (His, His, Asn, Ile) #status predicted

Query Match 34.0%; Score 1224; DB 1; Length 663;

Best Local Similarity 37.8%; Pred. No. 2.2e-87;

Matches 260; Conservative 126; Mismatches 267; Indels 34; Gaps 9;

QY 1 MAKCRVSTGEACGAGTWDKVSIVGTHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60

DB 1 MGRYIRVATGAWLFGSGNVRVQLVVGTRGAEI-----ELQRPARGEEEFDDHVD 56

QY 61 VGTVMRLRVHKAPEVSLPLMSFRSDAFCRWFPELWLPQAA--LHFPQCYQWLEGAGELV 118

DB 57 LGLLQFVLRKHHV-----DDAFCDRTVQV--FGACAEVAFPCYRVVQGEDILS 107

QY 119 LRGAQVSWQDHPHTLQDQKELSRQKMSYKVTYIGWPRCLDHTETVKOLDLNIKY 178

DB 108 LPEGTARLPQDNLDMFQKHREKELDRQIYCWATWKEGLPLTIAADRKDDLPNNRPH 167

QY 179 AMKNKLPFKAHSAYTELVKGLDRTGLWRSIRMRRLFNFRKTPAAEVVFAHWQEDAF 238

DB 168 EEKRLDFEWTLKAGALEMAKRVYITLLSSNCLUEDFDQIFWGQKSALEAKVRCQWQDEL 227

QY 239 FASQFLNGPVLIRCHSLPNNFPVTDENVAPVLGFG-----TSIQALEKSGSLVDH 293

DB 228 FSVQFLNGANPMLRRSTSLPSRL-----VLPFGMEELRAQLEKELQNGSLFEADF 278

QY 294 GILSGVHTNINLKPQFSAAPMTLHQSGSGPLPIALQKQTPGPDNP---IFLPSDD 350

DB 279 ILDDGIPANVIRGEQYLAAPVLM--KMBPNGKLQPMWIQI--QPNPSSPTPTLFLSDP 336

QY 351 TWDMIAKTWRNSFEYIHAETHLAHLIPEVFAATLRLQPRCHPLFKLLIPIRYT 410

DB 337 PLAWLLAKSWRNSDFQLHEIQYHLLNTHLVAEIVAVATMRCPLGHLPIFKLPIHIRT 396

QY 411 LHINTLARELIVAPCKLIDKSTGLGTGGFSDLIKRNQMLNYSVLCIPEDIPARGVEDIP 470

DB 397 MEINTARTQLTISGGIFDKAVSTGGGGHVQLVLRRAAAQLTYCSLCPDDLADRLGLLP 456

QY 471 GYYRDCQWQIGATKSPVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGLGREGSSGMP 530

DB 457 GALYAHDAIRLWEIARIIVEGIVHLFYORDDIVKGDPLQAWCREITEVGLCOADRGP 516

QY 531 SILDTREALVOYITWVIFETCSAKHAAVSSGQFDSVMMPNLPPTMQLPPTTSKGOARPE 590

DB 517 VSFQSQSLCHFLTMCVCTTAQHAAINQGLQDMVAVPNAPCTWRMPPTTKEDVTWAT 576

QY 591 FIATLPAVNSSYHIALWLLSAEPDGRDPLGHPDEHFTEDAPRRSVAAPFORKLIQSK 650

DB 577 VMGSLPDRVQACLOQWAIWSHLSSRRQPMVPLGHHKERYFSGPKPRAVLNQFRTDLEK 636

QY 651 GIRENRGALPYTYLDPPLIENSYSI 677

DB 637 EITARNEQDWPYELKFSIENSVTI 663

RESULT 6

B54075

Arachidonate 12-lipoxygenase (EC 1.13.11.31), leukocyte [validated] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: B54075; I49439

R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.

J. Biol. Chem. 269, 13979-13987, 1994

A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure

A:Reference number: A54075; MUID:94245713; PMID:8188678

A:Accession: B54075

A:Molecule type: DNA; mRNA

A:Residues: 1-663 <CHE>

A:Cross-references: UNIPROT:P39654; GB:U04331; NID:9467216; PIDN:AAA20658.1; PID:9467217

A:Experimental source: strains C57BL/6 and ICR, spleen leukocytes

A:Note: removal or substitution of Ile-663 abolished enzyme activity

R:Freire-Moar, J.; Alavi-Naseab, A.; Ng, M.; Mulkins, M.; Sigal, E.

Biochim. Biophys. Acta 1254, 112-116, 1995

A:Title: Cloning and characterization of a murine macrophage lipoxygenase.

A:Reference number: I49439; MUID:95110857; PMID:7811740

A:Accession: I49439

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-36, 'N', 38-118, 'Q', 120-396, 'N', 398-663 <RES>

A:Cross-references: GB:L34570; NID:9509607; PIDN:AAA64930.1; PID:9763530

C:Comment: A second arachidonate 12-lipoxygenase from mouse platelets is shown in (PIR:A1

C:Genetics:

A:Map position: 11

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: oxidoreductase

Query Match 33.1%; Score 1192; DB 1; Length 663;

Best Local Similarity 37.5%; Pred. No. 6.9e-85;

Matches 261; Conservative 121; Mismatches 262; Indels 52; Gaps 12;

QY 1 MAKCRVSTGEACGAGTWDKVSIVGTHGSPVPLDHLGKFP--SAGAEEDFEVTL 58

DB 1 MGVIIRVSTGDSVYVAGSNNEVYLWLGQGEA-----SLCKLFRPCRNSEAEFKVDVS 54

QY 59 QDVGTVMRLRVHKAPEVSLPLMSFRSDAFCRWFPELWLP--PGAALHFPQCYQWLEGAGE 116

DB 55 EYLGPLLFVRVQK-----WHYLKEDAWFCNWSIVGKPGQDQSGSEYTPCYRVWQGT 106

QY 117 LVLRGAQVSWQDHPHTLQDQKELSRQKMSYKVTYIGWPRCLDHTETVKOLDLNTK 176

DB 107 LMLPGTGTCTVVEDSQGLFRNHRHELEBERRSLYRWGNWKGDTILNVAATISDL 166

QY 177 YSAMKNKLPFKAHSAYTELVKGLLD-----RTGLWRSIRMRRLFNFRKTPAAEY 228

DB 167 F--REDKRLFEFA-----QVLGTMDTVINFPKNTVTCWKSLLDDPNYVFKSGHTKMAER 218

QY 229 VFAHWQEDAFASQFLNGPVLIRCHSLPNNFPVTDENVAPVLGFG-----TSIQALE 293

Db 219 VNSNKEADFFGYQFLNGANPNVLRKSTCLPARL-----VFPNGEKLQAQDLDEL 269
Qy 284 EKSGLFVDHGLSGVHTNINLNGKPFQSAAPMTLLHQSSGGPLLPPIAIQLK--QTPGPD 341
Db 270 KKGTLFEADFFLDGIGKANVILCSQYLAAPLWML-KLPDQQLPPIAIQLKLPKSTGP 328
Qy 342 NPFLPSPDDTWLAKTWVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQRPCHPLFK 401
Db 329 PPIFTPLPDDMLLAKCWRSSDLQLHQAHLRLVAEFAVATMRCPLSPVHPFK 388
Qy 402 LLIPIRHTLHINTLARELLVAPGKLDKSTGLGTGGFSDLIKRNMEQLNYSVLCPLPEDI 461
Db 389 LVPVHLLTMEINVRADLISERGFQKWSGTGGGHLDLKQAGFTYSSLCPPDDL 448
Qy 462 RARGVEDIPGYRRDGMQINGAIFSVSEIYIYPSDTSVQDDQELQAWVREIFSEGF 521
Db 449 AERGLDDITCFYAKDALQMQVMNRYVGMFDLYKTDQAVQDDYELQSQMCBITEIGL 508
Qy 522 LGRESSGMSLDDREALVOYITWIFTCSAKHAAVSSGQFDSVWMPNLPTMQLPDPT 581
Db 509 QGAQDRGFPTLSQSAQAACHFTMCIPTCTAQHSSIHGLQDWMFYVNPAPCTMELRPPK 568
Qy 582 SKGQARPSFTATLPAVNSSVHIITALLSAPGQDQPLGHYPDEHFTEDAPRESVAF 641
Db 569 TK-DATMEKLMATLNPQSTLIQINVMLLGRQAVMPLQGHSEHPNPPEAKVLKPF 627
Qy 642 QRLTIQISGRIRNRGLALPYTLDPPPLIENSIVI 677
Db 628 REELAALDKIEIRNKSLDIPYELRPSLIVENSVAI 663
RESULT 7
S32825
arachidonate 12-lipoxygenase (EC 1.13.11.31), tracheal - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 13-Jan-1995 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S32825; S77975; A56770
R:de Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.
Am. J. Physiol. 262, L198-L207, 1992
A>Title: Cloning and expression of an airway epithelial 12-lipoxygenase.
A:Reference number: A56770; MUID:92170942; PMID:1533676
A:Contents: tracheal epithelium
A:Accession: S32825
A:Molecule type: mRNA
A:Residues: 1-663 <ACG>
A:Cross-references: UNIPROT:P27479; EMBL:S96247; NID:Q246172; PIDN:AAB21522.1; PID:G2461
A>Note: in the authors' translation residues 441-460 do not match the nucleotide sequence
A:Note: sequence extracted from NCBI backbone (NCBI:96247)
R:de Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.
submitted to the EMBL Data Library, December 1993
A:Reference number: S77975
A:Accession: S77975
A:Molecule type: mRNA
A:Residues: 1-440, 'GLIGVKSSFY', 441-450, 461-663 <DEM>
A:Cross-references: EMBL:S96247
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: leukotriene biosynthesis; oxidoreductase
Query Match 32.9%; Score 1187; DB 2; Length 663;
Best Local Similarity 38.4%; Pred. No. 1.7e-84;
Matches 265; Conservative 126; Mismatches 258; Indels 42; Gaps 15;
Qy 1 MAKCRVRYSTGACAGTWDKVSIVSGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
Db 1 MGLYRVRYSTGSSFCAGNNQVHLVGVHGEAAL-----GNVVRPARKEVFQDVSEY 56
Qy 61 VGTVLMLRVHKAPPEVSLPMSFRSDAFCRWFELEWLPQAA---LHFPYQWLEAGEL 117
Db 57 LGRLLFVKLRK-----HLLS--DDAFCNWSVQV-PGASGNEFRFPYRWVSGDGL 107
Qy 118 VLREGAAKVSQDHPHTTLODQKQELSRQKYSWKTYIBGWPRCLDHTVKDLDLNTKY 177

Db 108 SLPSGTGRVVDPPQLFKKHREBELAERRKYRWGNWKOGLIILNIAGATINDLPVDERF 167
Qy 178 SAMKNAKLFFKXH--SAYTELKVKGLDRTGLWSLSREMRRLFNFRKTPPAEYVFAHQOE 235
Db 168 --LEDKRIDFEASLTGKLADLAIKDSLNIILTKWKSLODDFNIRFCWGQSKLAERVRDSWKE 225
Qy 236 DAFASOFLANGINVLIRCHSLPN--NFPVTDENVAPVLGPGTSLQAELEK---GSLF 289
Db 226 DALFGYQFLNGTNMPLLRSSVRLPARLEFP-----PGMG---ELQAELEKELQOQGLF 275
Qy 290 LVDHGILSGVHTNINLNGKPFQSAAPMTLLHQSSGGPLLPPIAIQLKQTP---GPDNPFL 346
Db 276 EADFSLMGIAKANVILCTQCYVAAPLWML-KLPDQGLLPWAIQL-QLPHKGSPPPLFL 333
Qy 347 PSDTDWMLAKTWVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQRPCHPLFKLLIPH 406
Db 334 PTDPMTWLLAKCWRSSDFQLHSHLLRHLVAEIVATWRCPLSIHMPFKLLIPH 393
Qy 407 IRYTLHINTLARELLVAPGKLDKSTGLGTGGFSDLIKRNMEQLNYSVLCPLPEDIARGV 466
Db 394 LRYTMEINIRARTGLVSDSGVFDQVSTGGGHVELLQAGAFITYSSFCPPDDLDRL 453
Qy 467 EDIPGYRRDGMQINGAIFSVSEIYIYPSDTSVQDDQELQAWVREIFSEGPLGRES 526
Db 454 LGVKSFFAQDALRLWEILSRVYVSLHYKTTDESVRDDIELQAWCEDITEIGLGAQD 513
Qy 527 SGMSPLDTRREALVOYITWIFTCSAKHAAVSSGQFDSVWMPNLPTMQLPDPTSKQOA 586
Db 514 RGFVTLQSKDQLCHFVTCMCIPTCTQGHSSHLQDWSWVNPACTMRLPPPTTK-DV 572
Qy 587 RPESFIATLPAVNSSVHIITALLSAPGQDQPLGHYPDEHFTEDAPRSVAAPQRLI 646
Db 573 TLEKVMATLPNFHOASLQMSITWQRRQPTIMVALGOHEEYFSGPEPKAVLKPFRELA 632
Qy 647 QISKGIRERNRGLALPYTLDPPPLIENSIVI 677
Db 633 ALEKDIIRNAQLDWPYELRPSLIVENSVAI 663
RESULT 8
A31349
arachidonate 15-lipoxygenase (EC 1.13.11.33) - human
A:Alternate names: arachidonate omega-6 lipoxygenase
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: A31349; A28192; S19625; S19577; A61164; B61164
R:Sigal, E.; Craik, C.S.; Highland, E.; Grunberger, D.; Costello, L.L.; Dixon, R.A.F.; N.
Biochem. Biophys. Res. Commun. 157, 457-464, 1988
A>Title: Molecular cloning and primary structure of human 15-lipoxygenase.
A:Reference number: A31349; MUID:89076270; PMID:3202857
A:Accession: A31349
A:Molecule type: mRNA
A:Residues: 1-662 <SIG>
A:Cross-references: UNIPROT:P16050; GB:M23892; NID:G187190; PIDN:AAA36182.1; PID:G307135
A:Experimental source: reticulocyte
R:Sigal, E.; Grunberger, D.; Craik, C.S.; Caughey, G.H.; Nadel, J.A.
J. Biol. Chem. 263, 5328-5332, 1988
A>Title: Arachidonate 15-lipoxygenase (omega-6 lipoxygenase) from human leukocytes. Purifi
A:Reference number: A28192; MUID:88186828; PMID:3356688
A:Accession: A28192
A:Molecule type: protein
A:Residues: 3-16 <S12>
A:Experimental source: leukocyte
R:Izumi, T.; Radmark, O.; Joernvall, H.; Samuelsson, B.
Eur. J. Biochem. 202, 1231-1238, 1991
A>Title: Purification of two forms of arachidonate 15-lipoxygenase from human leukocytes.
A:Reference number: S19577; MUID:92111501; PMID:1662607
A:Accession: S19625
A:Molecule type: protein
A:Residues: 'X', 3-4, 'X', 6, 'X', 8-22, 38-45, 157-162, 'XX', 165-168, 627-631 <IZU>
A:Accession: S19577
A:Molecule type: protein
A:Residues: 'X', 3-25, 27-31 <IZI>

A>Note: there appear to be distinct chromatographic forms, at least one each from reticulor
R; Izumi, T.; Radmark, O.; Samuelsson, B.
Adv. Prostaglandin Thromboxane Leukotriene Res. 21, 101-104, 1990
A:Title: Purification of 15-lipoxygenase from human leukocytes, evidence for the presence
A:Reference number: A61164
A:Accession: A61164
A:Molecule type: protein
A:Residues: 'X', 3-4, 'X', 6, 'X', 8-12, 'X', 14-19, 'T', 21-22 <123>
A:Experimental source: leukocyte
A:Accession: B61164
A:Molecule type: protein
A:Residues: 'X', 3-25, 27-31 <123>
A:Experimental source: leukocyte
C:Genetics:
A:Gene: GDB:ALOX15
A:Cross-references: GDB:132454
A:Map position: 17pter-17qter
C:Function:
A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,11Z,13E)-(15S)-15-h
A:Pathway: leukotriene biosynthesis
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidore
F;360,365,540,544,662/binding site: iron (His, His, His, His, Ile) #status predicted

Query Match 32.9%; Score 1186.5; DB 1; Length 662;
Best Local Similarity 37.6%; Pred. No. 1.9e-84;
Matches 259; Conservative 126; Mismatches 266; Indels 37; Gaps 12;

QY 1 MAKCRVRYSTGEACGAGTWDKVSIVSGTHGESPLVPLDLHLGKEP--SAGAEDEFEVTL 58
DB 1 MGLYRIRVSTGASLVSNNQVLMVQGHGAA-----LGKRLWPARGKETELKVEVP 54

QY 59 QDVGTVMRLRVHKAPEVSLPLMSFRSDAFCRWFLEWLPGAA--LHPFCYQWLEGAGE 116
DB 55 EYLGLPLFVKLR-----HLLKDDAFCNWSVQG--PGAGDEVREPCRVWEGNV 105

QY 117 LVLRGAAGVSWDHHPTLQDQKELSRQKMSYKTYIEGWPRCLDHTETVKDLNLK 176
DB 106 LSLPEGTGRTGSDPQGLFKHREELERRKLYRWGNKDG--LILNAGAKLYDLPLVD 163

QY 177 YSNKNAKLFKHAISA--YTELKVGKLLDRTGLRWLSLRMRRLFNFRKTPAAEYVPAHWQ 234
DB 164 ERLEDRVDVFEVSLAKGLADLAIDKSLNVLTCWKDLDDFNRFWCGSKLAERVRDSWK 223

QY 235 EDALFASQFLNGINPVLRCHSLPNPF--PVTDEMVAFLPGPSTLQAELEKGSFLV 291
DB 224 EDALFGYQFLNGANPVVLRSAHLPARLVFPQMELOA-----QLSEKEGGTLFEA 276

QY 292 DHGILSGVHTNINLNGKQPFAAPMTLLHSGSGPLLPPIAOLK--OTPGPNPFLPSD 349
DB 277 DFLSDGIRKANVILCSQQHLAAPLVML--KLQPDGKLLPMVQLQLPRTGSPPPPLPLPTD 335

QY 350 DTWDMLLAKTWNRNSFYTHEAVTHLLHAHLIPEVPFALATLRLQRPCHPLFKLLPHIRY 409
DB 336 PPMALLAKCVRSSDFQLHQLSHLRGLHMAELFVAVATMRCLPSIHPIFKLIIPHLYR 395

QY 410 TLHINTLARELLVAPGKLDKSTGLGTGGSFSLIKRNMELQNVSVLCLPEDIRARVEDI 469
DB 396 TLEINVRARTGLVSDMGIFDQIMSTCGGHVQLLKQAGAFLYSYSCPPDDDLADRLGLGV 455

QY 470 PGYVYRDDGMQIWAIGKSFVSEIVSYTPSDTSVQDDQBLQAVRVEIFSEGFLGREGSQ 529
DB 456 KSFYQAQDALRLWEIIYRVVGVISLVHYKTDVAVKDDPELQWCRTBITGLQGAQDRGF 515

QY 530 PSLDRTREALVQVITWVITCSAKHAASVSGQFSDSCVWMPNLPPTTQLPPTTSGOARPE 589
DB 516 PVSLOAQDVQCHVETCTCTGQHASVHLGQLDWYSWPNAPCTMRLPPTTK--DATLE 574

QY 590 SFTATLPVNSSSYHIIALWLSAEPQDORPLGHYDEHFTEDAPRRSVAAFORKLIQIS 649
DB 575 TVWATLPNHOASLQNSITWQLGRRQVAVVQGHGEEYFSGPEKAVLKKEFEELALD 634

QY 650 KGIRERNGLALPYTYLDPPLIENSYSI 677
DB 635 KEIIRNAKLDMPYEYLRPSVENSVAI 662

RESULT 9
S30051
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S30051
R:Watanabe, T.; Medina, J.F.; Haeggstroem, J.Z.; Radmark, O.; Samuelsson, B.
Eur. J. Biochem. 212, 605-612, 1993
A:Title: Molecular cloning of a 12-lipoxygenase cDNA from rat brain.
A:Reference number: S30051; MUID:93185682; PMID:8444196
A:Accession: S30051
A:Molecule type: mRNA
A:Residues: 1-663 <WAT>
A:Cross-references: UNIPROT:Q02759; EMBL:L06040; NID:g205212; PIDN:AAA1532.1; PID:g20521
C:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: oxidoreductase

Query Match 32.7%; Score 1177; DB 1; Length 663;
Best Local Similarity 37.2%; Pred. No. 1e-83;
Matches 258; Conservative 127; Mismatches 261; Indels 48; Gaps 11;

QY 1 MAKCRVRYSTGEACGAGTWDKVSIVSGTHGESPLVPLDLHLGKEFSAGAEDEFEVTL 60
DB 1 MGVIYRIRVSTGDSKYAGSNNEVYLMVQGHGEASLGKLLRPCR---SEAEFKVDVSEY 56

QY 61 VGTVMRLRVHKAPEVSLPLMSFRSDAFCRWFLEWL--PGAAHLHFCYQWLEGAGELV 118
DB 57 LGPLLFVRVQK-----WHYLTDDAFCNWSIVKPGDQGSYMFPCYRVVQGRSILS 108

QY 119 LREGAAGVSWDHHPTLQDQKELSRQKMSYKTYIEGWPRCLDHTETVKDLNLKYS 178
DB 109 LPEGTGCTVDESQGLFRHREELERRSLYRWGNKDGSLNVAASISDLVDQRP- 167

QY 179 AMKNAKLFKHAISAYTELKVGKLLD-----RTGLWRSLRMRRLFNFRKTPAAEYV 230
DB 168 -REDKRIEFAS-----QVIGVMDTVVFPINTVTCWKSLLDDFNCVFKSGHTKMAEVR 220

QY 231 AHQEDAFASQFLNGINPVLRCHSLPNPFVTDENVAPVLGPG-----TSLQAELEK 285
DB 221 NSWKEDAFPGYQFLNGANPMVLRKSTCLPARL-----VFPPGMEKLOQLNKELQK 271

QY 286 GSLFLVDHGILSGVHTNINLNGKQPFAAPMTLLHSGSGPLLPPIAOLK--OTPGPNP 343
DB 272 GTLFEADFLDGIKANVILCSQQYLAAPLVML--KLMPDGQLLPPIAQLLEPKTGSTPPP 330

QY 344 IFLPSDDTMDMLAKTWNRNSFYTHEAVTHLLHAHLIPEVPFALATLRLQRPCHPLFKLL 403
DB 331 IFTPSDPPMDMLLAKCVRSSDLQLHQLSHLRGLHMAELFAVATMRCLPSVHPVKLL 390

QY 404 PHIRYTHINTLARELLVAPGKLDKSTGLGTGGSFSLIKRNMELQNVSVLCLPEDIRA 463
DB 391 VPHLLYTMETINVRASDLISERGFDFKAMSTGGGGLDILLKQAGAFLYTCSLCPDDLA 450

QY 464 RGVEDIPGYVYRDDGMQIWAIGKSFVSEIVSYTPSDTSVQDDQBLQAVRVEIFSEGFLG 523
DB 451 RGLDIDETCFYAKDALRLWQIMNRYVVGMPNLYHYKTDKAVQDDYELQSWCRITDIGLQ 510

QY 524 RESGMPSLDRTREALVQVITWVITCSAKHAASVSGQFSDSCVWMPNLPPTTQLPPTTSG 583
DB 511 AQDRGFPTSLQSAQACVFITWCTCTAQHSSVHLGQLDWYFVVPNAPCTMRLPPTTK 570

QY 584 GOARPESTIATLPVNSSSYHIIALWLSAEPQDORPLGHYDEHFTEDAPRRSVAAFOR 643
DB 571 -EATWEKLMATLPNPNQSTLQINNVVLLGRRQVAVVQGHGEEHFPNPEAKVLKCKFRE 629

QY 644 KLIQISKGIRERNGLALPYTYLDPPLIENSYSI 677
DB 630 ELAALQKIEIRNKSLDIPYEYLRPSVENSVAI 663

RESULT 10

152462
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat
C:Species: Rattus sp. (rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jun-1999
C:Accession: I52462
R:Hada, T.; Hagiya, H.; Suzuki, H.; Arakawa, T.; Nakamura, M.; Matsuda, S.; Yoshimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 221-228, 1994
A:Title: Arachidonate 12-lipoxygenase of rat pineal glands: catalytic properties and primary structure
A:Reference number: I52462; MUID:94162305; PMID:8117750
A:Accession: I52462
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-663 <RES>
A:Cross-references: GB:S69383; NID:g545793; PIDN:AAB30132.1; PID:g545794
A:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: oxidoreductase

Query Match 32.6%; Score 1176; DB 2; Length 663;
Best Local Similarity 37.3%; Pred. No. 1.2e-83;
Matches 259; Conservative 125; Mismatches 262; Indels 48; Gaps 11;

QY 1 MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEDEFVTLPDQ 60
DB 1 MGVRIRVSTGDSKYAGNNEVYLWLVGQHGSEASLGKLLRPCR-----SEAEFKVDVSGY 56
QY 61 VGTVMRLRVHKAPPEVSLPLMSFRSDAWFCRWFLEWL--PGAALHFFPCYQWLEAGELV 118
DB 57 LGPLLFVRVQK-----WHYLTDDANFCNWSVKVGDQGSSEYMFPCYRWQGRSILS 108
QY 119 LREGAAKVSQDHPHTLQDQKQKESQKMSYKTYIEGWPCRLDHTVTKDLDLNIKYS 178
DB 109 LPEGTGCTWEDSQGLFKRHEELEERSLYRWGNKDGSLNVAASISDLVDQRF- 167
QY 179 AMKNAKLFKAHSAYTELVKVGLLD-----RTGLWRLSLREMRRLNFRKTPAAEYVF 230
DB 168 -REDKRIEFAS-----QVIGVMDTVVNFPTVTCWKSLLDDFNCVFKSGHTKMAEVR 220
QY 231 AHQWDAFFAGQFLNGINPVLIRCHSLPNPNFPVTDENVAPVLGPG-----TSLOAELEK 285
DB 221 NSWKEDAFGGYQFLNGANPMWLKSTCLPARI-----VFPQMEKLAQLNKELOK 271
QY 286 GSLFLVDHGILSGVHTNLNGKQPSAAPTLLHQSSGSGPLLPATLQK--QTPGDPNP 343
DB 272 GTLPADFFLLDGIKANVLCSQQYLAAPLVML-KLMPDGLLPATLQLELPKGTSTPPP 330
QY 344 IFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAILPEVPALATLRLPCHPLFKL 403
DB 331 IFTPSDPPMDMLLAKCWVRSSDLQHLQALHLLRGLHMAEFVAVATMRCPLSPVHPFKLL 390
QY 404 IPIRYTILHINTLARELVAPGKLDKSTGLGTGGFSDLIKRNMEOQANYSVLCPLPDIRA 463
DB 391 VPHLLYTMEINVRASDLISERGFDAKWSGTGGGHLDLLLQAGAFLYTCLCPDDDLAE 450
QY 464 RGVEDIPGYVYRDDQMGWGAIKSPVSEIVSYIPSDTSVQDDQLQAVREIFSEGFLG 523
DB 451 RGLLDIETCFYAKDALRLQWIMNRVVGWFMNLHYKTDKAVQDDYELQSWCREITDIGQG 510
QY 524 RESSGMPSLDTRREALVQYITWVITCSAKHAUVSSGQFSDCVWMPNLPPTWQLPPTSK 583
DB 511 AQDRGFPTSLQSAQAQCYITWCITCTAQHSVHLGQDLDFWYVFNAPACTMRLPPTTK 570
QY 584 GQARPESTIATLPVNSSSYHIIALWLLSAEPGDQRPGLGHYDDEHFTEDAPRRSVAQR 643
DB 571 -EATMEKLMATLPNPNQSTLQINVMVLLGRQAVMVLPGQHSSEHFFNPKEAKVLKPRE 629
QY 644 KLIQISKIGIRNRGALPYTLDPLPIENSYSI 677
DB 630 ELAALDKIEIRNKSLLDIPYELRPSMVENSVAI 663

RESULT 11

A35087
arachidonate 12-lipoxygenase (EC 1.13.11.31) - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A35087
R:Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.; Tanabe, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 2142-2146, 1990
A:Title: Cloning and sequence analysis of the cDNA for arachidonate 12-lipoxygenase of porcine
A:Reference number: A35087; MUID:90192763; PMID:2315307
A:Accession: A35087
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-663 <YOS>
A:Cross-references: UNIPROT:P16469; GB:M31417
A:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: oxidoreductase

Query Match 32.3%; Score 1164; DB 1; Length 663;
Best Local Similarity 37.9%; Pred. No. 1.1e-82;
Matches 264; Conservative 119; Mismatches 261; Indels 52; Gaps 15;

QY 1 MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEDEFVTLPDQ 56
DB 1 MGLYRVSTGSSFYAGSQVQLWLVQHGAEALGWLCLRP-----ARGKETEFSDV 52
QY 57 LPQDVGTVMRLRVHKAPPEVSLPLMSFRSDAWFCRWFLEWLPGA---ALHPPCYQWLEG 113
DB 53 VSEYLGPLLFVKLRK-----HLLQDDDAWFCNWSVQV--PGANGDEPRFPCCYRWVEG 103
QY 114 AGELVLRGAAKVSQDHPHTLQDQKQKESQKMSYKTYIEGWPCRLDHTVTKDLDL 173
DB 104 DRIISLPEGTARTVDDPPQGLFKRHEELEERSLYRWGNKDGSLNVAASISDLVHLPV 163
QY 174 NIKYSAMKNAKLFKAHSA--YTELVKVGKLDLDRGLWRLSLREMRRLNFRKTPAAEYVFA 231
DB 164 DERF--LEDKRIEAFSLAKGLADLAVKDSLVNLSMNSLDSFNRIFWCGSGKLAQVRD 221
QY 232 HWQEDAFAGQFLNGINPVLIRCHSLPN--NFPVTDENVAPVLGPG--TSLOAELEK--- 285
DB 222 SKEDALFGYQFLNGTNPMLLRHSHVLPARKFP-----PGMEELQAQLEKELQ 270
QY 286 -GSLFLVDHGILSGVHTNLNGKQPSAAPTLLHQSSGSGPLLPATLQKTP---CPD 341
DB 271 GGTLPADFFLLDGIKANVLCSQQYLAAPLVML-KLPDQGLLPVMIQL-QLPREGSPL 328
QY 342 NPFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAILPEVPALATLRLPCHPLFK 401
DB 329 PPLFLPTDPPMVLAKCWVRSSDFQHLHSHLLRGLHMAEFVAVATMRCPLSPHPIFK 388
QY 402 LLIPIRYTILHINTLARELVAPGKLDKSTGLGTGGFSDLIKRNMEOQANYSVLCPLPEDI 461
DB 389 LLIPIRYTMEINVRARNGLVSDLIGIPQVVSTGGGHVLELRRAAALLTYSFCPPDDL 448
QY 462 RARVEDIPGYVYRDDQMGWGAIKSPVSEIVSYIPSDTSVQDDQLQAVREIFSEGFLG 521
DB 449 ADRLGLGVSSFYAQDALRLMEVISRVEGIVSLHYKTDESVKEDFELQACRETFEGL 508
QY 522 LGRSSGMPSLDTRREALVQYITWVITCSAKHAUVSSGQFSDCVWMPNLPPTWQLPPT 581
DB 509 LGADRGFPTSLQSKQKQLCHFPVTWCITCTGQHSNHLGQDLDFWYVFNAPACTMRLPPT 568
QY 582 SKQARPESTIATLPVNSSSYHIIALWLLSAEPGDQRPGLGHYDDEHFTEDAPRRSVAAR 641
DB 569 TK-DATLETVMATLPNPNQSTLQINVMVLLGRQAVMVLPGQHSSEHFFNPKEAKVLKTKF 627
QY 642 QRLIQISKIGIRNRGALPYTLDPLPIENSYSI 677
DB 628 REELAALDKIEIRNKSLLDIPYELRPSMVENSVAI 663

RESULT 12

JQ0018

arachidonate 15-lipoxygenase (EC 1.13.11.33), erythroid-specific - rabbit
N:Alternate names: carotene oxidase; lipoxidase
N:Contains: lipoxygenase peptides
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ0018; A61060; A27327; A61568; JCI513
R:Fleming, J.; Thiele, B.J.; Chester, J.; O'Prey, J.; Janetzki, S.; Aitken, A.; Anton, I.
Gene 79, 181-188, 1989
A:Title: The complete sequence of the rabbit erythroid cell-specific 15-lipoxygenase mRNA
A:Reference number: JQ0018; MUID:89378774; PMID:2777088
A:Accession: JQ0018
A:Molecule type: mRNA
A:Residues: 1-663 <FLE>
A:Cross-references: UNIPROT:P12530; GB:M27214; NID:G2642134; PIDN:AA86978.1; PID:g16490
R:Thiele, B.J.; Fleming, J.; Chester, J.; O'Prey, J.; Prehn, S.; Janetzki, S.; Rapoport, B.
Biomed. Biochim. Acta 49, s17-s24, 1990
A:Title: Structure of the mRNA and of the gene coding for the rabbit erythroid 15-lipoxygenase
A:Reference number: A61060; MUID:90351403; PMID:2386503
A:Accession: A61060
A:Molecule type: mRNA
A>Status: not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 2-605, 'P', 607-663 <TH>
A:Note: nucleotide sequence is given only for intron/exon boundaries
R:Thiele, B.J.; Fleming, J.; Kasuri, K.; O'Prey, J.; Black, E.; Chester, J.; Rapoport, B.
Gene 57, 111-119, 1987
A:Title: Cloning of a rabbit erythroid-cell-specific lipoxygenase mRNA.
A:Reference number: A27327; MUID:88112854; PMID:3123326
A:Accession: A27327
A:Molecule type: mRNA
A:Residues: 1-31 <TH2>
A:Cross-references: GB:M33291
R:Thiele, B.J.; Black, E.; Fleming, J.; Nack, B.; Rapoport, S.M.; Harrison, P.R.
Biomed. Biochim. Acta 46, S120-S123, 1987
A:Title: Cloning of reticulocyte lipoxygenase mRNA.
A:Reference number: A61568; MUID:87241419; PMID:3109402
A:Accession: A61568
A:Molecule type: mRNA
A:Residues: 1-40, 'SHEH', 540-582, 'S' <TH3>
A:Note: this clone was reevaluated in reference JQ0018 and is thought to represent a clone
R:O'Prey, J.; Chester, J.; Thiele, B.J.; Janetzki, S.; Prehn, S.; Fleming, J.; Harrison, P.
Gene 84, 493-499, 1989
A:Title: The promoter structure and complete sequence of the gene encoding the rabbit erythroid 15-lipoxygenase
A:Reference number: JCI513; MUID:90128296; PMID:2612916
A:Accession: JCI513
A:Molecule type: DNA
A:Residues: 1-112, 'T', 114-189, 'N', 191-193, 'I', 195-663 <OPR>
A:Cross-references: GB:M33291; NID:g164731; PIDN:AAA75014.1; PID:g164732
C:Comment: Rabbit reticulocyte lipoxygenase plays a role in the degradation of mitochondria
C:Comment: This enzyme catalyzes the dioxygenation of polyenoic fatty acids containing a
C:Genetics:
A:Gene: 15-lox
A:Introns: 45/3; 114/1; 141/2; 182/2; 217/1; 270/3; 318/3; 388/3; 417/3; 474/2; 515/1; 515/2
A:Superfamily: arachidonate 5-lipoxygenase
C:Keywords: erythrocyte; iron; oxidoreductase

Query Match 31.7%; Score 1144; DB 1; Length 663;
Best Local Similarity 37.5%; Pred. No. 3.9e-81;
Matches 260; Conservative 124; Mismatches 262; Indels 48; Gaps 14;

QY 1 MAKCRVSTGACGAGTWDKVSIVGTHGE-----SPLVPLDLHGKFSAGAEDEFEVT 56
DB 1 MGIVYCVSTGASIVAGSKNVELWVGQGEVGLGCLRP-----TRNKEBEFKVN 52

QY 57 LPQDVGTVMVLRVHKAPPEVSLPLMSFRSDAFRCWFEEWLPGA--LHPFCYOWLEG 113
DB 53 VSKYLGSLFLVRUKK-----HFLKEDAFNCNWSIQAL-GAEDKYWFPCRWVVG 103

QY 114 AGEVLVREGAAKVSQWDHPTLQDQKKELESQKMSYKTYIEGWPRCLDHFVTKDL 173
DB 104 DGVSQSLPVGIGCTVGD PQGLFQKHEQEELERRKLYQWGSKEG--LILNVAQSKLTDL 161

QY 174 NTKYSAMKNAKLPFFKAHSAY--TELKVGKLLDRTGLWLSRLRMFLNFRKTPAAEYVPA 231

162 PVDERFLEKKIDPEASLANGLAELALXDSLNLVAPWKTLDLDFNRIFWGSRSLARRVD 221
232 HWQEDAFASQFLNGINPVLIRRHCHSLPNPNFVTDPMVAPVLGPG-TSLQAELEK-----G 286
222 SWEEDSLFGYQFLNGANPMLRRSVPARL-----VFPFGMEELQAELEKELKAG 272
287 SLFLVDHGILSGVHTNINLNGPQPSAAWTLHQSSGSGPLPIAQL---KQTGPDNP 343
273 TLFEADFALLDNIRKANVILYCOQYLAAPLVM-LKLQPDGKLMWVLIQLHLPKIGSSPP-P 330
344 IFLPSDDTMDWLLAKTWNSEFYTHEAVTHLLHAHLIPEVFALATLRLQRPCHPLFKLL 403
331 LFLPTDPMWLLAKCWRRSDFQVHELNSHLRLHMAEVFTVATMCLPSIHFVKLI 390
404 IPHYRTYHINTARELVAPFKLIDKSTGLTGSGFSLIKRNMQLNSVLCLEPDIRA 463
391 VPHLYRTLEINVRANGLVSDGIFDQIMSTGGGHVQLQAGAFVRSFCPPDDLAD 450
464 RGVEDIPGYRRDGMQIWGAIKSFVSEIVSIYPSDTSVQDDQLOAVRWREIFSEGFLG 523
451 RGLLGVESSFYAQDALRLWEIISRYVOGIMGLYKTDRAVRDDELEQSWCREITIGLQG 510
524 RESSGMPSLDTRREALVOYITWVITFCSAKAAVSSGQFDSVMMNPPLPPTMQLPPPTSK 583
511 AQKQGFPSLOSVAQACHFTVMTCTCTGQSSIHGLQDLWFTWVPNAPCTWRLPPTTK 570
584 QGAPESFIATLPVNSSSYHIIALWLLSABFGDQRPGLGHPYDEHFTEDAPRRSVAQFOR 643
571 -DATLETVMATLPNLHQSSLQMSIVWQLGRDQIPVPLGQHQEYFSGPEPRAVLEKFE 629
644 KLIQISKIIRNRGLALPYTLDPLLENSVSI 677
630 ELAIMDKIEVRNEKLDIPYLRPSIVENSVAI 663

RESULT 13
T30903
arachidonate 8-lipoxygenase (EC 1.13.11.40) / prostaglandin-endoperoxide synthase (EC 1.1.1.61)
C:Species: Pterodroma homomalla
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T30903
R:Koljak, R.; Routaud, O.; Shieh, B.H.; Samel, N.; Braeh, A.R.
Science 277, 1994-1996, 1997
A:Title: Identification of a naturally occurring peroxidase-lipoxygenase fusion protein.
A:Reference number: Z20930; MUID:97451024; PMID:9302294
A:Accession: T30903
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1066 <KOL>
A:Cross-references: UNIPROT:O16025; EMBL:AF003692; NID:g2440001; PID:g2440002; PIDN:AAC4;
C:Function:
A:Description: converts arachidonic acid to an allene oxide with an 8R-hydroperoxide intermediate
C:Keywords: oxidoreductase

Query Match 29.0%; Score 1044.5; DB 2; Length 1066;
Best Local Similarity 33.0%; Pred. No. 4.7e-73;
Matches 233; Conservative 141; Mismatches 280; Indels 53; Gaps 11;

QY 6 VRVSTGEACGAGTWDKVSIVGTHGESPLVPLDH-LGKFSAGAEDEFEVTLPODVGTV 64
DB 378 VEVEGTGREHAGTDATITIRITGAKGRTDYKLDKWFHNDFAEGSKQYTVQ-GFDVGDI 436

QY 65 LMLRVHKAPPEVSLPLMSFRSDA-----WFC-RWFELEWLPFGAALHFPYCOWLEGA 114
DB 437 QLIELH-----SDGGGVSGSDPDMFVNRVLIISSTQDRVYSFPCFRVW--I 480

QY 115 GELVIREGAAKVSQWDHPTLQDQKKELESQKMSYKTYIEGWPRCLDHFVTKDLN 174
DB 481 KDWLPFGPEATLPFNEVPAIVSEQRQKELEKLYQWDSDDMPGNKAKTHDLDLPD 540

QY 175 IKYSAMKNAKLPFFKAHSAYTELKVGKLLDRTGLWLSRLRMFLNFRKTPAAEYVFAHQ 234
DB 541 VQFTDEKRSYQESKKAALVNLGIGSLFTMFENWSDYDHYLYRNWILGGTFNMDRWH 600

Qy 235 EDAPFASQFLNGINPVLIRCHSLPNNPPVTDEMVAIVLPGTSLQAELEKGSFLVDHG 294
Db 601 EDWFGYQFLGANGPVLIRCDALPSPNPNVNEHVNASLDRGNLDEIKDGHYIVDFK 660
Qy 295 ILSGV-----HTNILINGKPOFSAAPMTLLHQSSGSGPLPIAQLKQT 337
Db 661 VLVGAKSVGGVLEDIGYKVPDHLKHDEADIRYCAPIALFYVK-LGHLMPAIQINQE 719
Qy 338 PGPONPIPLPSDDT-WDWLLAKTWVRNSEFIHEAVTHLLHAHLIPEVFALATLRLQPRC 396
Db 720 PGPENPIWPHNEENHMMMAKFWLGVASNFHQLNTHLLTHLTSTESFALSTWRNLASA 779
Qy 397 HPLFKLLPIHRYTHINTLARELLVAPGKLDKSTGLTGTGSGFSLIKRNMQLNYSVLC 456
Db 780 HPVFKLLQPHIYGLAIDTIGKELIGSGGIVDQSLSLGGGSHVTFMEKCFEKNVLQDYH 839
Qy 457 LPEDIRARGVED---IPGVYRDDGMQJWGAIKSFVSEIVSYIYPSDTSVDDOELQAW 513
Db 840 LPNALKKGVDPSKLPFYRDDGLALWEAETFIGSIIAIFYKNDVDDVRDNEIQSWI 899
Qy 514 REIFSEGFL---GREGSMPSLDREALVQYITWVIFTCSAKHAASVSSGQFDSQVWMPN 570
Db 900 YDVHKGWVRNPGHODHGVASFSREQLKEVITSLVFTSCQHAAVNFSQKDHVGFPTN 959
Qy 571 LPPTMQLPPTSKGOARPESTIATLPAVNSSSYHIIALWLLSAEPGDORPLGHYPDEHFT 630
Db 960 APAVLRHPPPKKGATLQSLSTLPSKQAATATVYILTKFSEDERYLGNYSATAWE 1019
Qy 631 EDAPRSVAARFQKLIQISKGIRNRGLALPYTLDPLPIENSIVI 677
Db 1020 DKDALDAINRFQDKLEDISKIKQENLENLEVPYIYLLPERIPNGTAI 1066
RESULT 14
A:3499
probable lipoxigenase PA169 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: AB3499
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: AB3499
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-685 <STO>
A:Cross-references: UNIPROT:Q914G8; GB:AE004547; GB:AE004547; PIDN:AAG0455
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1169
Query Match 16.4%; Score 592; DB 2; Length 685;
Best Local Similarity 33.6%; Pred. No. 5.5e-38;
Matches 182; Conservative 67; Mismatches 210; Indels 82; Gaps 20;
Qy 193 YTEL--KVGLLDRTGL-----WRSLEWRRLPNFRKTPAAYVFAH 232
Db 171 FTELQTRVIAILTRVGLLVDDILKASNLVTRQGGQGLNRPRAVFGTLRLPE---VADS 227
Qy 233 WQEDAFASQFLNGINPVLIRCHSLPNNPPVTDEMVAIVLPGTSLQAELEKGSFLVD 292
Db 228 FDDDEAFYWRVAGNPLIRVDALPANFPFLGESQFRVRMGADDSLLAAASRLYLUD 287
Qy 293 HGIL-----SGVHTNILINGKPOFSAAPMTLLHQSSGSGPLPIAQLKQTGPDPNPIFL- 346
Db 298 YAELEKLPAGSAGVDKLLTG-TGFAVAPIALFALGKDRARLLPVALQCGODPA-THPMFVR 345
Qy 347 ----PSDDTWDLAKTWVRNSEFIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLPKL 402

Db 346 PAESESPLYWGMQAKTVQVAENYHEMFVHLAQTHLVSEAFCLATQRTLAPSHPLHVL 405
Qy 403 LIPHRYTHINTLARELLVAPGKLD-----KSTGLGTGSGFSLIKRNMQLNYSVL 455
Db 406 LAPFECTFLTNEGAARILLPSAGFIDVFAAPITQDTQATAG-----NRLGDFDYRG 458
Qy 456 CLPEDIARGVED---IPGVYRDDGMQJWGAIKSFVSEIVSYIYPSDTSVDDOELQAW 512
Db 459 MLPESLKARNVDDPLALPDYRDGDLVWNAIKQWAADYVAVYASDGDVTADVELAAM 518
Qy 513 VREIFSEGFLG---RESSGMPSLDREALVQYITWVIFTCSAKHAASVSSGQFDSQVWMPN 570
Db 519 VGEVIGSGKAGFPITG-----RSQLEVLTVWIFTASQAHAANFPQPSMNTYAPA 571
Qy 571 LPPTMQLPPTSK---KQQA-----RPESFIATLPAVNSSSYHIIALWLLSAEPGDORPLG 622
Db 572 ICAMSAAPADSPSGKSEADWLKMPPTLVA-LEKVN--IYHLLGS-VYHRLGADYRQTG 627
Qy 623 HYDHEHTEADPESVAA-----FORKLIQISKGIRNRGLALPYTLDPLPIENSIVI 676
Db 628 -FPYAPVPSD--RRVTASGGPLERFOARLKEVEATIRNQARRRPYELLPSPRIASTN 684
Qy 677 I 677
Db 685 I 685
RESULT 15
T07065
probable lipoxigenase (EC 1.13.11.12) (clone H3) - potato
N:Alternate names: 13-lipoxygenase
C:Species: Solanum tuberosum (potato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07065
R:Rojo, J.N.; Vancanneyt, G.; Perez, A.G.; Sanz, C.; Scormann, K.; Rosahl, S.; Sanchez-Se
J. Biol. Chem. 271, 21012-21019, 1996
A:Title: Characterization of three potato lipoxygenases with distinct enzymatic activitie
A:Reference number: Z15894; MUID:96355454; PMID:8702864
A:Accession: T07065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-914 <ROY>
A:Cross-references: UNIPROT:O24371; EMBL:X96406; NID:g1495803; PIDN:CAA65269.1; PID:g149
A:Experimental source: cv. Desiree; leaf
C:Function:
A:Description: catalyzes the hydroperoxidation of specific unsaturated fatty acids
C:Superfamily: lipoxygenase
C:Keywords: fatty acid oxidation; oxidoreductase
Query Match 15.4%; Score 555; DB 2; Length 914;
Best Local Similarity 26.6%; Pred. No. 6.6e-35;
Matches 205; Conservative 100; Mismatches 247; Indels 220; Gaps 33;
Qy 88 WFCWFLEWLPGAALHPFCYQWLEGAGELVREGAKVSWQDHHPTLQDQ-----R 139
Db 181 FFLESITIEGACGVPVHPPCNVQPK-----KOHGPKRIFFSNQPYLPDETETAGLSLR 235
Qy 140 OKELSES-----RQKMYSWKTYIE-GWP-----RCLDHE 166
Db 236 ERELRLDGDGKGVKLSRDYIDYINDLGNPKDIDFARPKLGGDDNVYPRECRSGR 295
Qy 167 TVKOLDLNI-----KYSAMKNKL----- 185
Db 296 VPTDITSAESRVEKPNPTVVRDEQPEESQNTFTSRLKAVLHNLPLSLMASISSNNH 355
Qy 186 FPKAHSAYTELKVGLLDRDTGLWLSLEMRRLFNFRKTPAAEYV----- 229
Db 356 DFKGFSIDNLYSGLLKLGLQDEV-----LKKLPLPKVSSIKEGDLLKYDTPKI 407
Qy 230 ----FAHQWQDAFASQFLNGINPVLIRCHSLPNNPPVTDEMVAIVLPGTSLQAELEKGSFLVDHG 274
Db 408 LSKOKFA-WLRDDEFARQAIAGVNPVSIEKLFQFPFPPVSKLDPEIYGPQESALKKEHILGH 466

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:41:37 ; Search time 114.351 Seconds
(without alignment)
3031.690 Million cell updates/sec

Title: US-10-688-676A-4

Perfect score: 3604

Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTLDPPLIENSVSI 677

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3604	100.0	677 1 LX1B_MOUSE	O35936 mus musculus
2	3255	90.3	677 2 Q8K4F2	Q8K4F2 rattus norv
3	2883.5	80.0	676 2 Q8IYQ2	Q8IYQ2 homo sapien
4	2880.5	79.9	676 1 LX1B_HUMAN	O15296 homo sapien
5	2767.5	76.8	667 2 Q9XTS9	Q9XTS9 bos taurus
6	1864	51.7	711 1 LXE3_HUMAN	Q9YJ11 homo sapien
7	1840	51.1	711 1 LXE3_MOUSE	Q9WV07 mus musculus
8	1775	49.8	701 1 LOXR_HUMAN	O75342 homo sapien
9	1770	49.1	701 1 LOXR_MOUSE	O70582 mus musculus
10	1666.5	46.2	686 2 Q6GJ74	Q6GJ74 xenopus lae
11	1450.5	40.2	673 1 LOX5_MOUSE	P48999 mus musculus
12	1447	40.1	672 1 LOX5_MESAU	P51399 mesocricetu
13	1447	40.1	672 1 LOX5_RAT	P25277 rattus norv
14	1441.5	40.0	673 1 LOX5_HUMAN	P09917 homo sapien
15	1355	37.6	670 2 Q7T2A9	Q7T2A9 brachydanio
16	1254	34.8	663 2 Q8BHG4	Q8BHG4 mus muscu
17	1247	34.6	662 1 LOXP_MOUSE	P39655 mus musculus
18	1224	34.0	663 2 Q8ISF8	Q8ISF8 homo sapien
19	1222	33.9	662 1 LOXP_HUMAN	P18054 homo sapien
20	1198	33.2	663 2 Q6PHB2	Q6PHB2 mus musculus
21	1191	33.0	662 1 LOXP_MOUSE	P39654 mus musculus
22	1186	32.9	662 1 LOXP_BOVIN	P27479 bos taurus
23	1185.5	32.9	661 1 LOX1_HUMAN	P16050 homo sapien
24	1176	32.6	662 1 LOX2_RAT	Q02759 rattus norv
25	1163	32.3	662 1 LOXP_PIG	P16469 sus scrofa
26	1145	31.8	662 1 LOX1_RABIT	P12530 oryctolagus
27	1139	31.6	662 1 LOXP_RABIT	O19043 oryctolagus
28	1129.5	31.3	662 1 LOXE_MOUSE	P55249 mus musculus
29	1129.5	31.3	662 2 Q91YW6	Q91YW6 mus musculus
30	1044.5	29.0	1066 1 AOSL_PLEHO	O6025 plexaura ho
31	1030.5	28.6	555 2 Q95103	Q95103 bos taurus

32	847	23.5	430	2	Q9BEG3	Q9BEG3 bos taurus
33	690	19.1	390	2	Q8C587	Q8C587 mus musculus
34	592	16.4	685	1	LOXA_PSEAE	Q3i498 pseudomonas
35	590	16.4	685	1	LOX_PSEAE	Q8rnt4 pseudomonas
36	561	15.6	896	1	LOX23_HORVU	Q8gsm2 hordeum vul
37	555	15.4	914	2	O24371	O24371 solanum tub
38	554	15.4	565	2	Q82V62	Q82V62 nitrosomona
39	553.5	15.4	881	2	Q6RSN2	Q6rsn2 carica papa
40	549.5	15.2	922	2	Q93YA9	Q93ya9 sesbania ro
41	546.5	15.2	881	2	Q9M463	Q9m463 cucumis sat
42	543.5	15.1	860	1	LOXA_LYCES	P38415 lycopersico
43	541	15.0	862	2	Q43191	Q43191 solanum tub
44	540.5	15.0	862	2	Q8W4X6	Q8w4x6 prunus dulc
45	540	15.0	926	2	Q9FNX8	Q9fnx8 arabidopsis

ALIGNMENTS

RESULT 1

ID	LX1B_MOUSE	STANDARD;	PRT;	677 AA.
AC	O35936;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Arachidonate 15-lipoxygenase, type II (EC 1.13.11.33) (15-LOX-2) (8S-			
DE	lipoxygenase) (8S-LOX).			
GN	Name=Alox15b; Synonyms=Alox8;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Epidermis;			
RX	MEDLINE=97450967; PubMed=9305900; DOI=10.1074/jbc.272.39.24410;			
RA	Jisaka M., Kim R.B., Boeglin W.B., Nanney L.B., Brash A.R.;			
RT	"Molecular cloning and functional expression of a phorbol ester-			
RT	inducible 8S-lipoxygenase from mouse skin.";			
RL	J. Biol. Chem. 272:24410-24416(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC	STRAIN=NMRI; TISSUE=Epidermis;			
RX	MEDLINE=98186642; PubMed=9518531; DOI=10.1016/S0005-2760(97)00214-2;			
RA	Krieg P., Kinzig A., Heidt M., Marks F., Fuerstenberger G.;			
RT	"cDNA cloning of a 8-lipoxygenase and a novel epidermis-type			
RT	lipoxygenase from phorbol ester-treated mouse skin.";			
RL	Biochim. Biophys. Acta 1391:7-12(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Skin;			
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01366;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriber L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E.A., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L.,			
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,			
RA	Negashima T., Numata K., Okido T., Pavan W.J., Portea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,			
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,			

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E) - (15S) -
CC 15-hydroperoxyicoso-5,8,11,13-tetraenoate.
CC -I- COFACTOR: Iron (By similarity).
CC -I- PATHWAY: Leukotrienes biosynthesis.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- TISSUE SPECIFICITY: Expressed in epidermis and brain. No
CC expression found in heart, spleen, liver, skeletal muscle, kidney
CC or testis.
CC -I- INDUCTION: By phorbol ester.
CC -I- SIMILARITY: Belongs to the lipoxigenase family.
CC -I- SIMILARITY: Contains 1 PLAT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U93277; AAC53356.1; -;
DR EMBL; Y14696; CAA75003.1; -;
DR EMBL; AK028724; BAC26085.1; -;
DR EMBL; BC015253; AAH15253.1; -;
DR HSSP; P12530; ILOX.
DR MGD; MGI:1098228; Alox15b.
DR GO; GO:0005622; C:intracellular; ISS.
DR GO; GO:0006917; P:induction of apoptosis; ISS.
DR GO; GO:0006629; P:lipid metabolism; ISS.
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
DR GO; GO:0030336; P:negative regulation of cell migration; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0045926; P:negative regulation of growth; ISS.
DR InterPro; IPR00907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase.
DR InterPro; IPR001885; Mam_lipoxigenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00467; MAMLIPOXGNASE.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Dioxigenase; Iron; Leukotriene biosynthesis; Oxidoreductase;
KW Polymorphism.
FT DOMAIN 2 125 PLAT.
FT METAL 374 374 Iron (By similarity).
FT METAL 379 379 Iron (By similarity).
FT METAL 554 554 Iron (By similarity).
FT METAL 677 677 Iron (By similarity).
FT VARIANT 32 32 E -> G (in clone K12).
FT VARIANT 38 38 L -> M (in clone G2).
FT VARIANT 58 58 P -> R (in clone K12).
FT VARIANT 76 76 V -> A (in clones G2, G5, G11 and K1).
FT VARIANT 413 413 I -> V (in clone K7).
FT VARIANT 536 536 R -> Q (in clones G2, G5 and G11).
SQ SEQUENCE 677 AA; 76230 MW; 780B1AC9C2F68399 CRC64;
Query Match 100.0%; Score 3604; DB 1; Length 677;
Best Local Similarity 100.0%; Pred. No. 1.5e-280;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMLRVHKAPPSVSLPLMSFRSDAWFCRWFLEWLPGAALHPFCQWLEGGAGELVLR 120
DB 61 VGTVLMLRVHKAPPSVSLPLMSFRSDAWFCRWFLEWLPGAALHPFCQWLEGGAGELVLR 120
QY 121 EGAARVSVQDHHTLTQDQORQKESRQWYWKTYIEGMPRCLDHETVKDLNLKYSAM 180
DB 121 EGAARVSVQDHHTLTQDQORQKESRQWYWKTYIEGMPRCLDHETVKDLNLKYSAM 180
QY 181 KNAKLFKAHSAYTELKVGGLDRTGLWRSREMRLEFNFRKTPAAEYVFAHWQDAPFA 240
DB 181 KNAKLFKAHSAYTELKVGGLDRTGLWRSREMRLEFNFRKTPAAEYVFAHWQDAPFA 240
QY 241 SQFLNGINPVLIRCHSLPNNFPVTVDEMVAIVLPGTSLQAELEKGSFLVDHGILSGVH 300
DB 241 SQFLNGINPVLIRCHSLPNNFPVTVDEMVAIVLPGTSLQAELEKGSFLVDHGILSGVH 300
QY 301 TNILNGKQFSAAPMTLLHQSSGGLPLPIALQKQTPGPNPIFLPSDDTDWDLAKTW 360
DB 301 TNILNGKQFSAAPMTLLHQSSGGLPLPIALQKQTPGPNPIFLPSDDTDWDLAKTW 360
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVPALATLQRPCHPLFKLLIPIHRYTLHINTLAREL 420
DB 361 VRNSEFYTHEAVTHLLHAHLIPEVPALATLQRPCHPLFKLLIPIHRYTLHINTLAREL 420
QY 421 LVAPGKLIDKSTGLGTGGFSDLIKENMEQLNYSVLCPLDIRARGVEDIPGYYYRDDGMQ 480
DB 421 LVAPGKLIDKSTGLGTGGFSDLIKENMEQLNYSVLCPLDIRARGVEDIPGYYYRDDGMQ 480
QY 481 IWGAIKSFVSEIVSYYPDSITSVQDDQELQAVRWREIFSEGFLGREGSGMPSLLDTREALV 540
DB 481 IWGAIKSFVSEIVSYYPDSITSVQDDQELQAVRWREIFSEGFLGREGSGMPSLLDTREALV 540
QY 541 QYITWVIFTCSAKHAHVSSGQFDS CVMPNPLPPTWQLPPPTSKGQARPESTIATLPVNS 600
DB 541 QYITWVIFTCSAKHAHVSSGQFDS CVMPNPLPPTWQLPPPTSKGQARPESTIATLPVNS 600
QY 601 SSYHIIALWLLSAEPGDORPLGHYDEHFTDAPRSVAARFKLIQISKGRERNRGLA 660
DB 601 SSYHIIALWLLSAEPGDORPLGHYDEHFTDAPRSVAARFKLIQISKGRERNRGLA 660
QY 661 LPYTYLDPPLIENSYSI 677
DB 661 LPYTYLDPPLIENSYSI 677

RESULT 2

```
Q8K4F2
ID Q8K4F2 PRELIMINARY; PRT; 677 AA.
AC Q8K4F2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 15-lipoxxygenase-2.
GN Name=Alox15b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Boeglin W.E., Schneider C., Brash A.R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; AF415240; AAN03708.1; -.
DR HSP; P12530; ILOX.
DR GO; GO:0005622; C:intracellular; ISS.
DR GO; GO:0006917; P:induction of apoptosis; ISS.
DR GO; GO:0006629; P:lipid metabolism; ISS.
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
DR GO; GO:0030336; P:negative regulation of cell migration; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0045926; P:negative regulation of growth; ISS.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO00907; Lipoxxygenase.
DR InterPro; IPRO01024; Lipoxxygenase_LH2.
DR InterPro; IPRO01885; Mam_lipoxxygenase.
DR InterPro; IPRO08976; PLAT_LH2.
DR Pfam; PF00305; Lipoxxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLOXGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Dioxxygenase; Oxidoreductase.
KW SEQUENCE 677 AA; 76145 MW; 49A47B47C491B8B1 CRC64;
Query Match 90.3%; Score 3255; DB 2; Length 677;
Best Local Similarity 89.2%; Pred. No. 1.7e-252;
Matches 604; Conservative 32; Mismatches 41; Indels 0; Gaps 0;
Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEDFEVTLPOD 60
Db 1 MAKFRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEDFEVTLPOD 60
Qy 61 VGTVMMLRVRKAPPEVSLPLMSRSDAWFCRWFLEWLPGAALHPCCYOWLEGAGELVLR 120
Db 61 VGTVMMLRVRKAPPEVSLPLMSRSDAWFCRWFLEWLPGAALHPCCYOWLEGAGELVLR 120
Qy 121 EGAARVSHQDHPHTLQDQKQELSRQKWSWKTYIEGWPRCLDHTETVKDLNLIKYSAM 180
Db 121 EGAARVSHQDHPHTLQDQKQELSRQKWSWKTYIEGWPRCLDHTETVKDLNLIKYSAM 180
Qy 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSIREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
Db 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSIREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
Qy 241 SOFLINGNPVLRCHSLPNPNFPVTDENAVPLGPTCSLOAEKGSFLVDHGLSGVH 300
Db 241 SOFLINGNPVLRCHSLPNPNFPVTDENAVPLGPTCSLOAEKGSFLVDHGLSGVH 300
Qy 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGPNPILPSPDDTMDLLAKTW 360
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGPNPILPSPDDTMDLLAKTW 360
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Qy 361 VRNSEFYTHEAVTHLHAHLIPEVFALATLRLQPRCHPLFLKLIPIHRYTHINTLAREL 420
Db 361 VRNSEFYTHEAVTHLHAHLIPEVFALATLRLQPRCHPLFLKLIPIHRYTHINTLAREL 420
Qy 421 LVAFCKLIDKSTGLGTGSGFSLIKRNMEQLNYSVLCPLPEDIRARGVEDIPGYVYRDDGQ 480
Db 421 LVAFCKLIDKSTGLGTGSGFSLIKRNMEQLNYSVLCPLPEDIRARGVEDIPGYVYRDDGQ 480
Qy 481 IWGAIKSFVSEIVSIYYPSTDSVODDQELQAVWEIIFSEGFLGSESSGMPSLDTRREALV 540
Db 481 IWGAIKSFVSEIVSIYYPSTDSVODDQELQAVWEIIFSEGFLGSESSGMPSLDTRREALV 540
Qy 541 QYITWVFTCSAKHAASVSSQFSCVWMPNLPPTMQLPPTPSKQARPESTFATLPVNS 600
Db 541 QYITWVFTCSAKHAASVSSQFSCVWMPNLPPTMQLPPTPSKQARPESTFATLPVNS 600
Qy 601 SSVHIIALWLSAEPGDPORPLGHYPDEHFTEDAPRRSVAAPQKLIQISKGIRERNRGLA 660
Db 601 SSVHIIALWLSAEPGDPORPLGHYPDEHFTEDAPRRSVAAPQKLIQISKGIRERNRGLA 660
Qy 661 LPYTYLDPPLIENSIVI 677
Db 661 LPYTYLDPPLIENSIVI 677
RESULT 3
Q8IYQ2 PRELIMINARY; PRT; 676 AA.
AC Q8IYQ2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Arachidonate 15-lipoxxygenase, second type.
GN Name=ALOX15B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzhanovskii M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: Iron (By similarity).
```

CC -|- SIMILARITY: Belongs to the lipoxigenase family.
 CC -|- SIMILARITY: Contains 1 PLAT domain.
 DR EMBL: BC035217; AAH35217.1; -;
 DR EMBL: BC063647; AAH63647.1; -;
 DR HSSP: P22530; ILOX.
 DR GO: GO:0005622; C:intracellular; ISS.
 DR GO: GO:0006917; P:induction of apoptosis; ISS.
 DR GO: GO:0006917; P:induction of apoptosis; ISS.
 DR GO: GO:0006629; P:lipid metabolism; ISS.
 DR GO: GO:0045786; P:negative regulation of cell cycle; ISS.
 DR GO: GO:0030336; P:negative regulation of cell migration; ISS.
 DR GO: GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR GO: GO:0045926; P:negative regulation of growth; ISS.
 DR InterPro: IPR003006; Ig MHC.
 DR InterPro: IPR000907; Lipoxigenase.
 DR InterPro: IPR001024; Lipoxigenase LH2.
 DR InterPro: IPR001885; Mam lipoxigenase.
 DR Pfam: PF00305; Lipoxigenase; 1.
 DR Pfam: PF01477; PLAT; 1.
 DR PRINTS: PRO0087; LIPOXYGENASE.
 DR PRINTS: PRO0467; MAMLIPOXYGENASE.
 DR SMART: SM00308; LH2; 1.
 DR PROSITE: PS00290; IG MHC; UNKNOWN 1.
 DR PROSITE: PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE: PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE: PS00095; PLAT; 1.
 DR DIOXYGENASE; Oxidoreductase.
 KW DIOXYGENASE; 676 AA; 75884 MW; 4F641D2FBB902C6 CRC64;
 SQ SEQUENCE

Query Match 80.0%; Score 2883.5; DB 2; Length 676;
 Best Local Similarity 78.2%; Pred. No. 1.2e-222;
 Matches 530; Conservative 68; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGACAGTWDKVSIVTGHGSPVLVPLDLHLCGKFSAGAEEDFEVTLPOD 60
 DB 1 MAEFVRVSTGAFAGTWDKVSIVTGRGSPPLDLNLKERTAGAEEDFQVTLRED 60
 QY 61 VGTVLMRLVHKAPPEVSVLMS - FRSDAWFCRWFLEWLPGAALHPFCYQWLEGAGELVL 119
 DB 61 VGRVLLLRVHKAPP - VLPGLGFLAPDAWFCRWFQLTTPRGGHLLPFCYQWLEGAGTLVL 118
 QY 120 REGAAKVSQDHPHTLQDORQELSRQMYSKWTIEGWPCCLDHETVKLDIAIKYSA 179
 DB 119 QEGTAKVSQADHPVLPQOQBELQARQEMYQWKAYNPWCPCLDEKTVEDLELNKYST 178
 QY 180 MNNAKLFKAGAYTELKVGKLLDTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAF 239
 DB 179 ANNAFYLOAGAPAEKMKLGLLDRKGLWRSLEMRRLFNFRTPAAEYVFAHWQEDAF 238
 QY 240 ASQFLNGINPVLIRCHSLPNNPVTDEMVAVLGPGTSLQAELEKGSFLVDHGLISGV 299
 DB 239 ASQFLNGINPVLIRCHSLPNNPVTDEMVAVLGPGTSLQAELEKGSFLVDHGLISGI 298
 QY 300 HTNINLCKQPSAAMPHTLHQSGSGPLPIALQIKOTGPDPNPFLPSDDTMDWLLAKT 359
 DB 299 QTNVINGKQPSAAMPHTLYQSGCGPLPLAQLQSLQSGTGPSPFLPTDDKWDMLAKT 358
 QY 360 WYRNSFYTHAVTHLLHAHLIPEVFALATRLQPRCHPLFKLLIPHIYTHINTLARE 419
 DB 359 WYRNEFSFHEATHLLHSHLLPEVFTLATLQPRCHPLFKLLIPHIYTHINTLARE 418
 QY 420 LLVAPGLKIDKSTGLGTGFSDLIKENMBQLNYSVLCLEPDIRARGVEDIPGYVYRDDGM 479
 DB 419 LLIVPGQVDRSTGIGIEGFSSELIQRMKQLNYSVLLCLPDIRTRGVEDIPGYVYRDDGM 478
 QY 480 QIWGALKSFVSEIVSYIYPSDTSVQDDQLQAWREIFSEGLGRSSGMPSLDTREAL 539
 DB 479 QIWGAVERFVSEIIGIYPSDESQVDDRELQAWREIFSKGFLNQGSSGIPSSLETRAL 538
 QY 540 VOYITWVITFCSAKHAASVSGQFDSVWPNLPPTWQLPPPTSKGQARPESTIATLPVNV 599
 DB 539 VOYITWVITFCSAKHAASVAGQFDSCAWPNLPPTSKGLATCEGTATLPVNV 598
 QY 600 SSSYHIIALLWLSAEFGDQRLPHGYPDEHFTEDAPRRSVAAFQKLIQISKGIERNRGL 659

DB 599 ATCDVILLWLSKEPQDRPLGTYPDHFTTEAPRRSIATFQSRLAQISRGIQERNRGL 658
 QY 660 ALPYTYLDPPLIENSVS 677
 DB 659 VLPYTYLDPPLIENSVS 676
 RESULT 4
 LX1B HUMAN
 ID LX1B HUMAN STANDARD; PRT; 676 AA.
 AC O15296; Q8TEV3; Q8TEV4; Q8TEV5; Q8TEV6; Q9UKM4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Arachidonate 15-lipoxygenase, type II (EC 1.13.11.33) (15-LOX-2) (15-lipoxygenase 2).
 GN Name=ALOX15B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Skin;
 RX MEDLINE=97322340; PubMed=9177185; DOI=10.1073/pnas.94.12.6148;
 RA Brash A.R., Boeglin W.E., Chang M.S.;
 RT "Discovery of a second 15S-lipoxygenase in humans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6148-6152(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;
 RA Krieg P., Marks F., Fuerstenberger G.;
 RT "A gene cluster encoding human epidermis-type lipoxygenases at chromosome 17p13.1: cloning, physical mapping, and expression.";
 RL Genomics 73:323-330(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
 RX MEDLINE=21975171; PubMed=11839751; DOI=10.1074/jbc.M11936200;
 RA Tang S., Bhatia B., Maldonado C.J., Yang P., Newman R.A., Liu J.,
 RA Chandra D., Traag J., Klein R.D., Fischer S.M., Chopra D., Shen J.,
 RA Zhou H.E., Chung L.W.K., Tang D.G.;
 RT "Evidence that arachidonate 15-lipoxygenase 2 is a negative cell cycle regulator in normal prostate epithelial cells.";
 RL J. Biol. Chem. 277:16189-16201(2002).
 RN [4]
 RP SEQUENCE OF 337-484 FROM N.A. (ISOFORM B).
 RX MEDLINE=20009393; PubMed=10542053;
 RA Kilty I., Logan A., Vickers P.J.;
 RT "Differential characteristics of human 15-lipoxygenase isozymes and a novel splice variant of 15S-lipoxygenase.";
 RL Eur. J. Biochem. 266:83-93(1999).
 CC -|- FUNCTION: Converts arachidonic acid exclusively to 15S-hydroperoxyicosatetraenoic acid, while linoleic acid is less well metabolized.
 CC -|- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E)-(15S)-15-hydroperoxyicosa-5,8,11,13-tetraenoate.
 CC -|- COFACTOR: Iron (By similarity).
 CC -|- PATHWAY: Leukotriene biosynthesis.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A;
 CC IsoId=O15296-1; Sequence=Displayed;
 CC Name=B; Synonyms=15-LOX2sv-b;
 CC IsoId=O15296-2; Sequence=VSP_003143;
 CC Name=C; Synonyms=15-LOX2sv-c;
 CC IsoId=O15296-3; Sequence=VSP_003144; VSP_003145;
 CC Name=D; Synonyms=15-LOX2sv-a;
 CC IsoId=O15296-4; Sequence=VSP_003142;
 CC -|- TISSUE SPECIFICITY: Expressed in hair, prostate, lung and cornea.
 CC -|- SIMILARITY: Belongs to the lipoxygenase family.
 CC -|- SIMILARITY: Contains 1 PLAT domain.


```
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
DR GO; GO:0030336; P:negative regulation of cell migration; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0045926; P:negative regulation of growth; ISS.
DR InterPro; IPR003006; Iq MHC.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR001885; Mam lipoxigenase.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
DR DIOXYGENASE; Oxidoreductase.
KW NON_TER 1
SQ SEQUENCE 667 AA; 75327 MW; B49141C82A0E79C8 CRC64;

Query Match 76.8%; Score 2767.5; DB 2; Length 667;
Best Local Similarity 75.3%; Pred. No. 2.5e-213;
Matches 503; Conservative 75; Mismatches 89; Indels 1; Gaps 1;

QY 10 TGEACGAGTWDKVSIVSGTHGESPLVPLDLHLGKFSAGAEDEFVTLPPDQVGTVMILRV 69
DB 1 TGEAFGVGTWDKISVIVSGTRGETPLPLDLRLGKFNAGPEDEFVTPEDVGRVLLVRV 60

QY 70 HKAPPEVSIPLMSFRSDAWFCWFELEWLPGLALHPPCWLEGAGELVLRGAAKVSWQ 129
DB 61 HKAPPAISAP-RALGRDADFCEWLVHTVTPRGGALCFPCYQWLEGRSLVLRGTAKISWE 119

QY 130 DHHTLQDQORQESLRQWYKWTYEGWPCRLDHTYKDLNLKYSAMKNALFFKA 189
DB 120 DHHTLQDQORRELOARRETYRWKTYIPGWPCRLDEETVKDLNLKYSVAKNTTFYLRG 179

QY 190 HSAYTELVKGLDRTGLWRSREMRLENFRKTPAAEYVFAHWQSDAFASQFLNGINP 249
DB 180 GSALAEKLGKLLDRKGLKSLKEMRRVFNFRKTPAVEYVCEHWQSDAFAYQFLNGLNP 239

QY 250 VLIRRHCHSLPNPPVPTDENVAPVLGPGTSLQAELEKSLFLVDHGLLSGVHYNILNGPQ 309
DB 240 VLIRRHCHLPFPNPVPTDENVAPVLGPGTSLQAELEKSLFLVDYDLLAGVRTNVINGRPQ 299

QY 310 FSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPIFLPSDDTWMLLAKTWVRNSEFYIH 369
DB 300 FSTAPMTLLYQRRGRLPLALQLSQTGPGNSPIFLPSDDKMDMLLAKTWVRNSEFSIH 359

QY 370 EAVTHLLHAHLIPEVPALATRLQPLCHPLFKLLIPHIYTHLINTLARELLVAPGKLID 429
DB 360 EALTHLLQALHVEVPALATRLQPLCHPLFKLLIPHIYTHLINTLARELLVAPGQVVD 419

QY 430 KSTGLGTGFGSGLIKKNMQLNSVLCLPDIARGVEDIPGVYRDDQMGWGAIKSVF 489
DB 420 RSTGLGIGFSFELIQNMQLNSVCLPDIARGVEDIPGVYRDDQMGWGAVERVF 479

QY 490 SETVSTYPSDTSVQDDQELQAVREIFSEGFLGRESSGWPISLDREALVOYITWIFT 549
DB 480 SEMIGIYPSDESVRDSDQLQAVREIFSEGFLGRESSGLPSTLGRALIOFVTWIFN 539

QY 550 CSAKHAASVSGQSDSCVWPNPPTTQQLPPPTSKGQARPESTIATLPVNSSSYHIIALW 609
DB 540 CSAKHAASVAGQDFAAWPNLPPSNQQLPPPTSKGQARLEGFLATLPVYNATCDVVIALW 599

QY 610 LLSAEFGDORPLGHYPDEHTEADAPRSVAAPFORKLIQISKGIRERNRGLALPYTVLDPP 669
DB 600 LLSKEPGRPLGTYPDEVFTTEAPRSVAAPFORSIAEISRDIOERNHSLALPYTVLDPP 659

QY 670 LIENSYSI 677
DB 660 LIENSYSI 667
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RESULT 6

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LXE3 HUMAN
ID LXE3 HUMAN STANDARD; PRT; 711 AA.
AC Q9BYJ1; Q9H4P2; Q9HC22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Epidermis-type lipoxigenase 3 (EC 1.13.11.-) (e-LOX-3).
GN Name=ALOXE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;
RA Krieg P., Marks P., Fuerstenberger G.;
RT "A gene cluster encoding human epidermis-type lipoxigenases at
RL chromosome 17p13.1: cloning, physical mapping, and expression.";
RL Genomics 73:323-330 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Brash A.R.; Boeglin W.E.;
RT "Human epidermal lipoxigenase, ortholog of mouse Alox3.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Krieg P., Fuerstenberger G.;
RT "cDNA cloning, genomic structure, and chromosomal localization of
RL human epidermis-type lipoxigenase-3.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP VARIANTS NCIE SER-396 AND PHE-500.
RX MEDLINE=21634626; PubMed=11773004; DOI=10.1093/hmg/11.1.1.107;
RA Jobard F., Lefevre C., Karaduman A., Blanchet-Bardon C., Emre S.,
RA Weissenbach J., Ozguc M., Lathrop M., Prud'homme J.-F., Fischer J.;
RT "Lipoxigenase-3 (ALOXE3) and 12(R)-lipoxigenase (ALOX12B) are mutated
RL in non-bullous congenital ichthyosiform erythroderma (NCIE) linked to
RL chromosome 17p13.1.";
RL Hum. Mol. Genet. 11:107-113 (2002).
CC -! FUNCTION: Introduces molecular oxygen into polyunsaturated fatty
CC acids. Exact substrate is not known.
CC -! COFACTOR: Iron (by similarity).
CC -! TISSUE SPECIFICITY: Predominantly expressed in skin.
CC -! DISEASE: Defects in ALOXE3 are a cause of nonbullous congenital
CC ichthyosiform erythroderma (NCIE) [MIM:242100]. NCIE is
CC characterized by prominent erythroderma and fine white,
CC superficial, semiadherent scales. As many as 90% of affected
CC individuals present at birth as collodion babies. Patients suffer
CC from palmoplantar keratoderma, often with painful fissures,
CC digital contractures, and loss of pulp volume. In half of the
CC cases, a nail dystrophy including ridging, subungal
CC hyperkeratosis, or hypoplasia has been described.
CC -! SIMILARITY: Belongs to the lipoxigenase family.
CC -! SIMILARITY: Contains 1 PLAT domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AJ305020; CAC34518.1; -.
CC EMBL; AJ305021; CAC34518.1; JOINED.
CC EMBL; AJ305023; CAC34518.1; JOINED.
CC EMBL; AJ305025; CAC34518.1; JOINED.
CC EMBL; AF182218; RAG16899.1; -.
CC EMBL; AJ269499; CAC12843.1; -.
CC HSSP; P12530; ILOX.
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Genew; HGNC:13743; ALOXE3.
 DR DR MIN; 607206; --
 DR DR MIN; 242100; --
 DR InterPro; IPR000907; Lipoxxygenase.
 DR InterPro; IPR001024; Lipoxxygenase LH2.
 DR InterPro; IPR001885; Mam_lipoxxygenase.
 DR Pfam; PF00305; Lipoxxygenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR PRINTS; PR00467; MAMLIPOXYGENASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS50095; PLAT; 1.
 DR Dioxxygenase; Disease mutation; Iron; Leukotriene biosynthesis;
 KW Oxidoreductase.
 FT DOMAIN 2 119 PLAT.
 FT VARIANT 396 396 R -> S (in NCIE).
 FT FT /FTID=VAR_015175.
 FT VARIANT 500 500 V -> F (in NCIE).
 FT FT /FTID=VAR_015176.
 FT CONFLICT 155 155 C -> R (in Ref. 3).
 FT CONFLICT 194 194 F -> L (in Ref. 2).
 FT SEQUENCE 711 AA; 80543 MW; BDED1B4ED5CF6783 CRC64;
 Query Match 51.7%; Score 1864; DB 1; Length 711;
 Best Local Similarity 50.1%; Pred. No. 1.1e-140;
 Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3

QY 1 MAKCRVRYSTCEACGAGTWDKVSIVGTHGSPVLPLDLHLGKEFSAGAEEDPEVTLPOD 60
 DB 1 MAVRLCVTTGYPYLRAGTLDNISVTLVGTGSGPQRLORMGRDPAGSVQKTKVRCYAE 60

QY 61 VGTVLMRLVRHKAPPEVSVLPLMSFRSDAWFCRWFELEWLPFGAALHPFCYOWLEGAGELVLR 120
 DB 61 LGELLALLRVHKE-----RYAFFRKRDSWCSRI CVTEPDGVSVHPFCYQWIEGCTVELR 114

QY 121 EGAAKVSHQDHPHTLODORQKESLRQMYSKWTIEGHPRLCDHETVKDDL----- 173
 DB 115 PGTARTICQDSLPLLLDHRTELRLARQRCYRWKIYAPGPPCMVDVNSFOEMSDKKFALT 174

QY 174 -----NIKYSAMKNAKLFFKAHSAYTELKVK 199
 DB 175 KTTTCVDOGSDSGNRYLPGPFPKIDI PSLMYMEPNRVYSATKISLLFNWAI PASLGMKLR 234

QY 200 GLLDRITGLWRSLEMRRLNFNRKTPAAEYVFAHQOEDAFFAQFLNGINPVLIRCHSLP 259
 DB 235 GLLDRKSGWKLLDDMQNIFWCHKITFTTKVTEHWCEDHFFGYQYLNGVNPVMLHCISLP 294

QY 260 NNFPVTDEMVAVLPGPTSLQAELEKGSLSFLVDHGILSGVHTNINLNGRQPSAAPMTLLH 319
 DB 295 SKLPVTNDMVAPLLGQDTCLOTELEBGNIFLADYWI LAEAPFHLNGRQYVAAFLCLLW 354

QY 320 QSSGSGPLLPITAIQLKQTPGDPNPFLPSSDDTMDLLAKTWVRNSEFYTHEAVTHLLHAH 379
 DB 355 LSP-QGALVPLAIQLSQTGPDSPFLFTDSEMDLLAKTWVRNSEFVHENTHFLCTH 413

QY 380 LIPEVPALATIRQLPRCHPLFKLLIPHTRYTLHIINTLARELLVAPGKLIKDKSTGLGTGFG 439
 DB 414 LLCEAFAMATIRQLPLCHPIYKLLPHTRYTLIQVNTIARATLLNPEGLVDQVTSIGRQGL 473

QY 440 SDLIKRNEQLNYSVLCPEDIRARGVEDIPGYVYRDDGMQIWGAIKSPVSEIVSIYTPS 499
 DB 474 IYLMSTGLAHPTYTNFCLPDSLRLARGVLAIPNHYRDDGLKILWAAIESPVSEIVGYTPS 533

QY 500 DTSVQDDDELQAWVREIFSEGFGLRGSSGMPSLDLTREALVOYITWVITFCSAKHAAYSS 559
 DB 534 DASVQDSELQAWTGEIIFAQFLRGSSGFPSSRLCTPGEMVKFLTAIFNCSQAHAAYNS 593

QY 560 GQFDSCVMPNLPPTMQILPPTPSKQQAPESTIATLPVNSSSYHIIALWLLSAPGDOR 619
 DB 594 GQHDFGAMNAPSSMRQPPQTKGTTTLTKTLDLPVNTISCNLLFLFWLSQBPQKOR 653

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Qy 620 PLGHPDEHTEADPRRSVAAFQKLIQISKGRTRNRGLALPYTYLDPPLIENSYSI 677
Db 654 PLGTPDEHTEAPRRSIAAFQSLAQISRDICQERNQGLALPYTYLDPPLIENSYSI 711

RESULT 7
LXE3_MOUSE STANDARD; PRT; 711 AA.
AC Q9WV07;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Epidermis-type lipoxigenase 3 (EC 1.13.11.-) (e-LOX-3).
GN Name=Aloxe3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NNRI; TISSUE=Skin;
RX MEDLINE=99296830; PubMed=10366447; DOI=10.1006/geno.1999.5816;
RA Kinzig A., Heidt M., Fuerstenberger G., Marks F., Kiege P.;
RT "cDNA cloning, genomic structure and chromosomal localization of a
RL novel epidermis-type lipoxigenase.";
RL Genomics 58:158-164(1999).
CC -1- FUNCTION: Introduces molecular oxygen into polyunsaturated fatty
CC acids. Exact substrate is not known.
CC -1- COPACTOR: Iron (By similarity).
CC -1- PATHWAY: Leukotrienes biosynthesis.
CC -1- TISSUE SPECIFICITY: Skin specific.
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y14695; CAB46101.1; -.
CC HSSP; P12530; ILOX.
CC MGD; MGI:1345140; Aloxe3.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR001024; Lipoxigenase_LH2.
CC InterPro; IPR001885; Mam_lipoxigenase.
CC Pfam; PF00305; Lipoxigenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC PRINTS; PR00467; MAMLIPOXGNASE.
CC SMART; SMO0308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS50095; PLAT; 1.
CC Dioxigenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT DOMAIN 2 119 PLAT.
SQ SEQUENCE 711 AA; 80578 MW; 6E2183C7C64540E0 CRC64;

Query Match 51.1%; Score 1840; DB 1; Length 711;
Best Local Similarity 49.7%; Pred. No. 9.4e-139;
Matches 357; Conservative 113; Mismatches 200; Indels 48; Gaps 3;

Qy 1 MAKCRVRVSTGECAGGTWQDKVSVISVTHGSEPLVPLDHLGKEFSAGAEDEPVTLPQD 60
Db 1 MAVYRLCVTTGSLYKAGTLDNIYATLVGTGCSFKQKLDKRVGRDFASGSQVKYKVRCEAE 60

Qy 61 VGTVLMRLRVHKAPEVSVLPLMSFRSDAWCFRFEWMLPGCAALHFFPCYOWLEGAGELVLR 120
Db 61 LGSEILLRLHKE-----RPAFFCKDPWYCSRICTVAPDGSVAHFPCYQWIDGYCTVLELR 114

121 EGAAKVSWDHPHTLODOROKELSESQKMYSWKTYIEGWPCRLDHTHTVKDLDL----- 173

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Db 115 PGARTICQDPLLLDHRKRLRQBCYRWKIFAPGPRMVDVVSFQEMESDKKFALT 174
Qy 174 -----NIKYSAMGNKALFFKAHSAYTELKVK 199
Db 175 KTVPCAEQDDNGNRYLPQGFPMKIDIPSLHMEPIRISATKTASLI FNALPASFGMKIR 234
Qy 200 GLLDRTGLWRSRLRMRRLFRNFKTPAAEYVFAHQEDAFFASQFLNGINPVLIRCHSLP 259
Db 235 GLLDKRGSKWRLDDIRNIFWCHKTFTSEVTEHWCEDSFFGQYLVGNVPVWLHCLSLP 294
Qy 260 NNFPVTDEWAVPLGFGTSLQABLKSGLFLVDHIGLSGVHTNIILNGKQFSAAPMTLH 319
Db 295 SKLPVTNDWVPLGPGTCLQTELRGHI FLADYWLAEAPVHCINSLQYVYTPFLCLLW 354
Qy 320 QSSGSGPLPIALQKOTGPNPFLPSDDTWMLLAKTWNRNSEFYIHEAVTHLLHAH 379
Db 355 LNP-QCVLLPLAIIQUSQTPGSPSIFLPTDCBLMLLAKTWNRNBEFLVHENTHFLCTH 413
Qy 380 LIPEVFALATLRLPRCHPLFLKLLPHIRYTHINTLARELVAPKGLDKSTGLGTGF 439
Db 414 LUCEAFSMATLQLPLCHPVYKLLPHTRYTLQVNTIARATLLNPDGLVDKVTSGRQGL 473
Qy 440 SLLIKRNEQLNYSVLCLPEDIRARGVEDIPGYTRDDGMQIWAIGKSFVSEIVSYIPS 499
Db 474 IYLMSTGLAHFTYTDPLSPDSIRARGVLTIPNHYRDDGLKIAAIAERFVSEIVSYIPS 533
Qy 500 DTSVODDQLOAWVREIFSEGFLGRESSGMPSLDTRREALVOYITWVIFCSAKHAAYSS 559
Db 534 DASVODDQLOAWGVIFQAQALGRESSGPPRLCTPGELVKILTALIFNCQAHAAFNS 593
Qy 560 GQFDSVCMWNPPLPTMQLPPTSKQARPESTIATLPVNSSYHIIALWLSABFGDQR 619
Db 594 GQHDFGAWNPAPSNRQPPQTKGDTTMSYLDTLPEVNTTCRNLLPWLVSQEPKQOR 653
Qy 620 PLGHYPDEHFTEDAPRRSVAARFQKLIQISGIRERNRGLALPYTYLDPPLIENSIVI 677
Db 654 PLGTYPDEHFTBEAPRQSAAFQNCIAQISKDIRNRQSLALPYALDPLPIENSIVI 711

RESULT 8
LOXR_HUMAN STANDARD; PRT; 701 AA.
AC O75342;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Archidonate 12-lipoxygenase, 12R type (EC 1.13.11.-) (Epidermis-type
GN Name=ALOX12B;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Hair follicle;
RX MEDLINE=99057919; PubMed=9618483; DOI=10.1073/pnas.95.12.6744;
RA Sun D., McDonnell M., Chen X.-S., Lakkis M.M., Li H., Isaacs S.N.,
RA Elisea S.H., Patel P.I., Funk C.D.;
RT "Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning,
RT expression, and gene chromosomal assignment.";
RL J. Biol. Chem. 273:33540-33547(1998).
RN [3]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP TISSUE=B-cell;
RX MEDLINE=98284002; PubMed=9837935; DOI=10.1074/jbc.273.50.33540;
RA Sun D., McDonnell M., Chen X.-S., Lakkis M.M., Li H., Isaacs S.N.,
RA Elisea S.H., Patel P.I., Funk C.D.;
RT "Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning,
RT expression, and gene chromosomal assignment.";
RL J. Biol. Chem. 273:33540-33547(1998).
RN [3]
SEQUENCE FROM N.A.
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```
RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;
RA Krieg P., Marks F., Fuerstenberger G.;
RT "A gene cluster encoding human epidermis-type lipoxygenases at
RL chromosome 17p13.1: cloning, physical mapping, and expression.";
RN Genomics 73:323-330(2001).
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Tong L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP VARIANTS NCIE PRO-426 AND GLN-578.
RX MEDLINE=21634626; PubMed=11773004; DOI=10.1093/hmg/11.1.107;
RA Jobard F., Lefevre C., Karaduman A., Blanchet-Bardon C., Emre S.,
RA Weissenbach J., Ozug M., Lathrop M., Prud'homme J.-F., Fischer J.;
RT "Lipoxygenase-3 (ALOXE3) and 12(R)-lipoxygenase (ALOX12B) are mutated
RL in non-bullous congenital ichthyosiform erythroderma (NCIE) linked to
RL chromosome 17p13.1.";
RL Hum. Mol. Genet. 11:107-113(2002).
CC -!- FUNCTION: Converts arachidonic acid to 12R-
CC hydroperoxyicosatetraenoic acid (12R-HPETE).
CC -!- COFACTOR: Iron (by similarity).
CC -!- PATHWAY: Leukotrienes biosynthesis.
CC -!- TISSUE SPECIFICITY: Expressed in B-cells, hair follicles, foreskin
CC keratinocytes and adult skin. Also expressed in psoriatic tissue.
CC -!- DISEASE: Defects in ALOX12B are a cause of nonbullous congenital
CC ichthyosiform erythroderma (NCIE) [MIM:242100]. NCIE is
CC characterized by prominent erythroderma and fine white,
CC superficial, semiadherent scales. As many as 90% of affected
CC individuals present at birth as collodion babies. Patients suffer
CC from palmoplantar keratoderma, often with painful fissures,
CC digital contractures, and loss of pulp volume. In half of the
CC cases, a nail dystrophy including ridging, subungal
CC hyperkeratosis, or hypoplasia has been described.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
CC EMBL; AF038461; AAC39770.1; -
CC EMBL; AF059250; AAC79680.1; -
CC EMBL; AJ050526; CAC34520.1; -
CC EMBL; AJ050527; CAC34520.1; JOINED.
CC EMBL; BC041058; AAH41058.1; -
CC HSSP; P12530; 1LOX.
CC Genew; HGNC:430; ALOX12B.
CC MIM; 603741; -
CC MIM; 242100; -.
```


DR PROSITE; PS00081; LIPOXYGENASE 2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase;
FT POLYMORPHISM. 2 119 PLAT.
FT METAL 398 398 Iron (By similarity).
FT METAL 403 403 Iron (By similarity).
FT METAL 578 578 Iron (By similarity).
FT METAL 701 701 Iron (By similarity).
FT VARIANT 9 9 A -> V (in strain C57BL/6 X SJL).
FT VARIANT 351 351 M -> V (in strain C57BL/6 X SJL).
FT VARIANT 361 361 T -> I (in strain C57BL/6 X SJL).
SQ SEQUENCE 701 AA; 80577 MW; FAE3AJB8DZAAL42E CRC64;

Query Match 49.1%; Score 1770; DB 1; Length 701;
Best Local Similarity 46.6%; Pred. No. 3.9e-133;
Matches 330; Conservative 130; Mismatches 210; Indels 38; Gaps 3;
QY 1 MAKCRVSTGACGAGTWDKVSIVGTHGSPVLVDHLGKFSAGAEDEFVTLPOD 60
DB 1 MATYKVKVATGDFPSGLTSLITVGTQBSHKQRLNHFGRDPATGAVDDYTVCCQD 60
QY 61 VCTVLMRLVHKAPPEVSLPMSFRSDAMFCRWFELWLPGAALHPCYQWLGAGELVLR 120
DB LGELIIIRLHKPHSF-----LAKDPWYCNVQICAPDCRVYHPFAYQWMDGYETLALR 114
QY 121 EGAAKVSWDHHTIQQDQKESRQKMYSWKT----- 154
DB 115 EATGKITADDTLPILLEHQQEIRAKOFYHWRVFGVGLPNVVDIPSYHPPRCRNPFR 174
QY 155 -----YIEGWPCLDHETVKDLDLNIKYSAMKNKALFFKAHSAYTELKVKGLLDRTGLWR 209
DB 175 PEWDGYPGFPILINIKATRFNLNSLRFSTASFFVRLGPMALAFKLGLVDRKRSWK 234
QY 210 SREWRRLNFKPTAAEVFAHQWEDAFQAFQFLNGINPVLIRCHSLPNNFPVYDEM 269
DB 235 RLKDKINFPATKSVVSVVAEHWTEDSFFGYQLNGINPGLIRCTQIPDKFPVYDEM 294
QY 270 APVLGPGTSLOAELEKSLFLVDHGLTSGVHTNINLNGKPFQSAAPMTLHQSSGGLLP 329
DB 295 APFLGEGTCLQAELEGNLYLADYRLDGIPTVELNGQQOHHCAPMCLLH-FGPDGNMWP 353
QY 330 IAIQLKQTPGPNPILPSDDTWMLLAKTWVRNSEFYIHEAVTHLHAHLIPEVFALAT 389
DB 354 IAIQLSQTGPGDPIPLPNDSEWMLLAKTWVRYAEFYSEAVHLLSHLIGEAFCLAL 413
QY 390 LRQLRCHPLKLLTPHYRYTLHINTARELVAQKLDKSTGLTGTGFSDLIKRMEQ 449
DB 414 LRNLPMCHPLKLLTPHYRYVQINSIGRALLNKGUSARAWSLGLEFAQVMVRGUSE 473
QY 450 LNVSVLCLPEDIRARGVEDIPGYVRDDGMQIWGAIKSFVSEIVSYIYPSDTSVQDDQL 509
DB 474 LYTKSLCINDFVERGVQDLPYFRDDSLAWYAMERVYIIITYYPNDAAVEGDPEL 533
QY 510 QAWREIFSEFGFLRGSSGMPSLDREALVQYITWVITCSAKHAHVSSGQFSDCVMP 569
DB 534 QCVQVQIFKECLLGRSSGFPCLRTIPELIEYVTVMVYTCARAAVNSGQLEYTSWMP 593
QY 570 NLPPTMQLPPPTSKGQARPESTIATLPAYNSSYHIIALLWSABGCDORPLGHYPDEH 629
DB 594 NFPSSNRNPMQTKGTLTQITQYTDMLTDPVKTTCIVLLVLTLCREPDPRRPLHFDIHF 653
QY 630 TEDAPRSVAAFORKLIQISKGIERNRGLALPYTLDPPLEIENSYSI 677
DB 654 VEEGPRRSIEAFQNLQNSHINRQNKCLTLPYYLDPVLIENSISI 701

RESULT 10

Q66J24 PRELIMINARY; PRT; 686 AA.
AC Q66J24;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE LOC446930 protein (Fragment).
GN Name=LOC446930;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Heltón E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Klein S., Gethard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; BC081087; AAH81087.1; -.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase LH2.
DR InterPro; IPR001885; Mam lipoxigenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxygenase; Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 686 AA; 77852 MW; 1892A4AEB51CCF9 CRC64;
Query Match 46.2%; Score 1666.5; DB 2; Length 686;
Best Local Similarity 46.2%; Pred. No. 7.9e-125;
Matches 313; Conservative 130; Mismatches 227; Indels 7; Gaps 2;
QY 1 MAKCRVSTGACGAGTWDKVSIVGTHGSPVLVDHLGKFSAGAEDEFVTLPOD 60
DB 17 MSTYKLEVTGKDLAATWDSISIVLIGSRGSKQKLDHWGKDFLPGARDRYEYKSKED 76
QY 61 VCTVLMRLVHKAPPEVSLPMSFRSDAMFCRWFELWLPGAALHPCYQWLGAGELVLR 120

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Db 77 LGELVRLYKE-----SPGSPESAWFCNSIKVTCSPGIYEFPFHLNLSGVTGTEIP 130
Qy 121 EGAKVSWQDHHPTLQDQKELSRQKQYKWKYIEGWPCRLDHTYKDLDMNKYSAM 180
Db 131 QGKGITLTSVSPAIKQRESELNTRQTHEWKTAKYAGPHCISADAVTDLSPNDRFSYK 190
Qy 181 KNAKLFFKAHSAAYELKVGKLLDRGLWSLRSLREMRLENFRKTPAAEVFAHWQEDAFFA 240
Db 191 KTSIFGFNLFSSGATLKGFLNCSWKDLNKKVFSIQWTKISDVLSELMNEDTPFG 250
Qy 241 SQFLNGINPLIRCHSLPNFPVTDENVAPVLGPGTSLQAELEKSGSLFVLDHGLSGVH 300
Db 251 YOYLNGLNPLMKCLRPDPNFPVDDVTVSATLGSITLQELQNGNIFLADYKILGIP 310
Qy 301 TNLNGKPFQGAAPMTLLHQSSGSLPLPIAQLKQTPGPNPILPSPDDTMDMLAKTW 360
Db 311 TNVINGERQYTAAPMCLLWKP-NDLILPIALQNLQTPGEEPILPTDSKMDWTAKIW 369
Qy 361 VRNSEFYHEAVTHLLHAHLIPEVPALATLQRPCHPLPKLLPHIRYTHINTFLAREL 420
Db 370 VRSEFQVHEIVSHLLYTHLAAEFNIAATRHLPMPGHPVYKLIIRPHLYTLEINTLARQT 429
Qy 421 LVAPGKLDKSTGTLGTGSGFSLIKRMEQLANSVLCLPEDIRARGVEDIPGVYVDDGQM 480
Db 430 LIGPKGLDQAVVTGNGVFPVLLARATESLTSYALCLPDDIQARGVESIPNFRYHDMGR 489
Qy 481 IWGAIKSVSEIVSIYPSDTSVQDQELQAVREIFSEGFLGREGSSGMPSLDITREALV 540
Db 490 IWEAMESPASIDVHYVYSDTSDVDEPDLQAVAEIFQEGFLSNKNSGIPSPATRVELT 549
Qy 541 QYITWVITCSAKHAASVSGQFSDSCVMNPLPPTNQLPPTSKGQARPESTIATLPVNS 600
Db 550 KYLTWMTCTQHAAVNSGQFDYVAMPNAPSTMRKPPPTAKGTTTYSILETLPAINT 609
Qy 601 SSVHIIALWLSABPGDORPLGHPYDEHFTEDAPRSVAAPQKLIQISKIRERNRGLA 660
Db 610 TATAMVTVSLSSKGLPDLQRLGRYKNKSVFEDVPKYYIEQFKELSEISQIQKRNKTK 669
Qy 661 LPYTVLDPLIENSVISI 677
Db 670 LTYHYLDEAVECSVISI 686

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RESULT 11

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LOX5 MOUSE
ID LOX5 MOUSE STANDARD; PRT; 673 AA.
AC P48999;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
GN Alox5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X 129/Sv; TISSUE=Peritoneal cavity;
RX MEDLINE=95355399; PubMed=7629107; DOI=10.1074/jbc.270.30.17993;
RA Chen X.-S., Naumann T.A., Kurte U., Jenkins N.A., Copeland N.G.,
RA Funk C.D.;
RT "cDNA cloning, expression, mutagenesis, intracellular localization,
RT and gene chromosomal assignment of mouse 5-lipoxygenase.";
RL J. Biol. Chem. 270:17993-17999(1995).
CC -|- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6E,8Z,11Z,14Z)-(5S)-5-
CC hydroperoxyicoso-6,8,11,14-tetraenoate.
CC -|- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z)-(5S)-5-hydroperoxyicoso-
CC 6,8,11,14-tetraenoate = (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicoso-
CC 7,9,11,14-tetraenoate + H(2)O.
CC -|- COFACTOR: Iron, also requires calcium and ATP for activity.
CC -|- PATHWAY: Leukotrienes biosynthesis; first step.

```

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CC -|- PATHWAY: Leukotrienes biosynthesis; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to the lipoxygenase family.
CC -|- SIMILARITY: Contains 1 Pfam domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; L42198; AAC37673.1; --
CC PIR; I49479; I49479.
CC HSSP; P12530; ILOX.
CC MGI; MGI:87999; Alox5.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0006691; P:leukotriene metabolism; IMP.
CC InterPro; IPR000907; Lipoxygenase.
CC InterPro; IPR001885; Mam_lipoxygenase.
CC Pfam; PF00305; Lipoxygenase; 1.
CC Pfam; PF01477; Pfam; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC PRINTS; PR00467; MAMLIPOXYGNASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS00095; Pfam; 1.
CC Calcium; Dioxxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0
FT DOMAIN 1 117
FT METAL 367 367 Iron (By similarity).
FT METAL 372 372 Iron (By similarity).
FT METAL 550 550 Iron (By similarity).
FT METAL 673 673 Iron (By similarity).
SQ SEQUENCE 673 AA; 77868 MW; 0B2910477A3B7085 CRC64;
Query Match 40.2%; Score 1450.5; DB 1; Length 673;
Best Local Similarity 42.5%; Pred. No. 1.7e-107;
Matches 288; Conservative 133; Mismatches 242; Indels 15; Gaps 6;
Qy 6 VRVSTGEACAGTWDKVSIVTGHGSPVLPDLH-LGKEFSAGAEDEFVTLPODVGV 64
Db 5 VTVATGSQWAGTDDYIYLSIGSAGCSEKHLLDKAFYNDPFGAVDSYDVTVDLGEI 64
Qy 65 LMLRVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPGAALHPFCYOWLEGAGELVLRGAA 124
Db 65 YLVKIEKR-----KYWLHDDWLYKVTILKTPHGDYIEFPFCYRWITGEGEIVLRDGRA 116
Qy 125 KVSQDHHPTLQDQKELSRQKQYKWKYIEGWPCRLDHTYKDLDMNKYSAMKNAK 184
Db 117 KLARDDQIHILKQHRKELEARQKQYRMMWNPGLPSIDAKCHKDLPRDQFQSEKGV 176
Qy 185 LFFKAHSAYTELKVGKLLDR-TGLWRSRLREMRLENFRKTPAAEVFAHWQEDAFASQF 243
Db 177 FVLNYSKAMENLFINRRFMHMFQSSWHDFADPEKIFVKISNTISERVKNHWQEDLMFGYQF 236
Qy 244 LINGINPLIRCHSLPNFPVTDENVAPVLGPGTSLQAELEKSGSLFVLDHGLSGVHTNI 303
Db 237 LNCNPNVLIRKCTALPKLPVTTWVECSLERQLSLQEVQEGNIFIVDYVLLDGDANK 296
Qy 304 LNC-KPQFSAAPMTLLHQSSGSLPLPIAQLKQTPGPNPILPSPDDTMDMLAKTW 362
Db 297 TDPCTHQLAAPICLLYKNL-ANKVPIAQLQNTPGESNPIFLPTDSKYDWLLAKIWR 355
Qy 363 NSEFYHEAVTHLLHAHLIPEVPALATLQRPCHPLPKLLIPIRYTHINTFLARELV 422
Db 356 SSDPHVHTHTLLRTHLVSEVFGIAYMRQLPFAVHPLFKLLVAHVRFTHIAINTKAREQLI 415

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QY 423 APGLKIDKSTGLTGTGFSDLIRKNMEQLNYSVLCLPEDIRARGV---EDIPGYVYRDDGM 479
Db 416 CEYGLFDKANATGGGHVQWQRAVQDLTYVSLCPPEAIKARGMDSTEDMPFVYRDDGL 475
QY 480 QIWGAIKSFVSEIYSIYSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRAL 539
Db 476 LWBEAIQSFTSEVSIYSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRAL 535
QY 540 VOYITWVIFTSKAAHAUVSSGQFSCVWMPNLPPTMOLPPPTSCKGQAPESFIATLPAVN 599
Db 536 SEYLTWVIFTASQAHAUVNFGQYDWCWSPNAPPTMRAPPTAKGVVTTIEQIVATLPDRG 595
QY 600 SSSYHIIALWLLSAPGQDQRLGHYPDEHFTEDAPRRSVAARFQKLIQISKIRENRGL 659
Db 596 RSCWHLGAVWALSQFQNEFLGMYPEEHFIEKPVKEAMIRFRKNLEAIVIAERNK 655
QY 660 ALPTYTLDPLPIENSIVI 677
Db 656 KLPYYLSPDRIPNSVAI 673

RESULT 12
LOX5_MESAU STANDARD; PRT; 672 AA.
AC PS1339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
GN Name=ALOX5;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian;
RX MEDLINE=97109716; PubMed=8951996; DOI=10.1016/S0952-3278(96)90008-3;
RA Kitzler J.W., Eling T.E.;
RT "Cloning, sequencing and expression of a 5-lipoxygenase from Syrian
hamster embryo fibroblasts.";
RL Prostaglandins Leukot. Essent. Fatty Acids 55:269-277(1996).
CC -1- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6E,8Z,11Z,14Z) - (5S) -5-
hydroperoxyicosoic acid.
CC -1- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z) - (5S) -5-hydroperoxyicosoic
acid + H(2)O = (7E,9E,11Z,14Z) - (5S,6S) -5,6-epoxyicosoic
acid.
CC -1- COFACTOR: Iron, also requires calcium and ATP for activity.
CC -1- PATHWAY: Leukotrienes biosynthesis; first step.
CC -1- PATHWAY: Leukotrienes biosynthesis; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the lipoxygenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
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CC -----
DR EMBL; U43333; AAA85257.1; -.
DR HSSP; P12530; ILOX.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR01024; Lipoxygenase LH2.
DR Pfam; PF001885; Mam_lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPQYGNASE.
DR PRINTS; PR00467; MAMLOXGNASE.
DR SMART; SM00308; LH2; 1.
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DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Calcium: dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 By similarity.
FT DOMAIN 1 116 PLAT.
FT METAL 366 366 Iron (By similarity).
FT METAL 371 371 Iron (By similarity).
FT METAL 549 549 Iron (By similarity).
FT METAL 672 672 Iron (By similarity).
SQ SEQUENCE 672 AA; 77741 MW; 1F7234B5C297B30F CRC64;

Query Match 40.1%; Score 1447; DB 1; Length 672;
Best Local Similarity 42.9%; Pred. No. 3.3e-107;
Matches 291; Conservative 127; Mismatches 244; Indels 16; Gaps 7;

QY 6 VRVSTGEACGAGTWDKVSIVGTHGESPLVLDH-LGKFSAGAEDEFVTLPODVGV 64
Db 5 VTVATGSQWPAFTDDYIYLSIGSAGSEKHLDDKAFYNDFERGAVDSYDVTVDDELGEI 64
QY 65 LMLRVHKAPPEVSLPLMSFRSDAWFCRWFELWLPGAALHPHPCYQWLEAGELVREGAA 124
Db 65 QLVRIEKR-----KYWLHDDWLYKYLTK-TFTDYIEPCYRWITGESEIVLDGEA 115
QY 125 KVSQDHHPTLQDQKQKESRQKMYSWKTYIEGWPCRLDHTVCLDLNINIKYSAMONAK 184
Db 116 KLARDQIHLKQHRKLEARQKQYRWENWNPGLSIDAKCHKDLPRDIQFDEKGV 175
QY 195 LFFKAHSAYTELKVGKLLDR-TGLWRSUREWRLNFRKTPAAEYVFAHWQDEDAFASQF 243
Db 176 PVLNYSKAMENLFINRFMHMFQSSWNPDPADFEKIFVKISNTISERVYKHWQEDLMFGYQF 235
QY 244 LINGINVLIRRHCHSLPNFPVTDEMVAFLPGTSLQAELEKGSFLVDHGLSGVHTNI 303
Db 236 LNCNPVLKRCRELPOKLPVTTEMVCSLEHLSLEQVEQEGNIFIVDYELLDGIDANK 295
QY 304 LNG-KPQFSAAPMTLLHSSGSLPLPIAIOIKQTPGPDNPFLPSDDTMDWLLAKTWVR 362
Db 296 TDPCTHQFLAAPICLLYKNL-ANKIVPIAQLNQAPGEKNPIFLPSDAKYDWLLAKIWR 354
QY 363 NSEFVIRHNAVTHLLHAHLIPEVAFALATROLPRCHPLKLLPHIRYTLHINTLARELLV 422
Db 355 SSDFVHVQITHTLLCTHLVSEVFGIYRQPAVHPFIKLLVAHVRFITAINTKAREQLI 414
QY 423 APGLKIDKSTGLTGTGFSDLIRKNMEQLNYSVLCLPEDIRARGV---EDIPGYVYRDDGM 479
Db 416 CEYGLFDKANATGGGHVQWQRAVQDLTYVSLCPPEAIKARGMDSTEDMPFVYRDDGL 474
QY 480 QIWGAIKSFVSEIYSIYSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRAL 539
Db 476 LWBEAIQSFTSEVSIYSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRAL 534
QY 540 VOYITWVIFTSKAAHAUVSSGQFSCVWMPNLPPTMOLPPPTSCKGQAPESFIATLPAVN 599
Db 536 SEYLTWVIFTASQAHAUVNFGQYDWCWSPNAPPTMRAPPTAKGVVTTIEQIVATLPDRG 594
QY 600 SSSYHIIALWLLSAPGQDQRLGHYPDEHFTEDAPRRSVAARFQKLIQISKIRENRGL 659
Db 596 RSCWHLGAVWALSQFQNEFLGMYPEEHFIEKPVKEAMIRFRKNLEAIVIAERNK 654
QY 660 ALPTYTLDPLPIENSIVI 677
Db 656 KLPYYLSPDRIPNSVAI 672

RESULT 13
LOX5_RAT
ID LOX5 RAT STANDARD; PRT; 672 AA.
AC P12527;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
```


RL Proc. Natl. Acad. Sci. U.S.A. 85:26-30(1988).
RN [3]
RP ERRATUM.
RA Matsumoto T., Funk C.D., Raadmark O., Hoeoeg J.-O., Joernvall H.,
RA Samuelsson B.; Proc. Natl. Acad. Sci. U.S.A. 85:3406-3406(1988).
RL [4]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89320027; PubMed=2526519;
RA Matsumoto T., Funk C.D., Raadmark O., Hoeoeg J.-O., Joernvall H.,
RA Samuelsson B.;
RT "Molecular cloning and amino acid sequence of human 5-lipoxygenase.";
RL Adv. Prostaglandin Thromboxane Leukotriene Res. 19:466-469(1989).
RN [5]
RN SEQUENCE OF 1-49 FROM N.A.
RX MEDLINE=89202374; PubMed=2565035;
RA Funk C.D., Hoshiko S., Matsumoto T., Raadmark O., Samuelsson B.;
RT "Characterization of the human 5-lipoxygenase gene.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:2587-2591(1989).
RL [6]
RN SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=91067649; PubMed=2251250;
RA Hoshiko S., Raadmark O., Samuelsson B.;
RT "Characterization of the human 5-lipoxygenase gene promoter.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:9073-9077(1990).
RL [7]
RN MUTAGENESIS OF SOME HISTIDINE RESIDUES.
RX MEDLINE=92042124; PubMed=1939225;
RA Nguyen T., Faigueyret J.-P., Abramowitz M., Riendeau D.;
RT "Evaluation of the role of conserved His and Met residues among
RT lipoxygenases by site-directed mutagenesis of recombinant human 5-
RT lipoxygenase.";
RL J. Biol. Chem. 266:22057-22062(1991).
RN [8]
RN MUTAGENESIS OF SOME RESIDUES.
RX MEDLINE=92171971; PubMed=1540191;
RA Ishii S., Noguichi M., Miyano M., Matsumoto T., Noma M.;
RT "Mutagenesis studies on the amino acid residues involved in the iron-
RT binding and the activity of human 5-lipoxygenase.";
RL Biochem. Biophys. Res. Commun. 182:1482-1490(1992).
CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6S,8Z,11Z,14Z) - (5S) - 5-
CC hydroperoxyicoso-6,8,11,14-tetraenoate.
CC -!- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z) - (5S) - 5-hydroperoxyicoso-
CC 6,8,11,14-tetraenoate = (7E,9E,11Z,14Z) - (5S,6S) - 5,6-epoxyicoso-
CC 7,9,11,14-tetraenoate + H(2)O.
CC -!- COFACTOR: Iron, also requires calcium and ATP for activity.
CC -!- PATHWAY: Leukotrienes biosynthesis; first step.
CC -!- PATHWAY: Leukotrienes biosynthesis; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
DR EMBL; J03600; AAA36183.1; -
DR EMBL; J03571; AAA65450.1; -
DR EMBL; J04520; AAA59522.1; -
DR EMBL; M38191; AAA63212.1; -
DR FIR; A28117; DAHUAL.
DR HSP; P12530; ILOX.
DR IntAct; P09917; -
DR Genew; HGNC:435; ALOX5.
DR MIM; 152390; -
DR GO; GO:0004051; F:arachidonate 5-lipoxygenase activity; TAS.
DR GO; GO:0006691; P:leukotriene metabolism; TAS.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.

DR InterPro; IPR001885; Mam_lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR PRINTS; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Calcium; Dioxigenase; Direct protein sequencing; Iron;
KW Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0
FT DOMAIN 0
FT METAL 1 117 PLAT.
FT METAL 367 367 Iron (By similarity).
FT METAL 372 372 Iron (By similarity).
FT METAL 550 550 Iron (By similarity).
FT METAL 673 673 Iron (By similarity).
FT MUTAGEN 358 358 D->N: No loss of activity.
FT MUTAGEN 362 362 H->S,N: Still some substantial activity.
FT MUTAGEN 367 367 H->S,N,A: No activity.
FT MUTAGEN 372 372 H->Q: No activity.
FT MUTAGEN 376 376 H->S,N: Still some substantial activity.
FT MUTAGEN 390 390 H->A: No activity.
FT MUTAGEN 399 399 H->S,N: Still some substantial activity.
FT MUTAGEN 399 399 H->A: No activity.
FT MUTAGEN 432 432 H->N,A: Almost no loss of activity.
FT MUTAGEN 550 550 H->N,A: No activity.
SQ SEQUENCE 673 AA; 77852 MW; 7DBB515D9A58F0EB CRC64;
Query Match 40.0%; Score 1441.5; DB 1; Length 673;
Best Local Similarity 42.8%; Pred. No. 9.2e-107;
Matches 291; Conservative 126; Mismatches 244; Indels 19; Gaps 7;
QY 6 VRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHR-LGKERSAGAEEDPEVTLPODVGV 64
Db 5 VTVATGQSWFAGTDYIYLSLVGSAGCSKHLDRPFYDFNFERGAVSDVTVDELGI 54
QY 65 LMLRVHKAPPEVSLPFLMFRSDAFCRMFLEWLPFGAALHFFCYQWLEGAGELVLRGAA 124
Db 65 QLVRIEKR-----KYWLNDWDYLTTLTPHGDYIEFFCYRWITGDVWVLRDGRA 116
QY 125 KVSQDHHTPTLDQKQKLESQKYSWKTYEGHPCLDHTVTVDLDLNKYSAMKNK 184
Db 117 KLARDQIHILKQHRKKELETRQKQYRMWENWPGFPLSIDAKCHKDLPDIQFSEKGYD 176
QY 185 LFFKAHSAYTELKVKGLDHR-TGLWRSLEMRRLNFRKTPAAEYVFAHQWDAEPASOF 243
Db 177 FVLNYSKAWENLFNRFMHMFQSSWDFADFEKI FVKISNTISERVMMHWQEDLMFGYQF 236
QY 244 LINGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKSGSLFLVDHGILSGVHTWI 303
Db 237 LNCNPNVILIRCTELPEKLPVTENVECSLERQLSLEQEVQGNIFIVDFELLDGIDAN- 295
QY 304 LMGKP---QPSAAPMTLHQSSGSGPLPIALQIKQTGPDNPPIFLPSDDTWDWLLAKTW 360
Db 296 -KTDPCTLQFLAAPICLLYKXL-ANKIVPIATQLNQIPGDENPIFLPSDAKDWLLAKTW 353
QY 361 VRNSEFYTHEAVTHLHAHLPEVAFALATLRQLPRCHPLFKLLIPIHRYTLHINTLAREL 420
Db 354 VRSSDFHVTHTLTHLSEVFGIAMYRQLPAVHPPIFKULVAHVHRTIINTKARQ 413
QY 421 LVAPGKLIDKSTGLGTGGFSDLIKENMEQLNYSVLCLPEDIRARGV---EDIPGYVRDD 477
Db 414 LICEGCLFDKANATGGGGHVQVQAMKDLTYASLCFFPEAIKARGMESKEDIPYYFYRDD 473
QY 478 GNOIWAIGKSFVSEIVSYIPSDTSVQDDQELQAWREIFSESGFLGREGSGMPSLLDTR 537
Db 474 GLLVWEAIRTFATAEVVDIYEGDQVVEDEPQLQDFVNDVYVGMGRKSGSPKSKVRE 533
QY 538 ALVQVITVWVIFTCSAKHAHVSSGQFSDSCVMMNLPPTMQLPPPTSKGOARPSFIATLPA 597
Db 534 QLSEYLTVWVIFTASAQHAHVNFQYDMCSWIPNAPPTMRAPPTAKGVVTIISQIVDTLPD 593

	Matches	280;	Conservative	119;	Mismatches	264;	Indels	14;	Gaps	6
QY	5	RVRVSTGEACGAGTWDKVSIVGTGHESPLVDHLHGKEFGSAGAEDEVTLFQDVGV	64							
		:::::								
		:::::								
		:::::								
Db	4	KTVATGTSEYSTNNVVVTLLIGEGKSERTLIDNPGLDFCRGAYDDIVKSDTDLGPL	63							
		:::::								
		:::::								
QY	65	LMLRVHKAPPEVSLPMSFRSDAFCRWPELEWLPC--AALHPPCCYWLEGAGELV-LRE	121							
		:::::								

122	GAANKVQWDDHPTLQDORQKELESROGKMYSWKTYITGWPRLCDHETVTKOLDLNKYSAMK	181
Qy		
115	GTAKKLSEBSLPLEMAHROSELOERQKTYRWAWAFGIPKCKIDAKSEALDPODARENEK	174
Db		
182	NAXLFFKAHSAYTELKVKGLLDRGT-LWRSLEMRRLFNFRKTPAAEYVFAHWQOEADFFA	240
Qy		
175	RSDFEGSLHYALLESLKKLATRFKGSNSDLEDFRIFWKLRSPIAEYTMHWWKEDWFFA	234
Db		
241	SQFLANGINPVLIRRHCHSLPNPNVPTDWMVAPVLGPGTSLQAELEKGSFLVADHGILSGVH	300
Qy		
235	YQFLNGSNPRNITRLKKVPSNPLVTGDMYQSSLIPTTTLNEELKKGNIPLVADHAILDGP	294
Db		
301	TNILNGKPOFSAAPMTWLHQSSGSGBLLDIAIOLKQTPGPDNPIPLPSDDTDWMDILLAKTW	360
Qy		
295	ANVIRNSPOYIAPLCLLYEPEKG-LIPAIQLEQKPKDKOTEPVLFSPDPPLAWLLAKOMW	353
Db		
361	VRNSEFVIEAHVTHLLAHILIPEVFALATLROLPRCHPLFKLLIPHRYTLHINTLAREL	420
Qy		
354	VRHAEFQVQLLSHLRTHLMVEVICATLRQLPDAVHPYIKLUTPHRYTLEINCGRQTQ	413
Db		
421	LVAPGKLIIDKSTGLGTGGFSDLIKRMEQUNYSVLCLPEDIARAGVEDIPGYYYRDDGMQ	480
Qy		
414	LLSPEGIFKRVVSTGGEGLLLLAQREYKVLTYRSLQPKPFDLDRGTVKVGYYVRYDSLM	473
Db		
481	IWGAIKFSVEISVIYYPDSYTSQDDQEOELQAWVREIFSEGFLOGRESSGMPSLDTRALV	540
Qy		
474	LMDVIQNFVSGIVSLYYQCDSDVOEDSELQAWTHDVAVEGVDVPBPEGLASDMKTKBELI	533
Db		
541	QYITMWIFTCSAKHAHVSSGQDSDSCVYMMNLPPTMQLPPPTSKGQARPSFIATLPAVNS	600
Qy		
534	TLUSVAIFETSTQAHAATNGQDFWCRAWNTPTCTMRHPPPRDKDAVTMWMIMDTLPDISQ	593
Db		
601	SSVHITALWLLSAEPGDQRPLGHPDEHFTEDAPRERSVAAFKLIQISKGIRERNRGLA	660
Qy		
594	SCVQMAITHWLGRAQPDALPMGYQYEQYTEPAALKVIDKFRKELKELEDKIMAQNEGLE	653
Db		
661	LPYTYLDPPLIENSVISI	677
Qy		
654	LOYLYLCPGRMENSIT	670
Db		

Search completed: July 18, 2005, 22:01:13
Job time : 116.351 secs

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PT New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed
PT additives for livestock, or as antigens for producing antibodies.
PS Example 2; Fig 6; 51pp; English.

CC The present sequence is mouse 8S-lipoxygenase (8-Lox) protein.
CC Lipoxygenases are a structurally related family of non-haeme iron
CC dioxygenases that function in the production of fatty acid
CC hydroperoxides. 8-Lox acts in the metabolism of arachidonic acid to 8S-
CC hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as
CC diagnostic tools to detect normal and abnormal DNA sequences derived from
CC patient cells, for detecting and isolating other members of the
CC polypeptide family and related polypeptides from a DNA library
CC potentially containing the sequences, as primers for hybridising to
CC related sequences for amplifying those sequences or for altering native
CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives
CC for livestock and as antigens for producing antibodies
XX Sequence 677 AA;

Query Match 100.0%; Score 3604; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGSPVLPLDLHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGSPVLPLDLHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAHLHPCYQWLEGAGELVLR 120
DB 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAHLHPCYQWLEGAGELVLR 120
QY 121 EGAAKVSWQDHHTLQDQKQKESRQKMYSKWTYIEGWPRCLDHTVXDLDLNLKYSAM 180
DB 121 EGAAKVSWQDHHTLQDQKQKESRQKMYSKWTYIEGWPRCLDHTVXDLDLNLKYSAM 180
QY 181 KNAKLFFKAHSAYTELKVKGLLDRDTGLMRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240
DB 181 KNAKLFFKAHSAYTELKVKGLLDRDTGLMRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240
QY 241 SOFLANGINVLIRCHSLNPNRPVTDENVAPVLGCTSLQAELEKSLPLVDHGLSGVH 300
DB 241 SOFLANGINVLIRCHSLNPNRPVTDENVAPVLGCTSLQAELEKSLPLVDHGLSGVH 300
QY 301 TWILNGKPOFSAAPMTLLHQSSGSPLLPIALQKOTPGDPNPFIPLPSDDTWDMLLAKTW 360
DB 301 TWILNGKPOFSAAPMTLLHQSSGSPLLPIALQKOTPGDPNPFIPLPSDDTWDMLLAKTW 360
QY 361 VRNSEFYIHEAVTHLHAHLIPEVFALATLRLPRCHPLFKLLIPIHRYTLHINTLAREL 420
DB 361 VRNSEFYIHEAVTHLHAHLIPEVFALATLRLPRCHPLFKLLIPIHRYTLHINTLAREL 420
QY 421 LVAPGKLIDKSTGLTGGSDDLIRNMEQLNYSVLCLPEDIARGVEDIPGVYRDDGNQ 480
DB 421 LVAPGKLIDKSTGLTGGSDDLIRNMEQLNYSVLCLPEDIARGVEDIPGVYRDDGNQ 480
QY 481 IWGAIKSFVSEIYSIYPDSVTQDDQELQAWREIFSEGFLGRSSGMPSLDTRREALV 540
DB 481 IWGAIKSFVSEIYSIYPDSVTQDDQELQAWREIFSEGFLGRSSGMPSLDTRREALV 540
QY 541 QYITWVIFCSAKHAASVSGQFSDSCVVMENLPTTQOLPPPTSKGARPPSFATIPAVNS 600
DB 541 QYITWVIFCSAKHAASVSGQFSDSCVVMENLPTTQOLPPPTSKGARPPSFATIPAVNS 600
QY 601 SSYHIITALLSNPCDQRLGHYPDEHETEDAPRRSVAAFORKLIQISKGRERNRGLA 660
DB 601 SSYHIITALLSNPCDQRLGHYPDEHETEDAPRRSVAAFORKLIQISKGRERNRGLA 660
QY 661 LPYTYLDPPLIENSUSI 677
DB 661 LPYTYLDPPLIENSUSI 677

RESULT 2
ADQ91765
ID ADQ91765 standard; protein; 677 AA.
XX
AC ADQ91765;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse 8S-lipoxygenase.
XX
KW lipoxygenase; iron ligand; arachidonic acid metabolism; mouse;
KW 8S-lipoxygenase; 8-Lox.
XX
OS Mus sp.
XX
PN US2004137483-A1.
XX
PD 15-JUL-2004.
XX
PF 18-NOV-2003; 2003US-00716204.
XX
PR 16-APR-1998; 98US-00061768.
PR 17-JAN-2001; 2001US-00764246.
XX
PA (BRAS/) BRASH A R.
PA (BOEG/) BOEGLIN W E.
PA (JISA/) JISAKA M.
XX
PI Brash AR, Boeglin WE, Jisaka M;
XX
XX WPI; 2004-533356/51.
DR N-PSDB; ADQ91764.
XX
XX New lipoxygenase nucleic acid segment comprises an isolated gene encoding
PT a lipoxygenase containing an iron ligand comprising a serine, useful for
PT arachidonic acid metabolism.
PS Claim 11; SEQ ID NO 4; 39pp; English.

CC The invention describes a nucleic acid segment (I) comprising an isolated
CC gene encoding a lipoxygenase containing an iron ligand comprising a
CC serine, or comprises at least a 10 nucleotides long contiguous stretch of
CC the nucleic acid sequence not given in the specification (SEQ ID NO. 1)
CC or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a
CC nucleic acid segment comprising at least 10 nucleotides long contiguous
CC stretch of the nucleic acid sequence not given in the specification (SEQ
CC ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is
CC a polypeptide having the amino acid sequence Trp-Leu-Leu-Ala-Lys (SEQ ID
CC NO. 5) and Gly-Gin-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxygenase nucleic
CC acids and proteins are useful in arachidonic acid metabolism. This is the
CC amino acid sequence of mouse 8S-lipoxygenase (8-Lox).

XX Sequence 677 AA;

Query Match 100.0%; Score 3604; DB 8; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGSPVLPLDLHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGSPVLPLDLHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAHLHPCYQWLEGAGELVLR 120
DB 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAHLHPCYQWLEGAGELVLR 120
QY 121 EGAAKVSWQDHHTLQDQKQKESRQKMYSKWTYIEGWPRCLDHTVXDLDLNLKYSAM 180
DB 121 EGAAKVSWQDHHTLQDQKQKESRQKMYSKWTYIEGWPRCLDHTVXDLDLNLKYSAM 180
QY 181 KNAKLFFKAHSAYTELKVKGLLDRDTGLMRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240
DB 181 KNAKLFFKAHSAYTELKVKGLLDRDTGLMRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240

QY 241 SQFLNGINPVLIRCHSLPNNPPVTDWVAPVLGRGTSLOALEKSGSLFVDHGILSGVH 300
DB 241 SQFLNGINPVLIRCHSLPNNPPVTDWVAPVLGRGTSLOALEKSGSLFVDHGILSGVH 300
QY 301 TNLNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPFLPSDDTDWMLLAKTW 360
DB 301 TNLNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPFLPSDDTDWMLLAKTW 360
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLAREL 420
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLAREL 420
QY 421 LVAPGKLDKSTGLTGTSFSDLIKRNMEQLNSVLCPLDIPARGVEDIPGYRRDDGMQ 480
DB 421 LVAPGKLDKSTGLTGTSFSDLIKRNMEQLNSVLCPLDIPARGVEDIPGYRRDDGMQ 480
QY 481 IWGALKSFVSEIVSYIYPSDTSVQDDQLOAWVRIFSEGFLGSSGMPSLDTRREALV 540
DB 481 IWGALKSFVSEIVSYIYPSDTSVQDDQLOAWVRIFSEGFLGSSGMPSLDTRREALV 540
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNPPTMQLPPTTSKGOARPESTIATLPVNS 600
DB 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNPPTMQLPPTTSKGOARPESTIATLPVNS 600
QY 601 SSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRERNRGLA 660
DB 601 SSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRERNRGLA 660
QY 661 LPYTYLDPLPIENSYSI 677
DB 661 LPYTYLDPLPIENSYSI 677

RESULT 3

AAW93832
ID AAW93832 standard; protein; 676 AA.

AC AAW93832;

DT 25-JUN-1999 (first entry)

DE Human 15S lipoxigenase PS213 protein.

KW Lipoxigenase; PS213; human; diagnosis; prostate disease; cancer;
metastases; benign prostatic hypertrophy; prostatic; immunoassay;
prostatic intraepithelial neoplasia; Cytotoxic agent; drug screening;
therapy.

OS Homo sapiens.

XX WO9913111-A1.

XX PD 18-MAR-1999.

XX PF 11-SEP-1998; 98WO-US018983.

XX PR 11-SEP-1997; 97US-00927978.

XX PA (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Ruseell JC;
PI Stroupe SD;

XX WPI; 1999-229254/19.

XX DR N-P5DB; AAX23827.

XX Diagnosis of prostatic disease using lipoxigenase PS213 as marker.

XX Claim 26; Page 94-96; 101pp; English.

XX This invention describes methods for diagnosing prostate disease using

CC the human 15S-lipoxigenase PS213, or its nucleic acid or specific
CC antibodies, as markers. Detecting the presence of PS213, a derived
CC amplicon, the encoded polypeptide or specific antibody, basically in
CC standard hybridization, amplification or immuno assays, indicates
CC prostatic disease. These methods are used for diagnosis, staging,
CC monitoring, prognosticating, in vivo imaging and determining
CC predisposition to prostatic cancer (and metastases), benign prostatic
CC hypertrophy, prostatic, and prostatic intraepithelial neoplasia. Host
CC cells transfected with PS213 are used to produce recombinant polypeptides
CC which are used to generate antibodies or as immunoassay reagents. The
CC antibodies, and their fragments, are also immunoassay reagents and can be
CC used therapeutically, either directly or as carriers for cytotoxic
CC agents. The recombinant polypeptides are also used for drug screening and
CC as targets for therapy

XX Sequence 676 AA;

Query Match 79.9%; Score 2880.5; DB 2; Length 676;

Best Local Similarity 78.0%; Pred. No. 2.8e-266;

Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGVTHGESPLVLDHLGKFSAGAEEDFVTLPOD 60
DB 1 MAEPRVRVSTGEACGAGTWDKVSIVGVTHGESPLVLDHLGKFSAGAEEDFVTLPOD 60
QY 61 VGTVMILRVKAPPEVSLPLMS-PRSDAWFCRWELEWLPGAALHFPYQWLEGAGELVL 119
DB 61 VGRVLLRLRVHKAPP--VLPGLGLAPDAWFCRWFQLTTPRGHLLFPYQWLEGAGTLLV 118
QY 120 REGAAKVSQWDDHPTLODROKESQKYSWKTYTEGWPRCLDHTVKDLNLIKYS 179
DB 119 QEGTAKSVADHHPVLQOOROELOARQEMQWKAYPEGWPHCLDEKVEDELELNKYST 178
QY 180 MNAKLFFKAHSAYTELKVKGLLDRITGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFF 239
DB 179 AKNANFYLQAGSAPEAKMKIKGLDRKGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFF 238
QY 240 ASQFLNGINPVLIRCHSLPNNPPVTDWVAPVLGRGTSLOALEKSGSLFVDHGILSGV 299
DB 239 ASQFLNGINPVLIRCHSLPNNPPVTDWVAPVLGRGTSLOALEKSGSLFVDHGILSGV 298
QY 300 HTNLLNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPFLPSDDTDWMLLAKT 359
DB 299 QTNVINGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPFLPSDDTDWMLLAKT 358
QY 360 WVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLARE 419
DB 359 WVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLARE 418
QY 420 LLVAPGKLDKSTGLTGTSFSDLIKRNMEQLNSVLCPLDIPARGVEDIPGYRRDDGM 479
DB 419 LLVAPGQVVDRTSTGIEGFSGLIQRNMKQNLNSVLCPLDIPARGVEDIPGYRRDDGM 478
QY 480 QIWGALKSFVSEIVSYIYPSDTSVQDDQLOAWVRIFSEGFLGSSGMPSLDTRREALV 539
DB 479 QIWGALKSFVSEIVSYIYPSDTSVQDDQLOAWVRIFSEGFLGSSGMPSLDTRREALV 538
QY 540 VQYITWVIFTCSAKHAASVSGQFSDSCVMMNPPTMQLPPTTSKGOARPESTIATLPVNS 599
DB 539 VQYITWVIFTCSAKHAASVSGQFSDSCVMMNPPTMQLPPTTSKGOARPESTIATLPVNS 598
QY 600 SSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRERNRGL 659
DB 599 ATCDVILALWLLSKPEGQDQPLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRERNRGL 658
QY 660 ALPYTYLDPLPIENSYSI 677
DB 659 VLPYTYLDPLPIENSYSI 676

RESULT 4

AAE00935

ID AAE00935 standard; protein; 676 AA.

XX AAE00935;
 XX 04-JUL-2001 (first entry)
 XX Human 15S-lipoxygenase (15-Lox-2) protein.
 XX Human; 15S-lipoxygenase; 15-Lox-2; non-haeme iron dioxygenase;
 KW arachidonic acid; feed additive; livestock; antigen.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Region 353..357
 FT Binding-site /note= "Consensus sequence"
 FT Binding-site 374
 FT Binding-site /note= "Iron ligand"
 FT Binding-site 379
 FT Binding-site /note= "Iron ligand"
 FT Region 507..511
 FT Binding-site /note= "Consensus sequence"
 FT Binding-site 553
 FT Binding-site /note= "Iron ligand"
 FT Binding-site 557
 FT Binding-site /note= "Iron ligand"
 FT Region 559..563
 FT Binding-site /note= "Consensus sequence"
 FT Binding-site 676
 FT Binding-site /note= "Iron ligand"
 XX US6204037-B1.
 XX 20-MAR-2001.
 XX 16-APR-1998; 98US-00061768.
 XX 16-APR-1998; 98US-00061768.
 XX (UYVA-) UNIV VANDERBILT.
 XX Brash AR, Boeglin WE, Jisaka M;
 XX WPI; 2001-289517/30.
 XX N-PSDB; AAD04501.
 XX New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed
 PT additives for livestock, or as antigens for producing antibodies.
 XX Claim 2; Fig 1; Sipp; English.
 XX The present sequence is human 15S-lipoxygenase (15-Lox-2) protein.
 CC Lipoxygenases are a structurally related family of non-haeme iron
 CC dioxygenases that function in the production of fatty acid
 CC hydroperoxides. 15-Lox-2 acts in the metabolism of arachidonic acid to
 CC 15S-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as
 CC diagnostic tools to detect normal and abnormal DNA sequences derived from
 CC patient cells, for detecting and isolating other members of the
 CC polypeptide family and related polypeptides from a DNA library
 CC potentially containing the sequences, as primers for hybridizing to
 CC related sequences for amplifying those sequences or for altering native
 CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives
 CC for livestock and as antigens for producing antibodies
 XX Sequence 676 AA;
 XX Query Match 79.9%; Score 2880.5; DB 4; Length 676;
 XX Best Local Similarity 78.0%; Pred. No. 2.8e-266;
 XX Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;
 QY 1 MAKCRVRVTGECAGTWDKVSIVGTGHSPLVPLDLHGKFSAGAEEDFEVTLPOD 60
 DB 1 MAEFRVRVSTGEAFGAGTWDKVSIVGTGHSPLVPLDLNLGKFTAGAEEDFQVTLPED 60

QY 61 VGTVLMLRVHKAPPEVSLPLMS -FRSDAWFCRWFLEWLPGNALHPCYQWLEGAGELVL 119
 DB 61 VGRVLLLRVHKAPP--VLPLLGPLADAWFCRWFOITPPRGHLLFPCCYQWLEGAGTLLV 118
 QY 120 REGAAKVSQDHHPTLODROKELESROKMTSWKTYIEGWPRCLDHEVTVKOLDLNIKYSA 179
 DB 119 QEGTRAKVSWADHHPVLQOORQEELQARQEMQWKAYNFGWPHCLDEKTVEDLELNKYST 178
 QY 180 MKNAKLFFKAHSAYTELKVKGLLDRDTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAPF 239
 DB 179 AKNANFYLAGSAPAEPMKIKGLLDRKGLWRSLENMKRIFFNFRTPAAEHAPEHWQEDAPF 238
 QY 240 ASQFLNGINPVLIRCHSLPNNFPVYDDEWAPVLPQCTSLQAELEKGSFLVDHGILSOV 299
 DB 239 ASQFLNGLNPVLIRCHYLPKNFPVYTDAMVASLLGPGTSLQAELEKGSFLVDHGILSGI 298
 QY 300 HTNILINGKQPSAAPMTLLHOSGSGPLLPALQIKOTPGDPNPFLPSSDDTDWMLLAKT 359
 DB 299 QTNVINGKQPSAAPMTLLYSQPGCPPLPLAIQSQTGPGNSPIFLPTDDKDWMLLAKT 358
 QY 360 WYRNSEFYIHEAVTHLLHAHLIPEVFPALATLRLQPRCHPLFKLLIPHIRYTLHINTLARE 419
 DB 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLRLQPRCHPLFKLLIPHTRYTLHINTLARE 418
 QY 420 LLVAPGKLIKSTGLTGTGFSGLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYYYRDDGM 479
 DB 419 LLIVPGQVDRSTGIGIEGFSGLIQRNMKQLNYSLLCLPEDIRTRGVEDIPGYYYRDDGM 478
 QY 480 QIWGAIKSPVSEIYIYPSDTSVODDOLOAWVREIFSEGFLGRESGMPSLDDTREAL 539
 DB 479 QIWGAVERFVSEIIGIYPSDESVDRELOAWVREIFSKGFLNQESSGIPSSLETREAL 538
 QY 540 VQYITWVITCSAKHAAVSSGQFDSVVMNPPLPTMQLPPPTSKQARPESFIATLPAYN 599
 DB 539 VQYVTWVITCSAKHAAVSAGQFDSQAWNPPLPPSQMLPPPTSKGLATCEGFIATLPVYN 598
 QY 600 SSSYHIIALWLLSABPGDORPLGHYPDEHFTEDAPRSVAATQKLIQISKGIRERNGL 659
 DB 599 ATCDVILALWLLSKEFGDQPLGTYPDEHFTTEAPRSIATFQSRLAQISRGIQERNGL 658
 QY 660 ALPTYLDPLPLIENSYSI 677
 DB 659 VLPYTYLDPLPLIENSYSI 676
 RESULT 5
 ABG61866
 ID ABG61866 standard; protein; 676 AA.
 XX AC ABG61866;
 XX DT 15-AUG-2002 (first entry)
 XX DE Prostate cancer-associated protein #67.
 XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX OS Mammalia.
 XX PN WO200230268-A2.
 XX PD 18-APR-2002.
 XX PF 12-OCT-2001; 2001WO-US032045.
 XX PR 13-OCT-2000; 2000US-00687576.
 XX PR 08-DEC-2000; 2000US-00733286.
 XX PR 08-DEC-2000; 2000US-00733742.
 XX PR 24-JAN-2001; 2001US-0263957P.
 XX PR 16-MAR-2001; 2001US-0276791P.
 XX PR 16-MAR-2001; 2001US-0276888P.
 XX PR 06-APR-2001; 2001US-0281922P.
 XX PR 24-APR-2001; 2001US-0286214P.


```
Db 1 MAEPRVRVSTGEAFGAGTWDKVSIVGTRGSPPLPLDNLGKEFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAAPPEVSPLMS - FRSDAWFCWFLEWLPGLAALHPFCYQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPLGLPLADAWFCWFQLTTPRGCHLLFPCCYQWLEGAGTLLV 118
QY 120 REGAAKVSQDHHPTLQDQORKELESQKQYKWKYIEGWPCRLDHETVKDLMLKYS 179
Db 119 QEGTAKVSWADHHPVLQOQRELOQRELOQRELOQRELOQRELOQRELOQRELOQRELO 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRTGLWRSLEMRLEFRKTPAAEVFAHMQEDAFF 239
Db 179 AKNAVFLQAGSAFAEMKIKGLLDRKGLWRSLEMRLEFRKTPAAEVFAHMQEDAFF 238
QY 240 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV 299
Db 239 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV 298
QY 300 HTNILINGKQFSAAPMTLLHQSSGSGPLPIAIQLKOTPGDNPFLPDDTDWMLLAKT 359
Db 299 QTNVINGKQFSAAPMTLLHQSSGSGPLPIAIQLKOTPGDNPFLPDDTDWMLLAKT 358
QY 360 WYRNSEFYTHAEVTHLLHAHLIPEVFALATLQRLPCHPLFKLLIPHRYTHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLQRLPCHPLFKLLIPHRYTHINTLARE 418
QY 420 LLVAPGKLIDKSTGLGTGFSDLIKRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db 419 LLVPGQVVDRTSGIGIEGFSLEIQRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 478
QY 480 QIWAIAKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGFLGRSSGMPSLDTRREAL 539
Db 479 QIWAVERFVSEIIGIYPSDESVDQDQELQAWREIFSKGFLNQBSSGIPSSLETREAL 538
QY 540 VQYITWVITCSAKHAASVSGQFDCVWMPNLPPTWQLPPPTSKGOARPESTIATLPVN 599
Db 539 VQYVTVWVITCSAKHAASVAGQFDCVWMPNLPPTWQLPPPTSKGLATCEGFIATLPVN 598
QY 600 SSSYHIALWLLSAEPGDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNGL 659
Db 599 ATCDVIALWLLSKFQDQRLGTYPDEHFTEDAPRRSVAATQSLAQISRGIQERNGL 658
QY 660 ALPYTYLDPLIENSIVI 677
Db 659 VLPYTYLDPLIENSIVI 676

RESULT 7
ADQ91763
ID ADQ91763 standard; protein; 676 AA.
AC ADQ91763;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human lipoxigenase 15-Lox-2.
DE
XX lipoxigenase; iron ligand; arachidonic acid metabolism; human;
XX lipoxigenase 15-Lox-2.
XX
XX Homo sapiens.
XX
XX US2004137483-A1.
XX
XX 15-JUL-2004.
XX
XX 18-NOV-2003; 2003US-00716204.
XX
XX 16-APR-1998; 98US-00061768.
XX
XX 17-JAN-2001; 2001US-00764246.
XX
XX (BRAS/) BRASH A R.
PA (BOEG/) BOEGLIN W E.
```

```
PA (JISA/) JISAKA M.
XX
XX Brash AR, Boeglin WE, Jisaka M;
XX
XX WPI; 2004-533356/51.
XX N-PSDB; ADQ91798.
XX
XX New lipoxigenase nucleic acid segment comprises an isolated gene encoding
XX a lipoxigenase containing an iron ligand comprising a serine, useful for
XX arachidonic acid metabolism.
XX
XX Claim 36; SEQ ID NO 2; 39pp; English.
XX
XX The invention describes a nucleic acid segment (I) comprising an isolated
XX gene encoding a lipoxigenase containing an iron ligand comprising a
XX serine, or comprises at least a 10 nucleotides long contiguous stretch of
XX the nucleic acid sequence not given in the specification (SEQ ID NO. 1)
XX or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a
XX nucleic acid segment comprising at least 10 nucleotides long contiguous
XX stretch of the nucleic acid sequence not given in the specification (SEQ
XX ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is
XX a polypeptide having the amino acid sequence Trp-Leu-Ala-Lys (SEQ ID
XX NO. 5) and Gly-Gln-Tyr-Asp-Tip (SEQ ID NO. 35). The lipoxigenase nucleic
XX acids and proteins are useful in arachidonic acid metabolism. This is the
XX amino acid sequence of human lipoxigenase 15-Lox-2.
XX
XX Sequence 676 AA;
XX
XX Query Match 79.9%; Score 2880.5; DB 8; Length 676;
XX Best Local Similarity 78.0%; Pred No. 2.8e-266;
XX Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGSPVLPLDHLGKFSAGAEEDFVTLPOD 60
Db 1 MAEPRVRVSTGEAFGAGTWDKVSIVGTRGSPPLPLDNLGKEFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAAPPEVSPLMS - FRSDAWFCWFLEWLPGLAALHPFCYQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPLGLPLADAWFCWFQLTTPRGCHLLFPCCYQWLEGAGTLLV 118
QY 120 REGAAKVSQDHHPTLQDQORKELESQKQYKWKYIEGWPCRLDHETVKDLMLKYS 179
Db 119 QEGTAKVSWADHHPVLQOQRELOQRELOQRELOQRELOQRELOQRELOQRELOQRELO 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRTGLWRSLEMRLEFRKTPAAEVFAHMQEDAFF 239
Db 179 AKNAVFLQAGSAFAEMKIKGLLDRKGLWRSLEMRLEFRKTPAAEVFAHMQEDAFF 238
QY 240 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV 299
Db 239 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV 298
QY 300 HTNILINGKQFSAAPMTLLHQSSGSGPLPIAIQLKOTPGDNPFLPDDTDWMLLAKT 359
Db 299 QTNVINGKQFSAAPMTLLHQSSGSGPLPIAIQLKOTPGDNPFLPDDTDWMLLAKT 358
QY 360 WYRNSEFYTHAEVTHLLHAHLIPEVFALATLQRLPCHPLFKLLIPHRYTHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLQRLPCHPLFKLLIPHRYTHINTLARE 418
QY 420 LLVAPGKLIDKSTGLGTGFSDLIKRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db 419 LLVPGQVVDRTSGIGIEGFSLEIQRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 478
QY 480 QIWAIAKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGFLGRSSGMPSLDTRREAL 539
Db 479 QIWAVERFVSEIIGIYPSDESVDQDQELQAWREIFSKGFLNQBSSGIPSSLETREAL 538
QY 540 VQYITWVITCSAKHAASVSGQFDCVWMPNLPPTWQLPPPTSKGOARPESTIATLPVN 599
Db 539 VQYVTVWVITCSAKHAASVAGQFDCVWMPNLPPTWQLPPPTSKGLATCEGFIATLPVN 598
QY 600 SSSYHIALWLLSAEPGDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNGL 659
```


DR N-PSDB; ACN42888.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein or the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 671 AA;

Query Match 51.8%; Score 1868; DB 8; Length 671;
Best Local Similarity 52.9%; Pred. No. 3.1e-169;
Matches 359; Conservative 112; Mismatches 199; Indels 8; Gaps 3;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHSGSPVLPDLHKGKFGAGAEDEFVTLPOD 60
DB 1 MAVYRLCVTTGPLYRAGTLDNISVTLVGTCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60
QY 61 VGTVMRLRVHKAPPEVSLPMLGFRSDAMFCRWFELWLPALHPPCYOWLGSAGELVLR 120
DB 61 LGELLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGVSVSHFPYQWIEGYCTVELR 114
QY 121 EGAAKVSWODHHTPLQDQKQKESRQKMY-SKVTYIEGWPRCLDHTVKDLDLNIKYSA 179
DB 115 PGRTARTICODSLPDLLDHRTRELRAQECYRSGNRYLPGFPMKIDIPSLMYEPNRYSA 174
QY 180 MKNAKLFYFAHSAYTELKVGKLDRLGLWRSJREMRRLFNFRKTPAAEYVFAHWQDAFP 239
DB 175 TKTISLLFNAPASLGMKRLGLLDKRGSKWKLDDMQNIFWCHKTPTTKVYTHWCEDHFF 234
QY 240 ASQFLNGINPVLIRCHSLPNFPVDEMVAVLPGTSLQAELEKGSFLVDHGLSGV 299
DB 235 GYQYLVGNVPVMLHCISLPSKLPVNDMVAPLLGQDTCLQTELRGNIFLADYWIIEA 294
QY 300 HTNILINGKQFSAAPMTLLHQSGSGFLPIALQKOTGPDPNPFLPSDDTDWMLLAKT 359
DB 295 PTHCLNGRQOYVAAPLCLLWLSL-QGALVPLAIQLSQTPGDPSPFLPTDSEWDLAKT 353
QY 360 WRNSEFYTHAEVTHLLHAHLIPEVFALATRLQPRCHPLFKLLIPIHYTLHINTLARE 419
DB 354 WRNSEFLVHNTNTHFCLTHLCEAFAMATRLQPLCHFIYKLLLPHYTYLQVNTIARA 413
QY 420 LLVAPGKLIDKSTGLGTGFSDLIKRNMBQLNYSVLCLPEDIARQVEDIPGYYYRDDGM 479
DB 414 TLLNPEGLVDQVTSIGRQGLIYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYRDDGL 473
QY 480 QIWGALKSFVSEIVSYIYSDTSVQDDQELQAWREIFSEGFLGRSSGMPSLLDTRAL 539
DB 474 KIWAATESFVSETVGYIYPSDSAVQDDSEIQAWTGEIFAQFLGRESSGFPRLCTPGEM 533
QY 540 VOYITWVIFTCSAKHAASVSGQFSDCVWMPNLPPTWQLPPTSKQARPSFIATLPAVN 599
DB 534 VKFLTAIFNCSAQHAHVNSGGQHDFGAWPNAPSSMRQPPQTKGTTTLKTYLDTLPEVN 593
QY 600 SSSYHIIALLWSAEQDQRPGLGHYPDEHFTEDAPRRSVAAFORKLIQISKGIRERNRGL 659

DB 594 TSCNNLLFWLVSQKQDRPLGTVPDHFTEEPARRSIAAPQSLRAQLSDIQRNOQL 653
QY 660 ALPTYLDPPLIENSVSI 677
DB 654 ALPTYLDPPLIENSVSI 671
RESULT 10
AAB19379
ID AAB19379 standard; protein; 711 AA.
XX AAB19379;
AC AAB19379;
DT 06-MAR-2001 (first entry)
DE Amino acid sequence of a human lipoxxygenase protein.
XX Human; lipoxxygenase; leukotriene; lipid; chemotactic agent; inflammation;
KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;
KW cancer; acne; psoriasis.
XX Homo sapiens.
OS Homo sapiens.
XX WO2000061765-A2.
PN 19-OCT-2000.
XX 12-APR-2000; 2000WO-US009657.
XX 12-APR-1999; 99US-0128817P.
PR 24-AUG-1999; 99US-0150454P.
XX (LEXI-) LEXICON GENETICS INC.
XX Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
PI WPI; 2000-665134/64.
DR N-PSDB; AAC61747.
XX Novel polynucleotides encoding human lipoxxygenase proteins useful for
PT producing transgenic animals preferably mouse.
XX Claim 3; Page 58-60; 83pp; English.
XX AAB19379-92 represent novel human lipoxxygenase proteins. Lipoxxygenases
CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
CC receptors and trigger biological effects. Leukotrienes influence a
CC variety of biological processes, and can serve as, inter alia, potent
CC chemotactic agents and mediators of inflammation, smooth muscle
CC contractions, etc. Lipoxxygenases and leukotrienes are implicated in a
CC variety of diseases and disorders, such as asthma, eye diseases,
CC arthritis, lung disease, cancer, acne, psoriasis, etc
XX
XX Query Match 51.7%; Score 1864; DB 3; Length 711;
Best Local Similarity 50.1%; Pred. No. 8.1e-169;
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHSGSPVLPDLHKGKFGAGAEDEFVTLPOD 60
DB 1 MAVYRLCVTTGPLYRAGTLDNISVTLVGTCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60
QY 61 VGTVMRLRVHKAPPEVSLPMLGFRSDAMFCRWFELWLPALHPPCYOWLGSAGELVLR 120
DB 61 LGELLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGVSVSHFPYQWIEGYCTVELR 114
QY 121 EGAAKVSWODHHTPLQDQKQKESRQKMY-SKVTYIEGWPRCLDHTVKDLDL----- 173
DB 115 PGRTARTICODSLPDLLDHRTRELRAQECYRSGNRYLPGFPMKIDIPSLMYEPNRYSA 174
QY 174 -----NIKYSAMKNKALFFKAHSAYTELKVK 199

Db	594	QGHDFGAMNPAPSSMRQPPQTKGTTTLTKTYLDTLPVNI SCNNLLLFWLVSQBPQDQR	653
QY	620	PLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRERNRGLALPYTYLDPPLIENS VSI	677
Db	654	PLGTYPDEHFTEDAPRRSVAARQKLIQISKGIRERNRGLALPYTYLDPPLIENS VSI	711
RESULT 12			
AB04578			
XX	ABB04578	standard; protein; 711 AA.	
XX	ABB04578;		
XX	21-MAR-2002	(first entry)	
XX	Human lipoxigenase	46638.	
XX	Human; lipoxigenase; 46638; cytostatic; antiarrhythmic; hypotensive;		
XX	antiatherosclerotic; cardiast; vasotropic; hypertensive;		
XX	antiinflammatory; neuroprotective; nootropic; antiparkinsonian;		
XX	anticonvulsant; hepatotropic; dermatological; antipsoriatic; fungicide;		
XX	antiidiarrhaic; antiulcer; antidiabetic; antiasthmatic; antiarthritic;		
XX	antirheumatic; osteopathic; antithyroid; antiallergic; gene therapy;		
XX	ophthalmological; antianaemic; analgesic; virucide; anorectic; vulnery;		
XX	immunomodulator.		
OS	Homo sapiens.		
XX	WO200190323-A2.		
XX	29-NOV-2001.		
XX	21-MAY-2001;	2001WO-US016380.	
XX	19-MAY-2000;	2000US-0205675P.	
XX	(MILL-) MILLENNIUM PHARM INC.		
PA	Meyers RA;		
PI	WPI; 2002-083104/11.		
DR	N-PSDB; ABA05868.		
XX	Novel human lipoxigenase family member polypeptide and polynucleotide for		
PT	diagnosing, treating immune, blood vessel, cardiovascular, inflammatory,		
PT	ovarian, lung, colon, skin disorders and disorders involving placenta.		
XX	Claim 9; Page 102; 118pp; English.		
XX	The present invention provides the protein and coding sequences of a		
CC	human protein, which is a member of lipoxigenase family, and is referred		
CC	to as 46638. The sequences can be used in the treatment of immune, blood		
CC	vessels, cardiovascular, inflammatory, cell differentiation, and		
CC	neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,		
CC	disorders associated with bone metabolism, pain or metabolic disorders,		
CC	disorders involving the placenta and viral diseases. The present sequence		
CC	is the protein of the invention		
XX	Sequence 711 AA;		
QY	Query Match	51.7%; Score 1864; DB 5; Length 711;	
Db	Best Local Similarity	50.1%; Pred. No. 8.1e-169;	
XX	Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;		
QY	1 MAKCRVSTGACGAGTWDKVSIVTGHGSPVLPDLHLGKERSAGAEDEFVTLPOD	60	
Db	1 MAVYRLCVTTGTYLAGTLDNISVTLVGTCGSPKQRLDRMGDRDFAGSVQKYKVRCTAE	60	
QY	61 VGTVMRLRVHKAPPEVSLPLMFSRDAWFCRWFELWLPALHPFCYOWLESGAGELVLR	120	
Db	61 LGELLRLRVHKE-----RYAFRKDSVCSRICVTEPDGVSHPFCYQWIEGYCTVELR	114	
QY	121 EGAAKVSWQDHHTLQDQRQKLESQRKMYSWKTYIEGWPRCLDHETVKDLDL-----	173	

Db	115	PETARTICQDSLPLLDHRTRELARQECYRWKIYAPGPFPCWVDVNSQEMESDKKFAIT	174
QY	174	-----NIKYSAMNNAKLFFKAHSAYTELKVK	199
Db	175	KTYCVDGDSGGRYLPGPWKIDIPSLMYNEPNVRSATYKISLLFNAPASLGMKLR	234
QY	200	GLLDRGTGLWRLREMRRLNFRKTPAAEYVFAHQOEDAFFAQFNGINPVILIRCHSLP	259
Db	235	GLLDRKGSWKLLDDMONIFWCHKTFTTKYVTEHWCEDHFFGYQLNGVNPVLMHCISLSP	294
QY	260	NNFPVTDEMVAIVLPGTSLQAELEKGSFLVDHCGILSGVHTNINLNGKPSAAPTLLH	319
Db	295	SKLPVTNDMVAIVLPGQDTCLQTELEGRNIFLADYWIABEPHCLNGRQYVVAAPFLCLLW	354
QY	320	QSSGSGPLLPALIAOLKOTPGDNPFLPSDDTDWMLLAKTWVRNSEFYTHEAVTHLLAH	379
Db	355	LSP-QGALVPAIAIQSQTPGDSPIFLPTDSEWMLLAKTWVRNSEFLVHNNTHFLCTH	413
QY	380	LIPEVFPALATLRQPRCHPLFKLIPHIRYTLHINTLARELLVAPGKLIDKSTGLGTGF	439
Db	414	LLCEAFAMATLRQLPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGROGL	473
QY	440	SDLIKRMEQLNYSVLCPEDIRARGVEDIPGYYYRDDGMQIWAIGAKSFVSEIYIYPS	499
Db	474	IYLMSTGLAHFTYTNFCLPDSLRARGVLAIPNYHYRDDGLKIMAAIESFVSEIYIYPS	533
QY	500	DTSVQDDOELQAWVREIFSEGFLGRESGMSLLDTREALVQYITWVITFCSAKAAVSS	559
Db	534	DASVOOSELQAWTGEIIPAQLGRESGFSRLCTPGEMVKFLTAIFLNCQAHAANVS	593
QY	560	QGFDSVVMNLPPTMQLPPTSKQARPESFIATLPVNSSSYHIIALWLSAEPDQR	619
Db	594	QGHDFGAMNPAPSSMRQPPQTKGTTTLTKTYLDTLPVNI SCNNLLLFWLVSQBPQDQR	653
QY	620	PLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRERNRGLALPYTYLDPPLIENS VSI	677
Db	654	PLGTYPDEHFTEDAPRRSVAARQKLIQISKGIRERNRGLALPYTYLDPPLIENS VSI	711
RESULT 13			
AAE39890			
ID	AAE39890	standard; protein; 711 AA.	
AC	AAE39890;		
XX	18-DEC-2003	(first entry)	
XX	Human lipoxigenase,	46638.	
XX	Human; cytochrome p450; dehydrogenase/reductase; osteomalacia; psoriasis;		
XX	lipoxigenase; hydrtase; proliferative disorder; haematopoietic disorder;		
XX	differentiative disorder; carcinoma; sarcoma; leukaemia; immune disorder;		
XX	anorexia nervosa; neural degeneration; muscular disorder; lipid disorder;		
XX	multiple sclerosis; encephalomyelitis; metabolic disorder; osteoporosis;		
XX	myasthenia gravis; bone metabolism; immunomodulator; obesity; anorectic;		
XX	eating disorder; osteodystrophy; arthritis; diabetes; anabolic; rickets;		
XX	milk fever; diabetes mellitus.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Domain	267..703	
FT		/note= "Lipoxigenase domain"	
XX	US2003092658-A1.		
XX	15-MAY-2003.		
XX	20-JUN-2002;	2002US-00175696.	
XX	02-FEB-2001;	2001US-0266140P.	
PR	04-FEB-2002;	2002US-00067668.	

CC	reductases 21509 (ADQ48409-ADQ48411) and 33770 (ADQ48412-ADQ48414);	
CC	lipoygenase 4638 (ADQ48418-ADQ48420) and hydratase 50090 (ADQ48424-ADQ48426) . The sequences are useful for diagnosing and treating	
CC	disorders, such as genetic disorders of the membrane transport	
CC	(aminocidurias, cystinosis) . CNS disorders (Alzheimer's disease,	
CC	epilepsy, Parkinson's disease), liver disorders, skeletal muscle	
CC	disorders, cellular proliferative and/or differentiative disorders	
CC	(cancer), hormonal disorders (diabetes, thyroid disorders), immune and	
CC	inflammatory disorders (rheumatoid arthritis, osteoarthritis, ulcer),	
CC	cardiovascular disorders, blood vessel disorders, neutrophil disorders,	
CC	(neutropenia, lupus), testicular disorder (mumps) and platelet disorders.	
CC	The present sequence is a lipoygenase of the invention.	
XX		
SQ	Sequence 711 AA;	
	Query Match	51.7%; Score 1864; DB 8; Length 711;
	Best Local Similarity	50.1%; Pred. No. 8.1e-169;
	Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;	
Qy	1 MAKCRVSTGEACGAGCTWQKVSIVSVITGHGESPLVDLHGLGKFSAGAEEDFVTL	PD 60
Db	1 MAVYRLCVTTGPLYRAGTLDNISVTLVGTGCESPKQRLDRMGDRDFAFGSVQKYKVRCTAE	60
Qy	61 VGTVLMURVHKAPPEVSLPLMSFRSDAWFCRWFLEWLPGAALHFPQYQWLEGAGELVLR	120
Db	61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPTDGSVSHFPQCYQWIEGYCTVELR	114
Qy	121 EGAAKVSWQDHPHTLQDOROKELSRQKWSYKWTYIEGWPRCLDHEVTVKOLDL-----	173
Db	115 PGTARTTCQSLPLDLLDHRITRELRAQECYRWKIYAFGFCQWVDVNSQFQMESDKFKALT	174
Qy	174 -----	
Db	175 KTTTCVDQGDSSGNRYLPGPFMKIDIFSLMYMEFNRYVSATKTTLSLAFNAIPASLGMKLR	234
Qy	200 GLDRTGLKSLREMRRLFNRKTPPAAYFAHWQEDAFPAQSPQINGINPVLIRRHCHSLP	259
Db	235 GLDRLKSGWKLLDDMQNIFWCHKFTTKYVTEHWCEDHFFQCYQLNGVNPVMLHCISSLP	294
Qy	260 NNPFVTDENVAPVLPGCTSLQAELEKSLFLVDHGILSGVHTNTLNGKQFQPSAAPTMLLH	319
Db	295 SKLPVTNDMVAPLLGQDTCLQTELRGNIFLADYWIILAEAPTHCINGRQQVAAAPLCILW	354
Qy	320 QSSGSGPLLPALIAIKQTPGPDNPIFLPSDDTDWLLAKTWVRNSEFVIEAVTHLLHAH	379
Db	355 LSP-QGALVPLAIQLSQTTPGSDSPIFLPTDSEWDLAKTWVRNSEFLVHENTHFLCTH	413
Qy	380 LIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHNTLARELLVAPGKLIDKSTGLGTGGF	439
Db	414 LLCEAFAMATLRLQLPCHPIYKLLPLHTRVTLQVNTIARATLNLPEGLVDQVTSIGRQGL	473
Qy	440 SDLIKRWEQLNYSVLCIPEDIRARGVEDIPGYIYRDDGQWQICAKISFVSEIYIYPS	499
Db	474 IYLMSTGLAHFTYTNFCLPDSLRARGVLAIPNHYIRDDGLKIWAIESFVSEIYGYIYPS	533
Qy	500 DTSVQDDQELQAWREIFSFSGFLGREGSGMPSLLDTRREALVOYITWVTFCSAKHAAVSS	559
Db	534 DASVQDSELQAWTGELFPAQAFLGREGSGPSRLCTPGWVKFITALIFNCSSAQHAAVNS	593
Qy	560 GQFDSVCVMNPLPPTMQLPPTPSKGOARPEFIATLPVNVSSSYHIIALMLLSAEPGDQR	619
Db	594 GQHDFGAWMENAPSSMRQPPPTQKGTTLTKYTLDTLPEVNISCNLLFLWVSQEPKQDR	653
Qy	620 PLGHYPDEHTEADAPRSVAAFQRLQIQSKGIERNRGLALPTYILDPLPIENSVI	677
Db	654 PLGTYPDEHFTPEAPRSIAAFQSLAQISRDIOERNQGLALPTYILDPLPIENSVI	711
RESULT 15		
AAAB19390		
ID	AAAB19390 standard; protein; 867 AA.	
XX		
AC	AAAB19390;	

XX	06-MAR-2001 (first entry)	
XX	Amino acid sequence of a human lipoxxygenase protein.	
DE	Human; lipoxxygenase; leukotriene; lipid; chemotactic agent; inflammation;	
XX	smooth muscle contraction; asthma; eye disease; arthritis; lung disease;	
KW	cancer; acne; psoriasis.	
KW		
XX	Homo sapiens.	
OS		
XX	W0200061765-A2.	
PN		
XX	19-OCT-2000.	
XX		
XX	12-APR-2000; 2000WO-US009657.	
PF		
XX		
PR	12-APR-1999; 99US-0128817P.	
PR	24-AUG-1999; 99US-0150454P.	
XX	(LEXI-) LEXICON GENETICS INC.	
PA		
XX	Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;	
PI		
XX	WPI; 2000-665134/64.	
DR	N-PSDB; AAC61758.	
DR		
XX		
XX	Novel polynucleotides encoding human lipoxxygenase proteins useful for	
PT	producing transgenic animals preferably mouse.	
PT		
XX	Claim 3; Page 74-76; 83pp; English.	
PS		
XX	AAB19379-92 represent novel human lipoxxygenase proteins. Lipoxxygenases	
CC	oxidise lipids to produce leukotrienes. Leukotrienes bind cognate	
CC	receptors and trigger biological effects. Leukotrienes influence a	
CC	variety of biological processes, and can serve as, inter alia, potent	
CC	chemotactic agents and mediators of inflammation, smooth muscle	
CC	contractions, etc. . Lipoxxygenases and leukotrienes are implicated in a	
CC	variety of diseases and disorders, such as asthma, eye diseases,	
CC	arthritis, lung disease, cancer, acne, psoriasis, etc	
XX		
XX	Sequence 867 AA;	
XX		
Query Match	51.7%; Score 1864; DB 3; Length 867;	
Best Local Similarity	50.1%; Pred. No. 1.1e-168;	
Matches	360; Conservative 112; Mismatches 198; Indels 48; Gaps 3	
Qy	1 MAKRRVYSTGACGATWQKVSIVGTGHSPLVPLDHLGKEFGAGAEDEFTVLPQD 60	
Db	157 MAVRYLCVTTGPLYRAGTLDNISVTLVGTGESPQRDLDRMGDRDFAPGSQVKYKVRCTAE 216	
Qy	61 VGTVLMLRVHKAPPEVSILPLMSFRSDAFCWFPLEWLPGAALHFFCYOWLEGAGELVLR 120	
Db	217 LGELLLLRVHKE-----RYAFFRKDSWYCSRICVTEPDGDSVSHFPYQWIEGYCTVELR 270	
Qy	121 EGAAKVSWDHHPTLDQOROKESRQWYSWKTYIEGWPRCLDHTVKDLDL-----173	
Db	271 PGTARTICQDSLPLLLDHTRELRAQECYRWKIYAPGFCWVDVNSFQWESDKKFALT 330	
Qy	174 -----NIKYSAMKNAKLFFKAHSAYTELKVK 390	
Db	331 KTTTCVDQDSSGNRYLPGPFWKIDIPSLMYEPNVRYSATKTSLLFNAIPASLGKMLR 390	
Qy	200 GLLDRTGLWRLSRLENRRILFNFRKTPAAEYVFAHQEDAFASQFLGGINVPLTRCHSLP 259	
Db	391 GLLDKRGSKWKLLDDMQNTFWCHKTFTTKYVTEHWCEDHFFGYQYGLNGWNPVMLHCISLSP 450	
Qy	260 NNFPVTDWMAVPLGPGTSLQAELEKGSFLVADHGISLVGHTNLNGKPOFSAAPMTLLH 319	
Db	451 SKLPVTNDMAVPLLGQDTCLOTELERGNIFLADTWILAEAPTHCLNGRQOYVAAPICLLW 510	
Qy	320 QSSGSGPLPIAQLKQTPGPNPFIPLPSDDTDWLLAKTWRNRSFYTHAEVTHLLHAH 379	

```
RESULT 15
AAB19390
ID  AAB1
XX
AC  AAB1
```


Db 511 LSP-QGALVPLAIQISOTPGDPSIFLPTDSEMDWLLAKTWVRNSEFLVHNNTHFLCTH 569
Qy 380 LIPEVPALATLQOLPRCHPLFKLLIPHRYTLHINTLARELLVAPKGLIDKSTGLTGGF 439
Db 570 LLCEAFAMATLRLQLPLCHPIYKLLPLHRYTLQVNTIARATLLNPEGLVDQVTSIGROGL 629
Qy 440 SDLIKRNNEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGMOIWGAIKSFVSEIYSIYVPS 499
Db 630 IYLMSTGLAHFTYTNFCLPDSLRARGVLAIPNYHYRDDGLKIWAIESFVSEIVGYIYVPS 689
Qy 500 DTSVQDDOELQAWVREIFSEGFLGRESSCMPSSLDTREALVQYITMWIFTCSAKHAAVSS 559
Db 690 DASVQDSELQAWTGEIIFAQFLGRESSGFFSRLCTPGEMVKFELTAIFNCSAQHAAVNS 749
Qy 560 GQFDSQVWMPNLPTMQLPPTTSKQARPEFIATLPVNSSSYHIIALWLLSABPGDQR 619
Db 750 GQHDFGAWNPAPSSMRQPPQTKGTTTKTYLDTLPEVNTSCNNLLFLWLVSQEPKQOR 809
Qy 620 PLGHYPDEHFTEDAPRRSVAAPORKLIQISKGIRERNEGLALPYTYLDPPLIENSVSI 677
Db 810 PLGTYPDEHFTTEAPRRSIAAPQSRLAQISRDIOERNQGLALPYTYLDPPLIENSVSI 867

Search completed: July 18, 2005, 21:57:22
Job time : 118.375 secs

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OM protein - protein search, using sw model

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(without alignments)
1637.384 Million cell updates/sec

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Perfect score: 3604
Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTLDPLIENSVSI 677

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3604	100.0	677	US-09-061-768A-4	Sequence 4, Appli
2	3604	100.0	677	US-09-764-246-4	Sequence 4, Appli
3	2883.5	80.0	679	US-09-949-016-8912	Sequence 8912, Ap
4	2880.5	79.9	676	US-09-061-768A-2	Sequence 2, Appli
5	2880.5	79.9	676	US-09-764-246-2	Sequence 2, Appli
6	2880.5	79.9	676	US-09-949-016-6027	Sequence 6027, Ap
7	1864	51.7	711	US-09-547-435-2	Sequence 2, Appli
8	1864	51.7	867	US-09-547-435-24	Sequence 24, Appli
9	1795	49.8	701	US-09-087-727-2	Sequence 2, Appli
10	1795	49.8	701	US-09-853-053-2	Sequence 2, Appli
11	1795	49.8	701	US-09-949-016-6026	Sequence 6026, Ap
12	1588	44.1	556	US-09-547-435-6	Sequence 6, Appli
13	1464	40.6	615	US-09-547-435-10	Sequence 10, Appli
14	1464	40.6	771	US-09-547-435-28	Sequence 28, Appli
15	1442.5	40.0	674	US-09-949-016-5980	Sequence 5980, Ap
16	1442.5	40.0	689	US-09-949-016-11692	Sequence 11692, A
17	1212	33.6	663	US-09-641-638-653	Sequence 653, App
18	1212	33.6	663	US-10-170-097-653	Sequence 653, App
19	1188	33.0	460	US-09-547-435-12	Sequence 12, Appli
20	1186.5	32.9	662	US-09-061-768A-25	Sequence 25, Appli
21	1186.5	32.9	662	US-09-764-246-25	Sequence 25, Appli
22	1077.5	29.9	489	US-09-547-435-4	Sequence 4, Appli
23	1077.5	29.9	645	US-09-547-435-26	Sequence 26, Appli
24	953	26.4	291	US-09-547-435-14	Sequence 14, Appli
25	801.5	22.2	334	US-09-547-435-8	Sequence 8, Appli
26	799.5	22.2	675	US-09-902-540-12713	Sequence 12713, A
27	710	19.7	360	US-09-949-016-8911	Sequence 8911, Ap

28	524	17.3	592	3	US-09-413-814-83	Sequence 83, Appli
29	598	16.6	692	4	US-03-252-991A-19668	Sequence 19668, A
30	553	15.3	195	4	US-09-547-435-20	Sequence 20, Appli
31	544.5	15.1	862	4	US-09-978-522-1	Sequence 1, Appli
32	534	14.8	859	4	US-09-978-522-3	Sequence 3, Appli
33	520	14.4	864	4	US-09-810-268-3	Sequence 3, Appli
34	518.5	14.4	857	4	US-09-751-687-17	Sequence 17, Appli
35	516.5	14.3	864	4	US-03-751-687-18	Sequence 18, Appli
36	495	13.7	865	4	US-09-751-687-16	Sequence 16, Appli
37	493	13.7	862	4	US-09-751-687-9	Sequence 9, Appli
38	486	13.5	862	4	US-09-751-687-12	Sequence 12, Appli
39	483	13.4	139	4	US-09-547-435-18	Sequence 18, Appli
40	460.5	12.8	901	4	US-09-714-767A-4	Sequence 4, Appli
41	457	12.7	839	4	US-03-751-687-15	Sequence 15, Appli
42	389	10.8	110	4	US-09-547-435-22	Sequence 22, Appli
43	166.5	4.6	69	4	US-09-547-435-16	Sequence 16, Appli
44	158.5	4.4	131	4	US-09-641-638-654	Sequence 654, App
45	158.5	4.4	131	4	US-10-170-097-654	Sequence 654, App

ALIGNMENTS

RESULT 1
US-09-061-768A-4
; Sequence 4, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 677 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-061-768A-4

Query Match 100.0%; Score 3604; DB 3; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVSVITGHGESPLVLDHLGKFSAGAEEDFEVTLFQD 60

Db 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPAAALHPPCYOWLEGAGELVLR 120
Db 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPAAALHPPCYOWLEGAGELVLR 120
QY 121 EGAAKVSWQDHHPTLQDQKQELSRQKMSWKTYIEGWPRCLDHTVTDKLDLNIKYSAM 180
Db 121 EGAAKVSWQDHHPTLQDQKQELSRQKMSWKTYIEGWPRCLDHTVTDKLDLNIKYSAM 180
QY 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
Db 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
QY 241 SQFLNGINPVLRCHSLPNNPVTDEMVAFLPGTSLQAELEKGSFLVDHGILSGVH 300
Db 241 SQFLNGINPVLRCHSLPNNPVTDEMVAFLPGTSLQAELEKGSFLVDHGILSGVH 300
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420
Db 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420
QY 421 LVAPGKLDKSTGLTGTFSDLIKRNMEQLNYSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
Db 421 LVAPGKLDKSTGLTGTFSDLIKRNMEQLNYSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
QY 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFGLGREGSGMPSLLDTREALV 540
Db 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFGLGREGSGMPSLLDTREALV 540
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNLPPTMQLPPPTSGQARPSFIATLPVANS 600
Db 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNLPPTMQLPPPTSGQARPSFIATLPVANS 600
QY 601 SSVHIIALLWSAEPGDQRLPGHYDEHFTEDAPRSVAAFORKLQISKGRIRNRGLA 660
Db 601 SSVHIIALLWSAEPGDQRLPGHYDEHFTEDAPRSVAAFORKLQISKGRIRNRGLA 660
QY 661 LPYTYLDPPLIENSUSI 677
Db 661 LPYTYLDPPLIENSUSI 677

RESULT 2

US-09-764-246-4
; Sequence 4, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: AKLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-764-246-4
Query Match 100.0%; Score 3604; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
Db 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPAAALHPPCYOWLEGAGELVLR 120
Db 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPAAALHPPCYOWLEGAGELVLR 120
QY 121 EGAAKVSWQDHHPTLQDQKQELSRQKMSWKTYIEGWPRCLDHTVTDKLDLNIKYSAM 180
Db 121 EGAAKVSWQDHHPTLQDQKQELSRQKMSWKTYIEGWPRCLDHTVTDKLDLNIKYSAM 180
QY 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
Db 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
QY 241 SQFLNGINPVLRCHSLPNNPVTDEMVAFLPGTSLQAELEKGSFLVDHGILSGVH 300
Db 241 SQFLNGINPVLRCHSLPNNPVTDEMVAFLPGTSLQAELEKGSFLVDHGILSGVH 300
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420
Db 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420
QY 421 LVAPGKLDKSTGLTGTFSDLIKRNMEQLNYSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
Db 421 LVAPGKLDKSTGLTGTFSDLIKRNMEQLNYSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
QY 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFGLGREGSGMPSLLDTREALV 540
Db 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFGLGREGSGMPSLLDTREALV 540
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNLPPTMQLPPPTSGQARPSFIATLPVANS 600
Db 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMNLPPTMQLPPPTSGQARPSFIATLPVANS 600
QY 601 SSVHIIALLWSAEPGDQRLPGHYDEHFTEDAPRSVAAFORKLQISKGRIRNRGLA 660
Db 601 SSVHIIALLWSAEPGDQRLPGHYDEHFTEDAPRSVAAFORKLQISKGRIRNRGLA 660
QY 661 LPYTYLDPPLIENSUSI 677
Db 661 LPYTYLDPPLIENSUSI 677

RESULT 3

US-09-949-016-8912
; Sequence 8912, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8912
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8912

Query Match 80.0%; Score 2883.5; DB 4; Length 679;

Best Local Similarity 78.2%; Pred. No. 1e-316;

Matches 530; Conservative 68; Mismatches 77; Indels 3; Gaps 2;

Qy 1 MAKCRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHGKFSAGAEEDFEVTLPOD 60
Db 4 MAEPRVSTGEAFGAGTWDKVSIVGTRGESPLDLNLGKFTAGAEEDFQVTLPE 63
Qy 61 VGTVMRLRVHKAPEVSVSLPLMS - FRSDAFCRWFLEWLPGAALHFPVQWLEGAGELVL 119
Db 64 VGRVLLLRVHKAPP - VLPGLGLAPDAWFCRWFQLTTPRGHLLFPVQWLEGAGTLLV 121
Qy 120 REGAAKVSQDHHPTLQDQROKELSRQKYSWKTYIEGWPCRLDHTVTKDLNLKYS 179
Db 122 QEGTAKVSWADHHPVLQOQROEELQARQEMQKAYNPGWPHCLDEKTVDELNLKYST 181
Qy 180 MKNAKLFFKAHSAYTELKVKGLLDRGTGLWRSLEMRRLFNFRKTPAAEYVFAHQEDAFF 239
Db 182 AKNANFYLOAGSAPAEKIKGLLDRKGLWRSLEMRRLFNFRRTPAAEHAFHWQEDAFF 241
Qy 240 ASQFLNGINPVLIRCHSLPNNFPVTDMSVAPVLGPGTSLQAELEKSGSLFLVDHGILSGV 299
Db 242 ASQFLNGINPVLIRCHYLKPNFPVTDANVASVLGPGTSLQAELEKSGSLFLVDHGILSGI 301
Qy 300 HTNLLNGKPFSAAPMTLLHSGSGPLLPALIAQLKQTPGPDNPIFLPSSDDTWDWLLAKT 359
Db 302 QTNVINGKPFSAAPMTLLYQSPGGLPLPLAIQLSQTPGNSPIFLPDDKDWLLAKT 361
Qy 360 WYRNSFYIHEAVTHLLHAHLIPEVFALATLQRPCHPLFKLLIPHYRYTLHINTLARE 419
Db 362 WYRNBFSFHEALTHLLSHLLPEVFTLATLQRPCHPLFKLLIPHYRYTLHINTLARE 421
Qy 420 LLVAPGKLIDKSTGLGTGSGDLIKRNEQLNYSVLCLPEDIRARGVEDIPGYYYRDDGM 479
Db 422 LLVPGQVDRSTGIGIEGSELQRNNKQNLNLSLCLPEDIRTRGVEDIPIGYYYRDDGM 481
Qy 480 QIWGAIKSFVSEIYSYPSDTSVQDDQLQAWREIFSEGFLGRESSGMPSLDITREAL 539
Db 482 QIWGAVERFVSEIIGIYPSDESQDDRELQAWREIFSKGLNQGESSGIPSSLETREAL 541
Qy 540 VOYITWJFTCSAKHAAVSSGQFDSQVWMPNLPTWMLPPPTSKGQAPSPESIATLPVAV 599
Db 542 VOYITWJFTCSAKHAAVSAGQFDSQVWMPNLPPSMQLPPPTSKGLATCEGIATLPVAV 601
Qy 600 SSSVHIALWLLSAPGQORPLGHVPDEHFTEDAPRRSVAAPFQKLIQISGIRENRGL 659
Db 602 ATCDVILALWLLSKPQORPLGTYPDEHFTTEAPRRSIATFQSKRLAQISRGIOERNRGL 661

Qy 660 ALPTYLDPLPIENSIVI 677
Db 662 VLPYTYLDPPLPIENSIVI 679

RESULT 4

US-09-061-768A-2
; Sequence 2, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-061-768A-2

Query Match 79.9%; Score 2880.5; DB 3; Length 676;

Best Local Similarity 78.0%; Pred. No. 2.2e-316;

Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

Qy 1 MAKCRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHGKFSAGAEEDFEVTLPOD 60
Db 1 MAEPRVSTGEAFGAGTWDKVSIVGTRGESPLDLNLGKFTAGAEEDFQVTLPE 60
Qy 61 VGTVMRLRVHKAPEVSVSLPLMS - FRSDAFCRWFLEWLPGAALHFPVQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP - VLPGLGLAPDAWFCRWFQLTTPRGHLLFPVQWLEGAGTLLV 118
Qy 120 REGAAKVSQDHHPTLQDQROKELSRQKYSWKTYIEGWPCRLDHTVTKDLNLKYS 179
Db 119 QEGTAKVSWADHHPVLQOQROEELQARQEMQKAYNPGWPHCLDEKTVDELNLKYST 178
Qy 180 MKNAKLFFKAHSAYTELKVKGLLDRGTGLWRSLEMRRLFNFRKTPAAEYVFAHQEDAFF 239
Db 179 AKNANFYLOAGSAPAEKIKGLLDRKGLWRSLEMRRLFNFRRTPAAEHAFHWQEDAFF 238
Qy 240 ASQFLNGINPVLIRCHSLPNNFPVTDMSVAPVLGPGTSLQAELEKSGSLFLVDHGILSGV 299

Db 239 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASLGGTSLQAELEKSGSLFLVDHGILSGI 298
QY 300 HTNILNGKQFQSAAPMTLLHQSSGGLPLPIAIQLKQTEGPDNPFLPSSDDTWDMLLAKT 359
Db 299 QTNVINGKQFQSAAPMTLLYSPGCGPLPLAIQLSQTGPNPFLPDDDKWMLLAKT 358
QY 360 WYRNSEFYIHEAVTHLLHAHLIPEVPALATLQRLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNABFSFHEALTHLLHSHLLPEVFTLATLQRLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLAAPKLDKSTGLTGCGFSDLIKENMEOLANYSLCLPEDIRANGVEDIPGYVYRDDGM 479
Db 419 LLIIVPGQVDRSTGIGIEGSELIQNMKQLNYSLLCLPEDIRANGVEDIPGYVYRDDGM 478
QY 480 QIWAITSFVSEIVSYIYPSDTSVQDDQELQAWVREIFSEGFLGRESSGMPILLDTREAL 539
Db 479 QIWAVERFVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNCESSIPSSLETREAL 538
QY 540 VQYITWVIFTCSAKHAHVSSGQFDSVMMNPPLPPTWQLPPTSKGQARPESTIATLPVN 599
Db 539 VQYVTVMTVIFTCSAKHAHVSSGQFDSVMMNPPLPPTWQLPPTSKGQARPESTIATLPVN 598
QY 600 SSSYHIIALWLSAEPDORPLGHPYDEHFTEDAPRRSVAAPORKLIQISKGIERNRGL 659
Db 599 ATCDVILALWLSKEPQDQRLGTYPDEHFTEDAPRRSVAAPORKLIQISKGIERNRGL 658
QY 660 ALPTYTLDPLPIENSYSI 677
Db 659 VLPYTYLDPLPIENSYSI 676

RESULT 5
US-09-764-246-2
; Sequence 2, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; NAME: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-764-246-2
Query Match 79.9%; Score 2880.5; DB 4; Length 676;
Best Local Similarity 78.0%; Pred. No. 2.2e-316;
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVSTHGESPLVPLDLHLGKEFSAGAEEDFEVTLPOD 60
Db 1 MAEFVRVSTGEACGAGTWDKVSIVSTHGESPLVPLDLNLGKEFTAGAEEDFEVTLPED 60
QY 61 VGTVMMLRVHVKAPPEVSLPLMS-FRSDAWFCRWFLEWLPGLAALHFPYQWLEGAGELVL 119
Db 61 VGRVLLLRVHVKAPP-VLPFLGLPADAWFCRWFQLTTPRGHLLFPYQWLEGAGTLLV 118
QY 120 REGAAKVSQDHPHTLOQROKELSRKMYSWKTYIEGWPRCLDHEVTVDLNLKYSY 179
Db 119 QEGTAKVSWADHPVLOQROQELQARQEMTQWKAYNFGWPHCLDEKTVEDLELNKYST 178
QY 180 MKNAKLFFKAHSAYTELKVKGLDRTGLWRSLSREMRRLFNFRKTPAAEYVFAHWQEDAFF 239
Db 179 AKNANFYLAGSAFAEMKIKGLDRKGLWRSLSNEMKRIFNFRRTPAEHAPEHWQEDAFF 238
QY 240 ASQFLNGINPVLIIRCHSLPNNFPVTDENAPVLGPGTSLQAELEKSGSLFLVDHGILSGV 299
Db 239 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASLGGTSLQAELEKSGSLFLVDHGILSGI 298
QY 300 HTNILNGKQFQSAAPMTLLHOSGGLPLPIAIQLKQTEGPDNPFLPSSDDTWDMLLAKT 359
Db 299 QTNVINGKQFQSAAPMTLLYSPGCGPLPLAIQLSQTGPNPFLPDDDKWMLLAKT 358
QY 360 WYRNSEFYIHEAVTHLLHAHLIPEVPALATLQRLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNABFSFHEALTHLLHSHLLPEVFTLATLQRLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLAAPKLDKSTGLTGCGFSDLIKENMEOLNYSVLCLPEDIRANGVEDIPGYVYRDDGM 479
Db 419 LLIIVPGQVDRSTGIGIEGSELIQNMKQLNYSLLCLPEDIRANGVEDIPGYVYRDDGM 478
QY 480 QIWAITSFVSEIVSYIYPSDTSVQDDQELQAWVREIFSEGFLGRESSGMPILLDTREAL 539
Db 479 QIWAVERFVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNCESSIPSSLETREAL 538
QY 540 VQYITWVIFTCSAKHAHVSSGQFDSVMMNPPLPPTWQLPPTSKGQARPESTIATLPVN 599
Db 539 VQYVTVMTVIFTCSAKHAHVSSGQFDSVMMNPPLPPTWQLPPTSKGQARPESTIATLPVN 598
QY 600 SSSYHIIALWLSAEPDORPLGHPYDEHFTEDAPRRSVAAPORKLIQISKGIERNRGL 659
Db 599 ATCDVILALWLSKEPQDQRLGTYPDEHFTEDAPRRSVAAPORKLIQISKGIERNRGL 658
QY 660 ALPTYTLDPLPIENSYSI 677
Db 659 VLPYTYLDPLPIENSYSI 676

RESULT 6
US-09-949-016-6027
; Sequence 6027, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6027
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6027

Query Match 79.9%; Score 2880.5; DB 4; Length 676;
Best Local Similarity 78.0%; Pred. No. 2.2e-316;
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

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QY 1 MAKCHVRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
Db 1 MAFPRVSTGEAFAGTWDKVSIVGTHGESPLVPLDLNLGKEFTAGAEEDFQVTLPE 60
QY 61 VGTVLMRLVHKAPPEVSLPLMS-PRSDAWFCRWFELEWLPAAALHPFCVQWLEGAGELVL 119
Db 61 VORVLLLRVHKAPP--VLPLGLPADDAWFCWFOITPPRGHLLFPQVQWLEGAGTULV 118
QY 120 REGAAKVSQDHPHTLOPQORQKESRQKYSWKTYIEGWPCRLDHETVKOLDLMIKYS 179
Db 119 QEGTAKVSMADHPVLQOQOELOARQOEYQWKAYNFGWPHCLDEKTVEDLELNKYST 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRTGLWRSLEMRRLFNFRKTPAAAYVFAHWOEDAFF 239
Db 179 AKNANFYLAQSAFAEMKIKGLLDRKGLWRSLEMRKIFNFRRTPAASHAFEHWOEDAFF 238
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Db 239 ASQFLNGINPVLIIRCHSLPNNFVPTDEMVAAPVLPGGTSLQAELEKSGSLFLVDHGILSGI 298
QY 300 HTNILINGKQPSAAPTMLLHOSGSGPLLPALAIQKOTPGDNPFLPSSDDTWDWLLAKT 359
Db 299 QTNVINGKQPSAAPTMLLYQSPGGLPLPALAIQKOTPGDNPFLPSSDDTWDWLLAKT 358
QY 360 WVRNSEFYHRAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLARE 419
Db 359 WVRNAEFSFEALTHLLSHLLPEVFTLATLRLQPRCHPLFKLLIPIHRYTLHINTLARE 418
QY 420 LLVAPGLIKDSTGLTGCGFSDLIKRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db 419 LLVPGQVQVDRSTGIGTSGFSELIQRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 478
QY 480 QIWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFLGREGSGMPSSLDLTREAL 539
Db 479 QIWGAVERFVSEIIGIYPSDESQDDRELQAWVREIFSKGFLNQESSGIPSSLETRAL 538
QY 540 VOYITWVFTCSAKHAAVSSGQFDSVCMWPNLPPTMQLPPTTSKQARPESFIATLPVAVN 599
Db 539 VOYVTVWVFTCSAKHAAVSAGQFDSVCMWPNLPPTMQLPPTTSKGLATCEGFIATLPVAVN 598
QY 600 SSSVHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRENRGL 659
Db 599 ATCDVILALWLLSKGPGQORPLGTYPDEHFTEDAPRRSVAAPFQKLIQISKGIRENRGL 658
QY 660 ALPTYLDPPPLIENSVS 677
Db 659 VLPYLDPPPLIENSVS 676
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RESULT 7

US-09-547-435-2
; Sequence 2, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-2

Query Match 51.7%; Score 1864; DB 4; Length 711;
Best Local Similarity 50.1%; Pred. No. 3.3e-201;
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;

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QY 1 MAKCHVRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
Db 1 MAVYRLCVTTGTPYLRAGTLDNISVTLVGTGCEPKQRLDRMGDRDPAGSVQKYKVRCTAE 60
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPAAALHPFCVQWLEGAGELVL 120
Db 61 LGELLRLVRHKE-----RVAFPRKDSWYCSRICVTEPDGVSHPPCYQWIEGYCTVEIR 114
QY 121 EGAAKVSWQDHPHTLOPQORQKESRQKYSWKTYIEGWPCRLDHETVKOLDL----- 173
Db 115 PGTARTICQDLSLPLLDHRTRELRQECYRWKIYAPGFCMVVDVNSFQEMESDKKFAIT 174
QY 174 -----NIKYSAMNAKLPFKAHSAVTELVK 199
Db 175 KTTTCVQDSSGNRYLPGGPMKIDIPSLMYMENVRYSATKTSLLFNATPASLGMLK 234
QY 200 GLLDRTGLWRSLEMRRLFNFRKTPAAAYVFAHWOEDAFFASQFLNGINPVLIIRCHSLP 259
Db 235 GLLDRKSGWKLLDQWNIQFWCHKTFTTKYVTEHWCEDEHFFGQYLVGNVPMVLMHCISL 294
QY 260 NNPVTVDEMVAAPVLPGGTSLQAELEKSGSLFLVDHGILSGVHTNILINGKQPSAAPTMLLH 319
Db 295 SKLPVTNDMVAAPLQDTCQLQTELEGNIFLADYWIABEAPTHCLNGRQQVVAAPLCLLW 354
QY 320 QSSGSGPLLPALAIQKOTPGDNPFLPSSDDTWDWLLAKTWRNSEFYHRAVTHLLHAH 379
Db 355 LSP-QGALVPLAIQKOTPGDNPFLPSSDDTWDWLLAKTWRNSEFYHRAVTHLLHAH 413
QY 380 LIPEVFALATLRLQPRCHPLFKLLIPIHRYTLHINTLARELLVAPGLIKDSTGLTGCGF 439
Db 414 LLCEAFAMATLRLQPRCHPLFKLLIPIHRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL 473
QY 440 SLLIKRNMQLNYSVLCLPEDIRARGVEDIPGYVYRDDGMQIWAIGAKSFVSEIYIYPS 499
Db 474 IYLMSTGLAHFTYTNFCLPSLRARGVLAIPNHYRDDGLKIWAIAIESFVSEIYIYPS 533
QY 500 DTSVQDDQELQAWVREIFSEGFLGREGSGMPSSLDLTREALVOYITWVFTCSAKHAAYSS 559
Db 534 DASVQDSELOQWTCGEIIPAQAFLEGREGSGPSPRLCTGEMVKFLTAIFNCSAQHAAYSS 593
QY 560 GQFDSVCMWPNLPPTMQLPPTTSKQARPESFIATLPVAVNSSVHIIALWLLSAEPGQOR 619
Db 594 GQHDFGAWMPNAPSSMRQPPQTKGTTTLTKYTLDTLPVNVISCNLLFLWVSQEPKQOR 653
QY 620 PLGHYPDEHFTEDAPRRSVAAPFQKLIQISKGIRENRGLALPTYLDPPPLIENSVS 677
Db 654 PLGTYPDEHFTEDAPRRSVAAPFQKLIQISKGIRENRGLALPTYLDPPPLIENSVS 711
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RESULT 8

US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael

APPLICANT: Turner, C. Alexander, Jr.

APPLICANT: Zambrowicz, Brian

APPLICANT: Nehls, Michael

APPLICANT: Friedrich, Glenn

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: 7705.0009-00000

CURRENT APPLICATION NUMBER: US/09/547,435

CURRENT FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28

LENGTH: 771

TYPE: PRT

ORGANISM: Homo sapiens

US-09-547-435-28

Query Match 40.6%; Score 1464; DB 4; Length 771;
Best Local Similarity 47.5%; Pred. No. 7.6e-156; Indels 48; Gaps 3;
Matches 286; Conservative 95; Mismatches 173;

Qy 1 MAKCRVRYSTGACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60

Db 157 MAVYELCVTTGPLYLAGTLDNISVLVTGTCESPKQRLDRGRDPAGSVQKYKRCRTAR 216

Qy 61 VGTVLMLRVHAKPPEVSLPMSFRSDAWFCRWFELWLPGAALHPPCYQWLEGAGELVLR 120

Db 217 LGELLRLVRKE-----RYAFFRRKDSWCYRICVTEPDGSGVSHPPCYQWLEGAGELVLR 270

Qy 121 EGAKVSHODHHTPLQDOROKELSRQKMYSKTYIEGWPRCLDHTETVKDLDL----- 173

Db 271 PGTARTICODSLFLDLHRTRELRAQRCYRWKIYAPGPPCMVDVNSFOEMESDKKFALT 330

Qy 174 -----NIKYSAMNNAKLPFAKHSAYTELKVK 199

Db 331 KTTTCVDOGSSGNRYLPGFPKIDIPSLMYMEPNVRYSAKTSILLFNAIPASLGMLR 390

Qy 200 GLLDRTGLWRSLRMRRLFNFRKTPAAEYVFAHWQEDAFQAFQFLNGINPVLIRCHSLP 259

Db 391 GLLDRKSGWKKLDDMQNIFWCHKTFTTKYVTEHWCEDEHFFGQYLVNGVNPVMLHCISLP 450

Qy 260 NNPVTDWAPVLPVPGTSLQAELEKSLFLVDHGLSGVHTNINLNGKPOPSAAPMTLLH 319

Db 451 SKLPVTDWAPVLPVPGTSLQAELEKSLFLVDHGLSGVHTNINLNGKPOPSAAPMTLLH 510

Qy 320 QSSGSGPLLPATLQLOKTPGPNPFLPSDDTMDLLAKTWVRNSEFYTHEAVTHLHAH 379

Db 511 LSP-QGALVPLAIQUSQTPGDPSPFLPTDSEWDLAKTWVRNSEFYTHEAVTHLHAH 569

Qy 380 LIPEVFALATLQPRCHPLFKLLPHIRYTHLINTLARELIVAPGKLIDKSTGLTGTF 439

Db 570 LLCEAFAMATLQPRCHPLFKLLPHIRYTHLINTLARELIVAPGKLIDKSTGLTGTF 629

Qy 440 SDLIKRNEQLNYSVLCPEDIRARGVEDIPGYVYRDDGMQIWGAIKSFVSEIVSIYPS 499

Db 630 IYLMSTGLAHTYTNFCLPDSLRARGVLAIPNYHYRDDGLKIWAIESFVSEIVSIYPS 689

Qy 500 DTSVODDLOQAWVREIFSEGLGREGSGMPSLLDREALVOYITWVLTCSAKHAAYSS 559

Db 690 DASVODDLOQAWVREIFSEGLGREGSGMPSLLDREALVOYITWVLTCSAKHAAYSS 749

Qy 560 GQ 561

Db 750 GQ 751

RESULT 15

US-09-949-016-5980

Sequence 5980, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5980

LENGTH: 674

TYPE: PRT

ORGANISM: Human

US-09-949-016-5980

Query Match 40.0%; Score 1442.5; DB 4; Length 674;
Best Local Similarity 42.6%; Pred. No. 1.6e-153; Indels 19; Gaps 7;
Matches 292; Conservative 126; Mismatches 248;

Qy 1 MAKCRVRYSTGACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPO 59

Db 1 MPSYTVVATGVSQWFAAGTDDYIYLSVGSAGCSEKHLDDKPFYNDFERGAVDSYDVTVDE 60

Qy 60 DVGTVLMLRVHAKPPEVSLPMSFRSDAWFCRWFELWLPGAALHPPCYQWLEGAGELV 119

Db 61 ELGEIQLVRIEKR-----KYWLNDOWLYKTYLTTPHGDYIEFPYCRWITGDEVV 112

Qy 120 REGAAKVSQWQHHTPLQDOROKELSRQKMYSKTYIEGWPRCLDHTETVKDLDLNIK 179

Db 113 RDRAKLARDQIHLKQHRREKLETRQKQYRWMEWNPFPPLSIDAKCHKDLPDIOQD 172

Qy 180 MNAKLFPKASHAYTELKVKGLDRL-TGLWRSLSRMRLEFNFRKTPAAEYVFAHWQEDAF 238

Db 173 EKVDFVLNYSKAMENLFINRPMFMFQSSWNDADFEXIFVKISNTISERVVNHQEDLM 232

Qy 239 FASQFLNGINPVLIRRHCHSLPNNFPVTDWAPVLPVPGTSLQAELEKSLFLVDHGLSG 298

Db 233 FGQFLNGCNFVLIRRHCHSLPNNFPVTDWAPVLPVPGTSLQAELEKSLFLVDHGLSG 292

Qy 299 VHTNINLNGP---QFSAAPMTLLHQSSGSGPLPIAIOLKOTPGDNPFIPLSDDTWDL 355

Db 293 IDAN--KTDPCTLOFLAAPICLLYKNL-ANKIVPIAIQNLQIPGDNFIPLPSDAKYDL 349

Qy 356 LAKTWVRNSEFYTHEAVTHLHAHLIPEVPALATLQPRCHPLFKLLPHIRYTHLHNT 415

Db 350 LAKTWVRNSEFYTHEAVTHLHAHLIPEVPALATLQPRCHPLFKLLPHIRYTHLHNT 409

Qy 416 LARELLVAPGKLIDKSTGLTGTFSDLIKRNEQLNYSVLCPEDIRARGV---EDIRGY 472

Db 410 KARQLICECLGFDKANATGGGHVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 469

Qy 473 YRRDGMQIWGAIKSFVSEIVSIYIPSDTSVQDDQELQAWVREIFSEGLGREGSGMPSL 532

Db 470 FYRDDGLLWMEAIRFTAEEVDIYVEGQVVEEDPELODFVNDVYVYVYVYVYVYVYV 529

Qy 533 LDTREALVOYITWVLTCSAKHAAYSSQFSDSCVWMPNLPTMQLPPTSPGQARPESEFI 592

Db 530 VKSEQLSEYITWVLTCSAKHAAYSSQFSDSCVWMPNLPTMQLPPTSPGQARPESEFI 589

Qy 593 ATLPAVNSSSYHIIALMLLSAEPGQPRGLHYPDEHFTEDAPRRSVAAFQKLIQISKI 652

Db 590 DTLPRGSCWHLGAVWALSQFQENELFLGNYPEHFIKPKVKEAMARFRKNLEAIVSVI 649

Qy 653 RERNRGLALPYTYLDPPLIENSIVI 677

Db 650 AERNKKQLPYTYLDPPLIENSIVI 674

Search completed: July 18, 2005, 22:03:22

Job time : 32.8647 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:53:28 ; Search time 105.244 Seconds

(without alignments)
2497.095 Million cell updates/sec

Title: US-10-688-676A-4

Perfect score: 3604

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Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1736639 seqs, 368188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22:	/cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3604	100.0	677	9	US-09-764-246-4
2	3604	100.0	677	16	US-10-716-204-4
3	3604	100.0	677	16	US-10-688-676A-4
4	2880.5	79.9	676	9	US-09-764-246-2
5	2880.5	79.9	676	16	US-10-716-204-2
6	1864	51.7	711	9	US-09-862-658-2
7	1864	51.7	711	14	US-10-175-696-23
8	1864	51.7	711	14	US-10-422-264-2
9	1864	51.7	711	15	US-10-776-871-23
10	1864	51.7	867	14	US-10-422-264-24
11	1858	51.6	711	15	US-10-275-998-3

12	1795	49.8	701	9	US-09-853-053-2
13	1795	49.8	701	15	US-10-445-484-2
14	1588	44.1	556	14	US-10-422-264-6
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23	1227	34.0	663	17	US-10-741-600-1500
24	1212	33.6	663	15	US-10-170-097-653
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28	1186.5	32.9	662	16	US-10-716-204-25
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32	1077.5	29.9	645	14	US-10-422-264-26
33	953	26.4	291	14	US-10-422-264-14
34	801.5	22.2	334	14	US-10-422-264-8
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42	605.5	16.8	399	17	US-10-498-788-27
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44	568.5	15.8	807	14	US-10-132-350-42
45	568.5	15.8	807	14	US-10-132-350-44

ALIGNMENTS

RESULT 1

US-09-764-246-4
; Sequence 4, Application US/09764246
; Patent No. US20010046672A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:

Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 14, Appli
Sequence 22, Appli
Sequence 16, Appli
Sequence 516, App
Sequence 517, App
Sequence 1499, Ap
Sequence 1500, Ap
Sequence 653, App
Sequence 653, App
Sequence 12, Appli
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Sequence 5, Appli
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Sequence 4, Appli
Sequence 26, Appli
Sequence 14, Appli
Sequence 8, Appli
Sequence 19529, A
Sequence 3, Appli
Sequence 19890, A
Sequence 19963, A
Sequence 4, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 352299,
Sequence 42, Appli
Sequence 44, Appli

TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-764-246-4

Query Match 100.0%; Score 3604; DB 9; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60

QY 61 VGTVLMRLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPGAALHPCYQWLEGAGELVLR 120
DB 61 VGTVLMRLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPGAALHPCYQWLEGAGELVLR 120

QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLNLIKYSAM 180
DB 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLNLIKYSAM 180

QY 181 KNAKLPFKHAHSAYTELKVGGLDRTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
DB 181 KNAKLPFKHAHSAYTELKVGGLDRTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFPA 240

QY 241 SQFLNGINPVLIRCHSLPNPFVTDWMAVPLGPTSLQAELEKGSFLVDHGILSGVH 300
DB 241 SQFLNGINPVLIRCHSLPNPFVTDWMAVPLGPTSLQAELEKGSFLVDHGILSGVH 300

QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
DB 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKQTPGDPNPIFLPSSDDTWDWLLAKTW 360

QY 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420

QY 421 LVAPGKLDKSTGLGTGGFSDLIKRMEQLNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB 421 LVAPGKLDKSTGLGTGGFSDLIKRMEQLNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480

QY 481 IWGAIKSFVSEIYSIYPSDTSVQDDQELQAWVREIFSEGFLGREGSSGMPSLDTRREALV 540
DB 481 IWGAIKSFVSEIYSIYPSDTSVQDDQELQAWVREIFSEGFLGREGSSGMPSLDTRREALV 540

QY 541 QYITWVIFTCSAKHAIVSSGQFSDSCVMNLPPTMQLPPTSGKQARPESFIATLPVNS 600
DB 541 QYITWVIFTCSAKHAIVSSGQFSDSCVMNLPPTMQLPPTSGKQARPESFIATLPVNS 600

QY 601 SSVHITALLSAPGQDQPLGHYPDEHTEADAPRSVAAFORFKLIQISKGIRERNRGLA 660
DB 601 SSVHITALLSAPGQDQPLGHYPDEHTEADAPRSVAAFORFKLIQISKGIRERNRGLA 660

QY 661 LPYTYLDPPLIENSVS I 677
DB 661 LPYTYLDPPLIENSVS I 677

RESULT 2
US-10-716-204-4
Sequence 4, Application US/10716204
Publication No. US20040137483A1
GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM E.
JISAKA, MITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/716,204.
FILING DATE: 18-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-716-204-4

Query Match 100.0%; Score 3604; DB 16; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60

QY 61 VGTVLMRLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPGAALHPCYQWLEGAGELVLR 120
DB 61 VGTVLMRLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPGAALHPCYQWLEGAGELVLR 120

QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLNLIKYSAM 180
DB 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLNLIKYSAM 180

QY 181 KNAKLPFKHAHSAYTELKVGGLDRTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFPA 240
DB 181 KNAKLPFKHAHSAYTELKVGGLDRTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFPA 240

QY 241 SQFLNGINPVLIRCHSLPNPFVTDWMAVPLGPTSLQAELEKGSFLVDHGILSGVH 300
DB 241 SQFLNGINPVLIRCHSLPNPFVTDWMAVPLGPTSLQAELEKGSFLVDHGILSGVH 300

QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKQTPGDPNPIFLPSSDDTWDWLLAKTW 360
DB 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKQTPGDPNPIFLPSSDDTWDWLLAKTW 360

QY 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420

QY 421 LVAPGKLDKSTGLGTGGFSDLIKRMEQLNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB 421 LVAPGKLDKSTGLGTGGFSDLIKRMEQLNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480

QY 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 540
DB 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 540
QY 541 QYITWVITCSAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 600
DB 541 QYITWVITCSAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 600
QY 601 SSSYHIIALWLLSAEPGQDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGLA 660
DB 601 SSSYHIIALWLLSAEPGQDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGLA 660
QY 661 LPYTYLDPPLIENSUSI 677
DB 661 LPYTYLDPPLIENSUSI 677

RESULT 3

US-10-688-676A-4
; Sequence 4, Application US/10688676A
; Publication No. US20040248794A1
; GENERAL INFORMATION:
; APPLICANT: Alcon, Inc.
; APPLICANT: Yanni, John M.
; APPLICANT: Gamache, Daniel A.
; APPLICANT: Miller, Steven T.
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo
; FILE REFERENCE: 2394 US
; CURRENT APPLICATION NUMBER: US/10/688,676A
; PRIORITY FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/435,988
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 677
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-688-676A-4

Query Match 100.0%; Score 3604; DB 16; Length 677;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
DB 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
QY 61 VGTVLMRLVRHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGAALHPPCYQWLEGAGELVLR 120
DB 61 VGTVLMRLVRHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGAALHPPCYQWLEGAGELVLR 120
QY 121 EGAAKVSQDHHPTLQDQKQELSRQKXWNTYIEGWPCRLDHTVVDLNLKYSAM 180
DB 121 EGAAKVSQDHHPTLQDQKQELSRQKXWNTYIEGWPCRLDHTVVDLNLKYSAM 180
QY 181 KNAKLPFAKHSAYTELKYGILLDRGLRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240
DB 181 KNAKLPFAKHSAYTELKYGILLDRGLRSREMRLENFRKTPAAEYVFAHWQEDAFPA 240
QY 241 SOFLNGINPVLIRCHSLPNNFPVTVDEMVAAPVLGPGTSLQAELEKGSFLVDHGLISGVH 300
DB 241 SOFLNGINPVLIRCHSLPNNFPVTVDEMVAAPVLGPGTSLQAELEKGSFLVDHGLISGVH 300
QY 301 TNLNGKQFQSAAPMTLLHQSSGSGPLPIAQLKQTPGPNPIPLPSDDTWDMLAKTW 360
DB 301 TNLNGKQFQSAAPMTLLHQSSGSGPLPIAQLKQTPGPNPIPLPSDDTWDMLAKTW 360
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLQPRCHPLFKLLIPIHRYTLHINTLREL 420
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVPALATLQPRCHPLFKLLIPIHRYTLHINTLREL 420

QY 421 LVAPGKLIKSTGLTGCTGFSDLIKRNMEQLNYSVLCIPEDIRARGVEDIPGYVYRDDGMQ 480
DB 421 LVAPGKLIKSTGLTGCTGFSDLIKRNMEQLNYSVLCIPEDIRARGVEDIPGYVYRDDGMQ 480
QY 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 540
DB 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 540
QY 541 QYITWVITCSAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 600
DB 541 QYITWVITCSAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFLGRESSGMPSLDITREALV 600
QY 601 SSSYHIIALWLLSAEPGQDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGLA 660
DB 601 SSSYHIIALWLLSAEPGQDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGLA 660
QY 661 LPYTYLDPPLIENSUSI 677
DB 661 LPYTYLDPPLIENSUSI 677

RESULT 4

US-09-764-246-2
; Sequence 2, Application US/09764246
; Patent No. US20010046672A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-764-246-2

Query Match 79.9%; Score 2880.5; DB 9; Length 676;

Best Local Similarity 78.0%; Pred. No. 5.1e-268;

Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60

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Db 1 MAEFRVSTGEAFAGTWDKVSIVGTRGSPPLDNLGKFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAPPEVSLPLMS - FRSDAWFCWFLEWLPGAALHPFPCYQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPGLGLPADAWFCWFQLTTPRGHLLFPYQWLEGAGTLVL 118
QY 120 REGAAKVSQDHHPTLDQORKELESROKYSWKTYIEGWPRCLDHTVTKDLNLKYS 179
Db 119 QEGTAKVSWADHHPVLVQOQRELOARQEMQWKAYNPGWPHCLDEKTVEDLELNKYST 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRGTGLWRSLEMRRLNFRKTPAAEYVFAHWQEDAFF 239
Db 119 QEGTAKVSWADHHPVLVQOQRELOARQEMQWKAYNPGWPHCLDEKTVEDLELNKYST 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRGTGLWRSLEMRRLNFRKTPAAEYVFAHWQEDAFF 239
Db 179 AKNANFYLAGSAPAEKIKGLLDKGLWRSLEMRRLNFRKTPAAEYVFAHWQEDAFF 238
QY 240 ASOFLNGINPVLIRCHSLPNNPVTDEMVAFLGPGTSLQAELEKGSFLVDHGILSGV 299
Db 239 ASOFLNGINPVLIRCHSLPNNPVTDEMVAFLGPGTSLQAELEKGSFLVDHGILSGI 298
QY 300 HTNILNGKPFQSAAPMTLLHSGSGPLLPALAIQLKQTPGPNPFLPSSDDTMDLLAKT 359
Db 299 QTNVINGKPFQSAAPMTLLYQSPGCGPLLPALAIQLSQTGPNSPFLPTDDKMDLLAKT 358
QY 360 WYRNSEFYIHEAVTHLLHAHLIPEVPALATIRQLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATRLQLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLVAPKGLDKSTGLTGCGFSDLIKNMEOLNYSVLCPLPDIRARGVEDIPGYVYRDDGM 479
Db 419 LLVPGQVVDRTGTGIEGSELIQKNMKQLNYSLLCLPDIRGVEDIPGYVYRDDGM 478
QY 480 QIWGAIKSFVSEIVSIYYPDSVQDDQLOAWVREIFSEGFLGRESGMPSLDITREAL 539
Db 479 QIWGAVERFVSEIIGIYYPDESQDDRELQAWVREIFSKGLNQGESSGIPSSLETREAL 538
QY 540 VOYITWVITCSAKHAASVSSGQFDSQVWMPNLPPTMQLPPTPSKGOARPESTIATLPVN 599
Db 539 VOYVTWVITCSAKHAASVSSGQFDSQVWMPNLPPTMQLPPTPSKGOARPESTIATLPVN 598
QY 600 SSSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRSVAAFQKLIQISKGIERNRGL 659
Db 599 ATCDVILALWLLSKPEGQORPLGTYPDEHFTEDAPRSVAATQSRLAQISRGIERNRGL 658

RESULT 5
US-10-716-204-2
; Sequence 2, Application US/10716204
; Publication No. US20040137483A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10716, 204
; FILING DATE: 18-Nov-2003
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-716-204-2

Query Match 79.9%; Score 2880.5; DB 16; Length 676;
Best Local Similarity 78.0%; Pred. No. 5,1e-268;
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGEAGAGTWDKVSIVGTHGESPLVLDHLGKFPKSAGAEEDFVTLPOD 60
Db 1 MAEFRVSTGEAFAGTWDKVSIVGTRGESPPPLDNLGKFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAPPEVSLPLMS - FRSDAWFCWFLEWLPGAALHPFPCYQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPGLGLPADAWFCWFQLTTPRGHLLFPYQWLEGAGTLVL 118
QY 120 REGAAKVSQDHHPTLDQORKELESROKYSWKTYIEGWPRCLDHTVTKDLNLKYS 179
Db 119 QEGTAKVSWADHHPVLVQOQRELOARQEMQWKAYNPGWPHCLDEKTVEDLELNKYST 178
QY 180 MKNAKLFFKAHSAYTELKVGLLDRGTGLWRSLEMRRLNFRKTPAAEYVFAHWQEDAFF 239
Db 179 AKNANFYLAGSAPAEKIKGLLDKGLWRSLEMRRLNFRKTPAAEYVFAHWQEDAFF 238
QY 240 ASOFLNGINPVLIRCHSLPNNPVTDEMVAFLGPGTSLQAELEKGSFLVDHGILSGV 299
Db 239 ASOFLNGINPVLIRCHSLPNNPVTDEMVAFLGPGTSLQAELEKGSFLVDHGILSGI 298
QY 300 HTNILNGKPFQSAAPMTLLHSGSGPLLPALAIQLKQTPGPNPFLPSSDDTMDLLAKT 359
Db 299 QTNVINGKPFQSAAPMTLLYQSPGCGPLLPALAIQLSQTGPNSPFLPTDDKMDLLAKT 358
QY 360 WYRNSEFYIHEAVTHLLHAHLIPEVPALATIRQLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATRLQLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLVAPKGLDKSTGLTGCGFSDLIKNMEOLNYSVLCPLPDIRARGVEDIPGYVYRDDGM 479
Db 419 LLVPGQVVDRTGTGIEGSELIQKNMKQLNYSLLCLPDIRGVEDIPGYVYRDDGM 478
QY 480 QIWGAIKSFVSEIVSIYYPDSVQDDQLOAWVREIFSEGFLGRESGMPSLDITREAL 539
Db 479 QIWGAVERFVSEIIGIYYPDESQDDRELQAWVREIFSKGLNQGESSGIPSSLETREAL 538
QY 540 VOYITWVITCSAKHAASVSSGQFDSQVWMPNLPPTMQLPPTPSKGOARPESTIATLPVN 599
Db 539 VOYVTWVITCSAKHAASVSSGQFDSQVWMPNLPPTMQLPPTPSKGOARPESTIATLPVN 598
QY 600 SSSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRSVAAFQKLIQISKGIERNRGL 659
Db 599 ATCDVILALWLLSKPEGQORPLGTYPDEHFTEDAPRSVAATQSRLAQISRGIERNRGL 658

QY 660 ALPTYTLDPPPLIENSYSI 677
Db 659 VLPYTYLDPPLIENSYSI 676
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RESULT 6

US-09-862-658-2
; Sequence 2, Application US/09862658
; Patent No. US20020137101A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 46638, A NOVEL HUMAN LIPOXYGENASE FAMILY
; FILE REFERENCE: 10448-053001
; CURRENT APPLICATION NUMBER: US/09/862,658
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/205,675
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-658-2

Query Match 51.7%; Score 1864; DB 9; Length 711;
Best Local Similarity 50.1%; Pred. No. 5.9e-170;
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;

Qy 1 MAKCRVSTGEACGAGTWDKVSIVGTHGESPLVDHLGKFSAGAEDEFVTLPOD 60
Db 1 MAVYRLCVTTGPLYRAGTLDNISVLTGTCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60

Qy 61 VGTVMRLVRHKAPEVSLPLMSFRSDAFRCWFLEWLPGAALHPPCYQWLEGAGELVLR 120
Db 61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGVSHPPCYQWIEGYCTVELR 114

Qy 121 EGAAKVSWQDHHPTLQDOROKELSRQMYSKWTYIEGWPRCLDHETVKDLDL----- 173
Db 115 PGTARTICQDSLPLLDHRTRELRAQECYRWKIYAPGPPCMVDVNSFQMESDKKFAIT 174

Qy 174 -----NIKYSAMKNAKLPFKAHSAYTELVKVK 199
Db 175 KTTTCVDQDSSGNRYLPGFPFKIDIPSLMYMEPNVRYSATKTSLLFNAIPASLGMKLR 234

Qy 200 GLLDRTGLWRLSRMRLEFNFRKTPAAEYVFAHQEDAFPAQFNGINPVLIRCHSLP 259
Db 235 GLLDRKSGWKKLDDMONIFWCHKTFTTKYVTEHWCEDEHFFGYQYLVNGVNPVWLHCISL 294

Qy 260 NNFVPTDWMVAPVLGPGTSLQAELEKSLFLVDHGLSGVHTNINLNGKPOPSAAPMTLLH 319
Db 295 SKLPVTDWMAVPLGQDTCLQTELERGNIFLADYWLAEAPTHCLNGRQYVVAAPLCILW 354

Qy 320 QSSGSGPLLPALIAQLKQTPGDPNPIFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAH 379
Db 355 LSP-QGALVPLAIQLSQTPGDPSPFLPTDSEMDWLLAKTWVRNSEFLVHNNTHFLCTH 413

Qy 380 LIPEFALATLQRLPRCHPLKLLPHRYTLHINTLARELLVAPKLIKSTGLGTGGP 439
Db 414 LLCEAFAMATLQRLPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGRQL 473

Qy 440 SDLIKRNQNLNYSVLCLPEDIRARGVEDIPCYVYRDDGMQIWAIGKSFVSEIYIYPS 499
Db 474 IYLMSTGLAHFTYTNFCLPDSLRAGVLAI PNHYRDDGLKWAIESFVSEIYIYPS 533

Qy 500 DTSVQDDQELQAWREIFSEGFLGREGSGMPSLDTRREALVQYITWVFTCSAKHAAYSS 559
Db 534 DASVQDSELQAWTGEIFAQFLGREGSGFSPRLCTPGEMVKFLTAIFNCSAQHAAYNS 593

Qy 560 GQFDSVVMNLPPTMQLPPTPSKQARPEFATLPVAVNSSVYHIALWLLSAPPGQR 619
Db 594 GQHDGAWNPAPSMRQPPQTKGTTTLTKTYLDTLPEVNISCNLLLFLLVLSQEPKQOR 653

Qy 620 PLGHYPDEHFTEDAPRRSVAAFORLQIISGIRERNEGLALPYTLDPPLIENSVS 677
Db 654 PLGTYPDEHFTEDAPRRSIAAQSRKLAQISRDIOERNQGLALPYTYLDPPLIENSVS 711

RESULT 7

US-10-175-696-23
; Sequence 23, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-696-23

Query Match 51.7%; Score 1864; DB 14; Length 711;
Best Local Similarity 50.1%; Pred. No. 5.9e-170;
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;

Qy 1 MAKCRVSTGEACGAGTWDKVSIVGTHGESPLVDHLGKFSAGAEDEFVTLPOD 60
Db 1 MAVYRLCVTTGPLYRAGTLDNISVLTGTCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60

Qy 61 VGTVMRLVRHKAPEVSLPLMSFRSDAFRCWFLEWLPGAALHPPCYQWLEGAGELVLR 120
Db 61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGVSHPPCYQWIEGYCTVELR 114

Qy 121 EGAAKVSWQDHHPTLQDOROKELSRQMYSKWTYIEGWPRCLDHETVKDLDL----- 173
Db 115 PGTARTICQDSLPLLDHRTRELRAQECYRWKIYAPGPPCMVDVNSFQMESDKKFAIT 174

Qy 174 -----NIKYSAMKNAKLPFKAHSAYTELVKVK 199
Db 175 KTTTCVDQDSSGNRYLPGFPFKIDIPSLMYMEPNVRYSATKTSLLFNAIPASLGMKLR 234

Qy 200 GLLDRTGLWRLSRMRLEFNFRKTPAAEYVFAHQEDAFPAQFNGINPVLIRCHSLP 259
Db 235 GLLDRKSGWKKLDDMONIFWCHKTFTTKYVTEHWCEDEHFFGYQYLVNGVNPVWLHCISL 294

Qy 260 NNFVPTDWMVAPVLGPGTSLQAELEKSLFLVDHGLSGVHTNINLNGKPOPSAAPMTLLH 319
Db 295 SKLPVTDWMAVPLGQDTCLQTELERGNIFLADYWLAEAPTHCLNGRQYVVAAPLCILW 354

Qy 320 QSSGSGPLLPALIAQLKQTPGDPNPIFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAH 379

1	MAVYRLCVTTGFLRAGTLDNI SVTLVGTGESPQRQLDRMGDRFAPGVSQYKYKRCRTAE	60
61	VGTVLMRLVRHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGAALHPFCPCWLEGGAGELVLR	120
61	LGEILLLRVHKE-----RYAFFRKDSVYCSRICVTEPDGVSVHPFCPCWLEIGYCTVELR	114
121	EGAAKSVQDHHPTLQDQRKELESQRXMYSKWITYIEGWPRCLDHETVKDLDL-----	173
115	PGTARTICQDSLPLLLDHRTELRLARQCERYRWKIYAPGFPQCMVDVNSPQEMESKKFALT	174
174	-----NIKYSAMKNVAKLFFKAHSAYTELKVK	199
175	KTTTCVQDQDSSGNRYLPFGFPMKIDIPSLMYMEPNVRYSATKTIISLLFNFAIPASLGMKLR	234
200	GLLDRTGLWRLSIREMRRLFNFRKTPAAEYVFAHMOEDAFFASQFQINGINPVLIRRCHSLP	259
235	GLLDRLKSGWKLLDDMONIFWCHKFTTKTYVTEHWCEDHFFGGQYLVGNVPVWLHCISSLP	294
260	NNFPVTDBMWAPVLPGGTSLQAEKGSFLVDHGIILSGVHTNIILNGKRPQFSAAPMTLLH	319
295	SKLPVTNDMWAPLLQDTCLOTELERGNIFLADYWI LAEPATHCLNGRQQYVAAAPLCILW	354
320	QSSSGGLPLPTAIQLKOTPGDNPFLPDSDDTWDMLLAKTWVRNSEFYTHEAVTHLLHAH	379
355	LSP-QGALVPLAIQLSOTPGDPSPIFLPTDSEMDWLLAKTWVRNSEFLVHNNTHFLCTH	413
380	LIPEVFALATLRLQPRCHPLFKLLIPHYRYTLIHNTLARELIVAPGKLDKDGSTGLGTGF	439
414	LLCEAFAMATLRLQPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGRQL	473
440	SDLIKRNMEQLNYSVYLCPEDIRARGVEDIPGYYYRDDGMQIWAIGAKFVSVEIVSYPS	499
474	IYLMSTGLAHFTYTNFCPLDRLARGVLAIAPNHYVRDDELGLKIWAATIESFVSEIVGYVPS	533
500	DTSVQDDOELQAWVREIIESEGLGHESSGMPSLDTRALVQYITWVFTCSAKAAVYS	559
534	DASVQDSELAQWAGEIIFAQAPLGHRESSGFFSRLCTPGEMVFKFLAIIPNCQAQAAVNS	593
560	GQFDSVVMNPLPPTMQLPPTPSKQARPESPIATLPVANSSSYHIIALWLLSASPQDOR	619
594	GQHDFGAWPNAPNSMRQPPQTGTTTLTKTYLDTLPVNTISCNLLLPWLVSQEPKQOR	653
620	PLGHYPDBEHFTEDAPRRSVAAPQRKLIQISKGIERNRGLALPYTYLDDPLIENSVSI	677
654	PLGYTPDEHFTTEAPRRSIAAFQSRLAISRDIQERNOCGLALPYTYLDDPLIENSVSI	711

```

RESULT 10
US-10-422-264-24
; Sequence 24, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zamdrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-24

```

Query Match	51.7%;	Score 1864;	DB 14;	Length 867;
Best Local Similarity	50.1%;	Pred. No. 8,1e-170;		

Matches	360;	Conservative	112;	Mismatches	198;	Indels	48;	Gaps	3																																															
QY	1	MAKRVRSVTEAGCAGT	WMDKVSVISVIGTHGES	PLVDHLHGKFSAGAE	DEFVTL	QD	60																																																	
Db	157	MAVRLCVTTGPIYRAG	TLDNISVTLVGTG	CGSPKQRLDR	GRDGFAPGS	VQKYKVR	TAE	216																																																
QY	61	VGVTLMLRVHKA	PPVSLPLMS	FRSDAWFCR	WPELWPG	AALHPPC	VQWLE	GAGELVLR	120																																															
Db	217	LGELLRLRVHKE	-----RYAF	RKDSWYCSRIC	VTPE	DGVS	HFPCYQ	WTEGYCTVELR	270																																															
QY	121	EGAAKVS	WODHHP	TLODOR	KELES	RKMSWK	TYIEG	MPRLD	HETVKIDL	173																																														
Db	271	PGTARTICQ	BSLPLLDH	RTREURAR	QCYRW	KIYAF	GC	WCV	DVNS	QFHESS	KK	FALT	330																																											
QY	174	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	199																																											
Db	331	KTTTCVDQ	DSSGN	RYLPG	FPMKID	IPSL	MYME	PNV	RYSAT	KTISL	L	FNAL	PAS	LG	MKL	390																																								
QY	200	GLLDR	TGLW	SLRE	MRL	FN	RKTP	AAE	YVAH	QED	AFF	ASQ	F	LNG	IN	PNV	LIR	CH	S	L	P	259																																		
Db	391	GLLDR	KSG	WKL	DD	MQNI	FW	CHK	TFT	KY	TEH	WC	ED	HF	FG	Y	L	NG	V	N	P	W	M	L	H	C	S	S	L	P	450																									
QY	260	NNP	PVT	DEM	V	PV	L	PG	TS	L	Q	A	E	K	S	L	F	V	D	H	G	I	L	S	V	H	T	N	I	L	N	G	K	P	S	A	P	M	T	L	L	H	319													
Db	451	SKL	PVT	N	D	M	V	A	P	L	L	G	D	T	C	L	Q	T	E	L	E	R	G	N	I	F	L	A	D	Y	M	I	L	A	E	A	P	H	C	L	N	G	Q	Q	V	A	A	P	L	C	L	L	W	510		
QY	320	QSSG	S	G	L	L	P	I	A	I	Q	L	K	T	P	G	D	N	P	I	F	P	S	D	D	T	W	D	L	L	A	K	T	W	R	N	S	E	F	I	H	E	A	V	T	L	L	H	A	H	379					
Db	511	LSP	-	Q	G	A	V	P	L	A	I	Q	S	T	P	G	D	S	P	I	F	L	T	S	E	W	D	L	L	A	K	T	W	R	N	S	E	F	L	H	N	T	H	F	L	C	T	H	569							
QY	380	L	I	P	E	V	A	L	A	T	R	L	Q	P	R	C	H	P	F	K	L	I	P	H	I	R	T	L	I	N	T	L	A	R	E	L	L	V	A	P	G	K	L	I	D	K	S	T	G	L	G	T	G	F	439	
Db	570	L	L	C	E	A	F	A	M	A	T	L	Q	L	P	C	H	P	I	Y	K	L	L	P	H	R	T	L	Q	V	T	I	A	R	A	T	L	L	N	P	E	G	L	V	D	Q	T	S	I	G	R	Q	L	629		
QY	440	S	D	L	I	K	R	N	E	Q	I	N	T	S	V	L	C	P	D	I	R	A	R	G	V	E	D	I	P	G	Y	R	D	D	G	H	O	I	W	A	I	K	S	F	V	S	E	I	S	I	Y	P	S	499		
Db	630	I	Y	L	M	S	T	G	L	A	H	F	T	T	N	F	C	L	P	D	S	L	R	A	R	G	V	L	A	P	N	H	R	D	D	G	L	K	I	M	A	A	I	E	S	F	V	S	E	I	V	G	Y	P	S	689
QY	500	D	T	S	V	O	D	D	E	L	Q	A	M	V	R	E	F	S	G	F	E	L	G	R	E	S	S	G	P	S	L	D	T	R	E	A	L	V	O	Y	I	T	M	I	T	F	C	S	A	H	A	V	S	559		
Db	690	D	A	S	V	Q	D	S	E	L	Q	A	M	T	G	E	L	F	A	Q	A	F	L	G	R	E	S	S	G	P	P	S	R	L	C	T	G	E	M	V	K	F	L	T	A	I	I	N	C	S	A	Q	H	A	V	S</

RESULT 11
US-10-275-998-3
Sequence 3, Application US/10275998
Publication No. US2004002354A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DAS, Debopriya
APPLICANT: REDDY, Roopa
APPLICANT: YAO, Monique G.
APPLICANT: NGUYEN, Dannel B.
APPLICANT: LU, Yan
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: AU-YOUNG, Janice
APPLICANT: LAL, Preeti
APPLICANT: KEARNEY, Liam
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: DING, Li
APPLICANT: THORNTON, Michael
TITLE OF INVENTION: LIPID METABOLISM ENZYMES

; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023354A1 7473234CD1
US-10-275-998-3

Query Match 51.6%; Score 1858; DB 15; Length 711;
Best Local Similarity 50.0%; Pred. No. 2.2e-169;
Matches 359; Conservative 112; Mismatches 199; Indels 48; Gaps 3;

QY 1 MAKCRVRVSTGEACAGTWDKVSIVCTHGESPLVDHLGKFSAGAEDEFVTLPOD 60
DB 1 MAVYRLCVTTGPVLRAGTLDNLSVLTGCGSPKQRLDRMGDRDPAGSVQKYKRCRTAE 60

QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPFGAALHPPCYQWLLEGAGELVLR 120
DB 61 LGELLLLRHKE-----RYAFPRKDSWYCSRICVTEPDGSGVSHPPCYQWIEGYCTVELR 114

QY 121 EGAAKVSWQDHHTLPDQORQKELSRQKMYSWKTYIEGMPRLCDHETVKDL----- 173
DB 115 PGTARTICQDSLPLLDHRTRELRAQECYRNKIYAPGPPCMVDVNSFQEMSDKKFALT 174

QY 174 -----NIKYSAMKNAKLFFKAHSAYTELKVK 199
DB 175 KTTTCVQDQSSGNRYLPFGPKIDIPSLMYMEPNVRYSATTTISLLFNAIPASLGMKLR 234

QY 200 GLLDRTGLWRSIREMRLENFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLP 259
DB 235 GLLDKSGSKLDDMQNI FACHKTFTTKVYTHWCEDHFFGQYQLNGVNPVLMHLCISLP 294

QY 260 NNFPVTDEMVAVLPGTSLQAELEKGSFLVDHGILSGVHTNINLNGKQFSAAPMTLLH 319
DB 295 SKLPVTNDMVAPLLGQDTCQTELERGNIFLADYWLAEAPTHCLNGRQYVAAAPLCILW 354

QY 320 QSSGSGPLPIALQKOTPGDNPFLPDDTDWMLLAKTWRNSEFYIHEAVTHLLHAH 379
DB 355 LSP-QGALVPLAIQSLQSGTPSPFLPTDSEWDMLLAKTWRNSEFYIHEAVTHLLHAH 413

QY 380 LIPEVPALATLQRLPCHPLFKLLIPIHRYTLHINTLARELLVAPGKLDKSTGLGTGTF 439
DB 414 LICEAFAMATLQRLPCHPIYKLLPHRYTYLQVNTIARATLNLPEGLVDQVTSIGRQL 473

QY 440 SLLIKENMBQLNYSVLCPLPEDIARGVEDIPGYYYRDGQWIGAIKSFVSIVSIYYP 499
DB 474 IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNVHYRDDGLKIWAALIESFVSIYGYYP 533

QY 500 DTSVQDDQELQAWRIESEGFLGRSSGMPSLDTRALVQYITWVITCSAKHAANVS 559
DB 534 DASVQDDSELAQWGTGIFAQFLGRSSGFPRLCTPGEMVFLTAIIFNCQAHAANVS 593

QY 560 GQFDSVCMWPNLPTTQKQARPEFIATLPVNSSSYHIIALWLSAEPGQORPLGHPYDHF 619
DB 594 GQMTLGAMFNAPSSWRQPPQTKGTTTLKTYLDLPEVNI SCNNLLLLFWLSQEPKQOR 653

QY 620 PLGHYPDEHFTEDAPRRSVAAFQKLIQISKIGIRERNRGLALPYTYLDPPLIENSVS 677

DB 654 PLGTYPDEHFTEDAPRRSIAAFQKRLAQISRDIOERNOGLALPYTYLDPPLIENSVS 711

RESULT 12
US-09-853-053-2
; Sequence 2, Application US/09853053
; Patent No. US20020037554A1
; GENERAL INFORMATION:
; APPLICANT: Braash, Alan
; APPLICANT: Boeglin, William
; APPLICANT: Kim, Richard
; TITLE OF INVENTION: ISOLATED AND PURIFIED 12R-LIPOXYGENASE PROTEIN AND NUCLEIC ACIDS
; FILE REFERENCE: Attorney Docket No. US20020037554A1 1242/7/2
; CURRENT APPLICATION NUMBER: US/09/853,053
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-053-2

Query Match 49.8%; Score 1795; DB 9; Length 701;
Best Local Similarity 47.9%; Pred. No. 2.6e-163;
Matches 339; Conservative 121; Mismatches 210; Indels 38; Gaps 3;

QY 1 MAKCRVRVSTGEACAGTWDKVSIVCTHGESPLVDHLGKFSAGAEDEFVTLPOD 60
DB 1 MATYKRVATGTDLLSGTRDSISLTI VGTQGESHKQLLNHFGRDPATGAVGQYTVQCQD 60

QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPFGAALHPPCYQWLLEGAGELVLR 120
DB 61 LGELLIIIRLHKE-----RYAFFPKDPWYCNVQVQICAPNGRIYHPAPQWMDGYETLALR 114

QY 121 EGAAKVSWQDHHTLPDQORQKELSRQKMYSWKTYIEGMPRLCDHETVKDL----- 154
DB 115 EATGKTTADDLSLPVLLEHREKBEIRAKQDFYHWRVFLPGLPSYVHIPSYRPPVRRHRPNR 174

QY 155 -----YIEGMPRLCDHETVKDLNLNIKYSAMKNAKLFFKAHSAYTELKVGLLDRTGLWR 209
DB 175 PEWNGYIPGFPILINFKATKFLNLMRYSLFKTASFFVRLGPMALAFKVRGLLDCCKHSWK 234

QY 210 SILREMRLENFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLPNNFPVTDEM 269
DB 235 RLKDIRKIFPGKSVSVYVAEHWAEEDTFGQYQLNGVNPGLIRCTRIPDKFPVTDMMV 294

QY 270 APVLPGTSLQAELEKGSFLVDHGILSGVHTNINLNGKQFSAAPMTLLHQSSGSGPLLP 329
DB 295 APFLGEGTCLQAELEKGNILADYRIMEGIPTVELSGRKHHCAPLCLLH-FGPEGKMP 353

QY 330 TAIQLKOTPGDNPFLPDDTDWMLLAKTWRNSEFYIHEAVTHLLHAHLIPEVPALAT 389
DB 354 TAIQLSQTGPGDPIFLPDSSEWDMLLAKTWRVYAEFYSHAEIAHLLETHLLIAEAFCLAL 413

QY 390 LRQLPRCHPLFKLLIPIHRYTLHINTLARELLVAPGKLDKSTGLGTGFSGLIKRNMEQ 449
DB 414 LENLPMCHPLYKLLIPIHRYTYVQINSIGRAVLNNEGGLSAGMSLGVGEFAGVMVRLSE 473

QY 450 LNYSVLCLPEDIARGVEDIPGYYYRDGQWIGAIKSFVSIVSIYYPSTSVQDDQBL 509
DB 474 LTYDSLPLPNDPVERGVQDLPGYYYRDSLSLWNALEKYVTEIITYYYPDAAVEGDPBL 533

QY 510 QAWVEIIESEGFLGRSSGMPSLDTRALVQYITWVITCSAKHAANVSQGFDSVCMVP 569
DB 534 QSWQEIIEKELGREGSGFPRLCTVPRLRYVTVIYITCSAKHAANVTQMEFTAMP 593

QY 570 NLPPTMQLPPTTQKQARPEFIATLPVNSSSYHIIALWLSAEPGQORPLGHPYDHF 629
DB 594 NFPASMRNPPTQKGLTLETFTFMDTLDPDKYTCITLLVLTLSRFPDDRRPLGHPDIHF 653

QY 630 TEDAPRRSVAAFQKLIQISKIGIRERNRGLALPYTYLDPPLIENSVS 677

US-10-422-264-10
; Sequence 10, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-10

Query Match 40.6%; Score 1464; DB 14; Length 615;
Best Local Similarity 47.5%; Pred.No.1.8e-131;
Matches 286; Conservative 95; Mismatches 173; Indels 48; Gaps 3;

QY	1	MAKCRVRVSTGEACGAGTWDKVSIVTGVTHGESPLVPLDLHLGKEFSAGAEDFEVTLPOD	60
DB	1	MAVYRLCVTTGYPYLRAGTLDNISVTLVGTGESPQRDLDMGRDPAGSVQYKVRCTAE	60
QY	61	VGTVLMLRVHKAPPEVSLPLMSFRSDANFCRWFELWLPFGAALHFPFCYQWLEGAGELVLR	120
DB	61	LGELJLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGVSVSHFPCYQWIEGYCTVELR	114
QY	121	EGAAKVSQDHHPTLQDQKQKLESRQKMYSWKTYIEGHPRLCDHETVKDLDL-----	173
DB	115	PGTARTICQDSLPLLLDHRTRELRARCQECYRWKIYAPGPPCMVDVNSFQEMESDKKALT	174
QY	174	-----NIKYSAMKNAKLFFKAHSAYTELKVK	199
DB	175	KTTTCVDQDSSGNRYLPGFPWKIDIPSLMYMEPNVRSATKTISSLFNAIPASLGMLR	234
QY	200	GLLDRITGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLP	259
DB	235	GLLDRKGSWKLLDDMQNIWFCHKFTTKYVTEHWCEDEHFFGYQLNGVNPVMLHCISLIP	294
QY	260	NNPVTVDENWAPVLGPGTSLQAELEKSLFLVDHGLISGVHTNILINGKQFSAAPMTLLH	319
DB	295	SKLPVTNDWVAPLLGQDTCLOTLELERNIFLADYWLAEAPTHCLNGRQQYVAAPLCLLW	354
QY	320	QSSGSGPLPIAQLKQTPGPNPIPLPSDDTDMDMLLAKTWVRNSEFYIHEAVTHLLHAH	379
DB	355	LSP-QQALVPLAIQUSQTGPGDSPIFPLPTDSEWMLLAKTWVRNSEFLVHENTHFLCTH	413
QY	380	LIPVFPALATRLQPLRCHPLFKLLPHIRYTHLINTLARELLVAPKLDKSTGLTGGF	439
DB	414	LLCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGRQL	473
QY	440	SLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYVRDDGMQIWGAIKSPVSEIVYIYPS	499
DB	474	IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYRDDGLKIWAALIESFVSEIVGYIYPS	533
QY	500	DTSVQDDQELQAWRIESEGFLGREGSCGMPSLDTRALVQYITWVIFTCSAKHAAYSS	559
DB	534	DASVQDDSELAQTGEIFAQFLGRESGSGPRLCTPGEMVRKFLTAIIFNCSAQHAAYNS	593
QY	560	GQ	561
DB	594	GQ	595

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